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(54) **METHODS OF TRANSCRIPTION ACTIVATOR LIKE EFFECTOR ASSEMBLY**

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USPC **506/26**; 435/91.41; 435/455; 435/471; 435/69.7

(57) **ABSTRACT**

The disclosure describes methods that include providing a first nucleic acid having a sequence encoding a first set comprising one or more transcription activator-like effector (TALE) repeat domains and/or one or more portions of one or more TALE repeat domains; contacting the first nucleic acid with a first enzyme, wherein the first enzyme creates a first ligatable end; providing a second nucleic acid having a sequence encoding a second set comprising one or more TALE repeat domains and/or one or more portions of one or more TALE repeat domains; contacting the second nucleic acid with a second enzyme, wherein the second enzyme creates a second ligatable end, and wherein the first and second ligatable ends are compatible; and ligating the first and second nucleic acids through the first and second ligatable ends to produce a first ligated nucleic acid, wherein the first ligated nucleic acid is linked to a solid support, and wherein the first ligated nucleic acid encodes a polypeptide comprising said first and second sets.

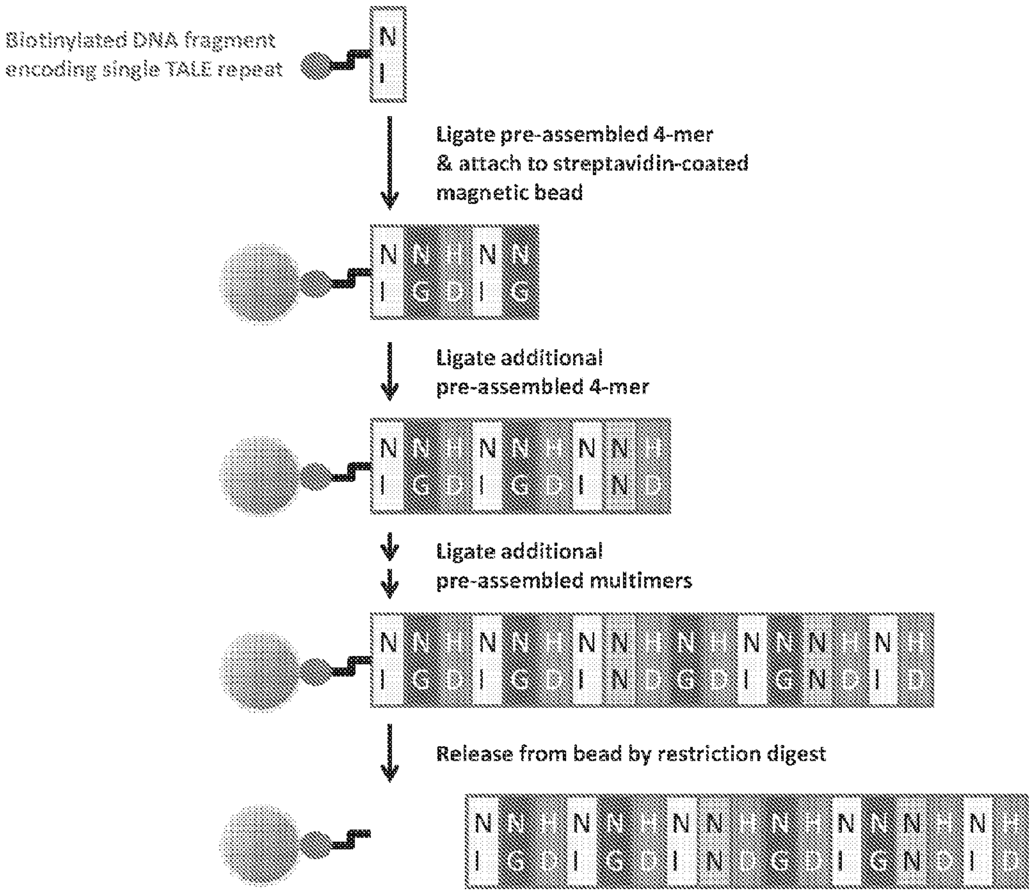
Biotinylated DNA fragment encoding single TALE repeat
Ligate pre-assembled 4-mer & attach to streptavidin-coated magnetic bead
Ligate additional pre-assembled 4-mer
Ligate additional pre-assembled multimers
Release from bead by restriction digest

FIG. 1

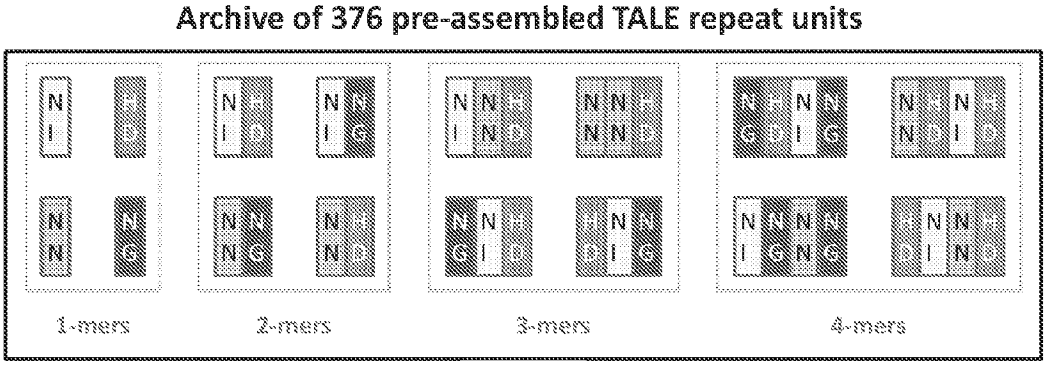
Archive of 376 pre-assembled TALE repeat units
1-mers
2-mers
3-mers
4-mers

FIG. 2

TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGT
CTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGG
CTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGC
ACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAA
GGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATT
AAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTCGAGCTCG
GTACCTCGCGAATGCATCTAGATATCGGATCCCGGGCCCGTCGACTGCAGAGGCCTGCATGCAAGCTT
GGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATAC
GAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTG
CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC
GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCG
TTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGAT
AACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCT
GGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC
GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT
CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG
CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCC
CCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC
TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA
GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT
GGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTT
TTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA
AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAG
TAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCG
TTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC
CCAGTGCTGCAATGATACCGCGAGAgCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTG
CCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCA
TCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTT
ACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
GTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCG
TAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCG
AGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCAT
CATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGT
AACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAA
ACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTT
CCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAA
ACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
(SEQ ID NO:1)

FIG. 3

FIG 4A

Type	SEQUENCE	SEQ ID NO:
α/ε	LTP**D**QVVAIASNIGGKQALETVQRLLPVLCQ**D**HG	2
β	LTP**E**QVVAIASNIGGKQALETVQRLLPVLCQ**A**HG	3
γ	LTP**D**QVVAIASNIGGKQALETVQRLLPVLCQ**A**HG	4
δ	LTP**A**QVVAIASNIGGKQALETVQRLLPVLCQ**D**HG	5

FIG 4B

Type	SEQUENCE	SEQ ID NO:
α/ε	CTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGC	6
Type β:	CTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGG	7
Type γ:	CTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGT	8
Type δ:	TTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGA	9

GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTA
TCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGAC
CGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTG
ACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTA
CATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCC
CATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCAGTACAT
CAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACA
TGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAG
TACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTG
TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGT
GTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAAT
ACGACTCACTATAGGGAGACCCAAGCTGGCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGA
CATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCT
ATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGC
GCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCT
TGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCG
GTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCA
GCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCG
CAATGCGCTCACCGGGGCCCCCTTGAACAGAGACGATTAATGCGTCTCGCTGACACCCGAACAGGTGGTCGCCATTGC
T**XXXXXXXXX**GGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTT
AACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCA
TGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCCCAACTAGT
CAAAAGTGAACTGGAGGAGAAGAAATCTGAACTTCGTCATAAATTGAAATATGTGCCTCATGAATATATTGAATTAAT
TGAAATTGCCAGAAATTCCACTCAGGATAGAATTCTTGAAATGAAGGTAATGGAATTTTTTATGAAAGTTTATGGATAT
AGAGGTAAACATTTGGGTGGATCAAGGAAACCGGACGGAGCAATTTATACTGTCGGATCTCCTATTGATTACGGTGTG
ATCGTGGATACTAAAGCTTATAGCGGAGGTTATAATCTGCCAATTGGCCAAGCAGATGAAATGCAACGATATGTCGAA
GAAAATCAAACACGAAACAAACATATCAACCCTAATGAATGGTGGAAAGTCTATCCATCTTCTGTAACGGAATTTAAGT
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GCTGTTCTTAGTGTAGAAGAGCTTTTAATTGGTGGAGAAATGATTAAAGCCGGCACATTAACCTTAGAGGAAGTCAGA
CGGAAATTTAATAACGGCGAGATAAACTTTTAAGGGCCCTTCGAAGGTAAGCCTATCCCTAACCCTCTCCTCGGTCTCG
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GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
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GGGCTCTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTG
ACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCC
CGTCAAGCTCTAAATCGGGGCATCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATT
AGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAA
TAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGA
TTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTA
GGGTGTGGAAAGTCCCCAGGCTCCCCAGGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGT
GTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTC
(SEQ ID NO:10)

FIG. 5A

FIG. 5B

AGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGC
TGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTT
TTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACA
ATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGCCTTTGTCTC
AAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCC
AGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGAA
CTCGTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAACA
GGGGCATCTTGAGCCCCTGCGGACGGTGTCGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCGATAGTGAA
GGACAGTGATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCA
CTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCT
TCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCC
AACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCAC
TGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTT
GGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAG
CATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCA
GTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC
TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG
GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG
AACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTC
AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC
CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACG
CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACC
GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG
GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC
TAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCG
GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAA
GAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAG
ATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAA
ACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTG
CCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGA
GACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTG
CAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCC
AACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCA
GAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAA
GATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCC
CGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGG
CGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCA
TCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGA
CACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGT
C (SEQ ID NO:11)

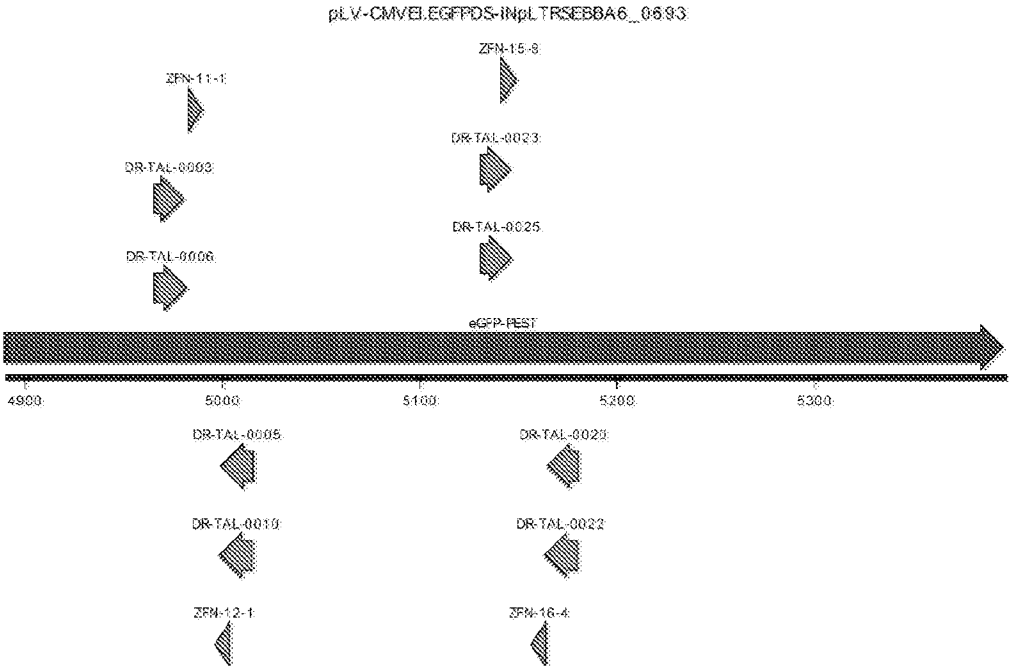

pLV-CMVEI.EGFPDS-INpLTRSEBBA6_0693
ZFN-15-8
ZFN-11-1
DR-TAL-0023
DR-TAL-0003
DR-TAL-0025
DR-TAL-0006
eGFP-PEST
4900
5000
5100
5200
5300
DR-TAL-0005
DR-TAL-0020
DR-TAL-0010
DR-TAL-0022
ZFN-12-1
ZFN-16-4

FIG. 6

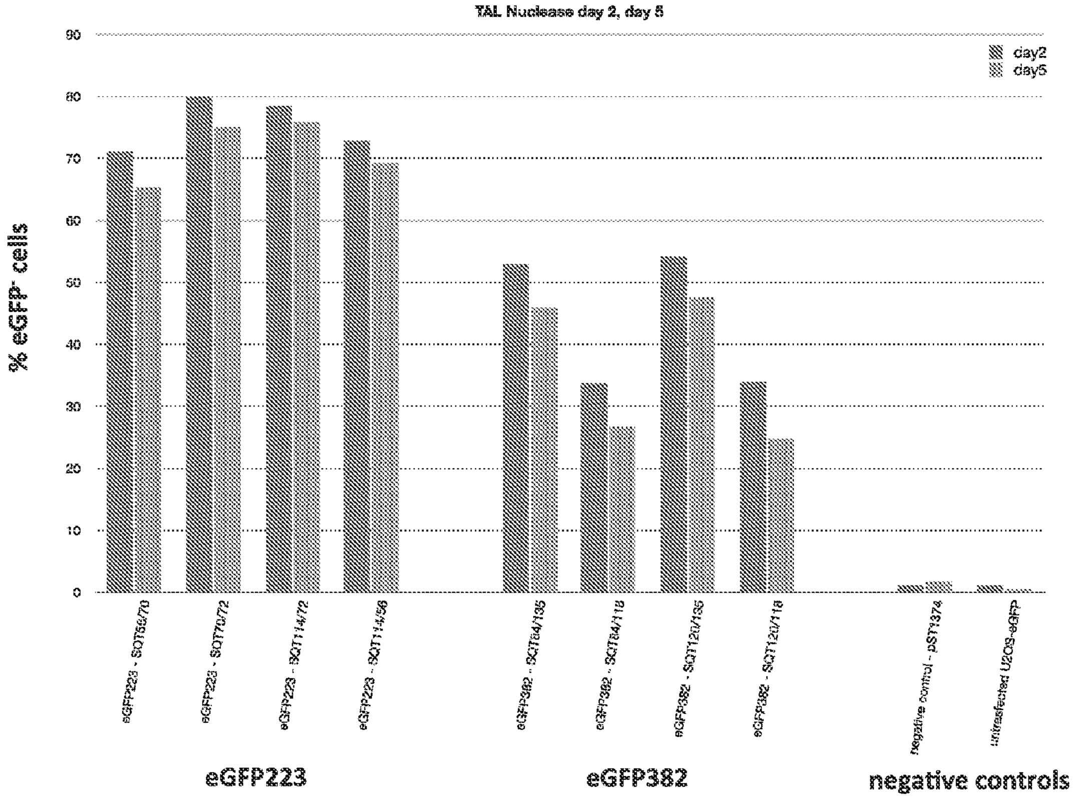

TAL Nuclease day 2, day 5
% eGFP- cells
90
80
70
60
50
40
30
20
10
0
▨ day2
▨ day5
eGFP223 - SQT55/70
eGFP223 - SQT70/72
eGFP223 - SQT114/72
eGFP223 - SQT114/56
eGFP382 - SQT84/135
eGFP382 - SQT84/118
eGFP382 - SQT120/135
eGFP382 - SQT120/118
negative control - pST1374
untransfected U2OS-eGFP
eGFP223
eGFP382
negative controls

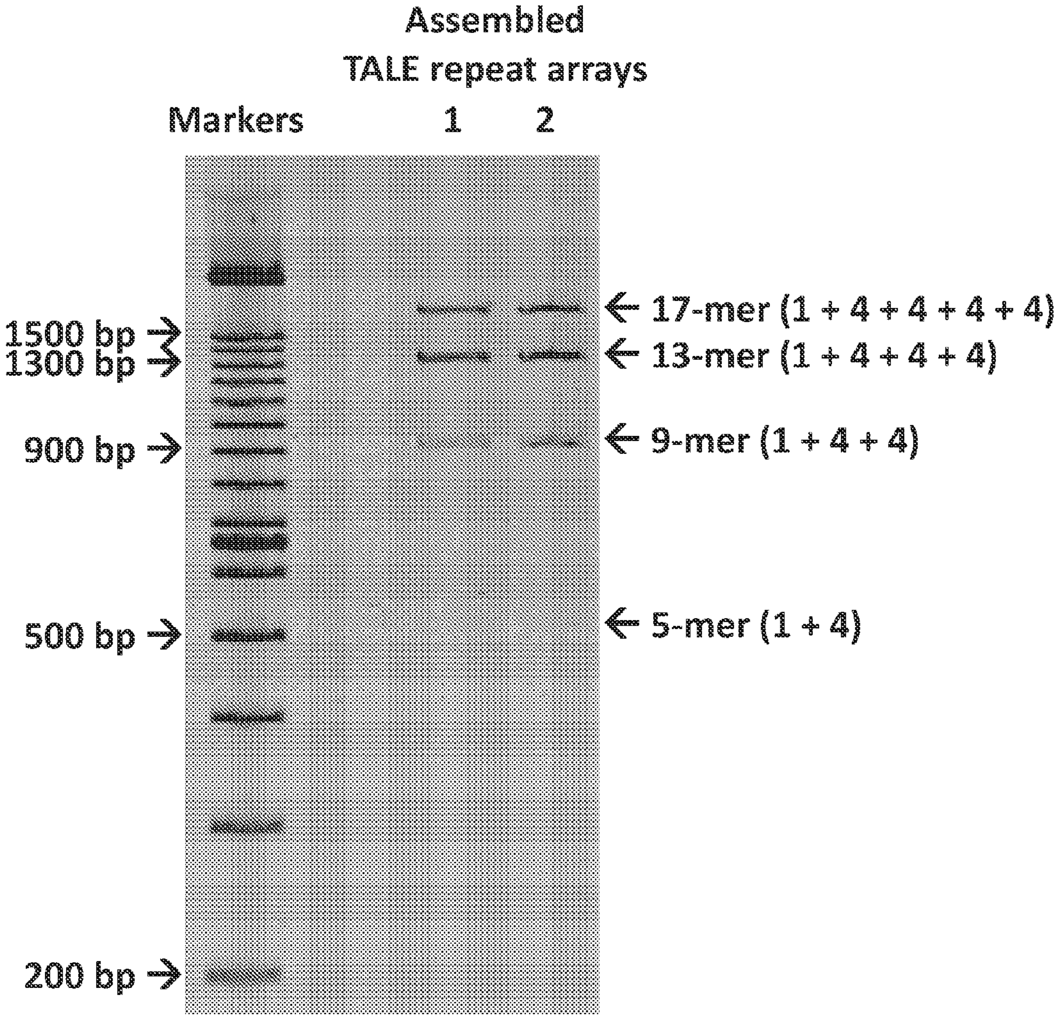
FIG. 7

14 of 30 sequences mutated. (46%)

Sequence	Δ SIZE	SEQ ID NO:
CTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	WT	12
CTACGGCGTGCAGTGCTTCAGCCGCTACCCCGA---CATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ3 (3X)	13
CTACGGCGTGCAGTGCTTCAGCCG----------------AAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ16	14
CTACGGCGTGCAGTGCTTCAGCCGCTAC---------------------GACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ21	15
CTACGGCGTGCAGTGCTTCAGCCGC----------------------ACGACTTCTTCCAGTCCGCCATGCCCGAAGGCTACNTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ22	16
CTACGGCGTGCAGTGCTTCAGC-------------------------------ACTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ30 (Δ31 and +1)	17
CTACGGCGTGCAG---------------------------------CACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ33	18
CTACGGCGTGCAG---------------------------------CACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ33	19
CTACGGCGTGCAGTGCTT---GCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ51	20
CTACGGCGTGCAGTGCTTCAGCC--GCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ54	21
CTACG--CCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	Δ60	22
CTACGGCGTGCAGTGCTT--CTTCAAGGA	Δ84	23
CTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA	+2	24

FIG. 8

FIG. 9


Assembled
TALE repeat arrays
Markers
1
2
1500 bp
1300 bp
900 bp
500 bp
200 bp
17-mer (1 + 4 + 4 + 4 + 4)
13-mer (1 + 4 + 4 + 4)
9-mer (1 + 4 + 4)
5-mer (1 + 4)

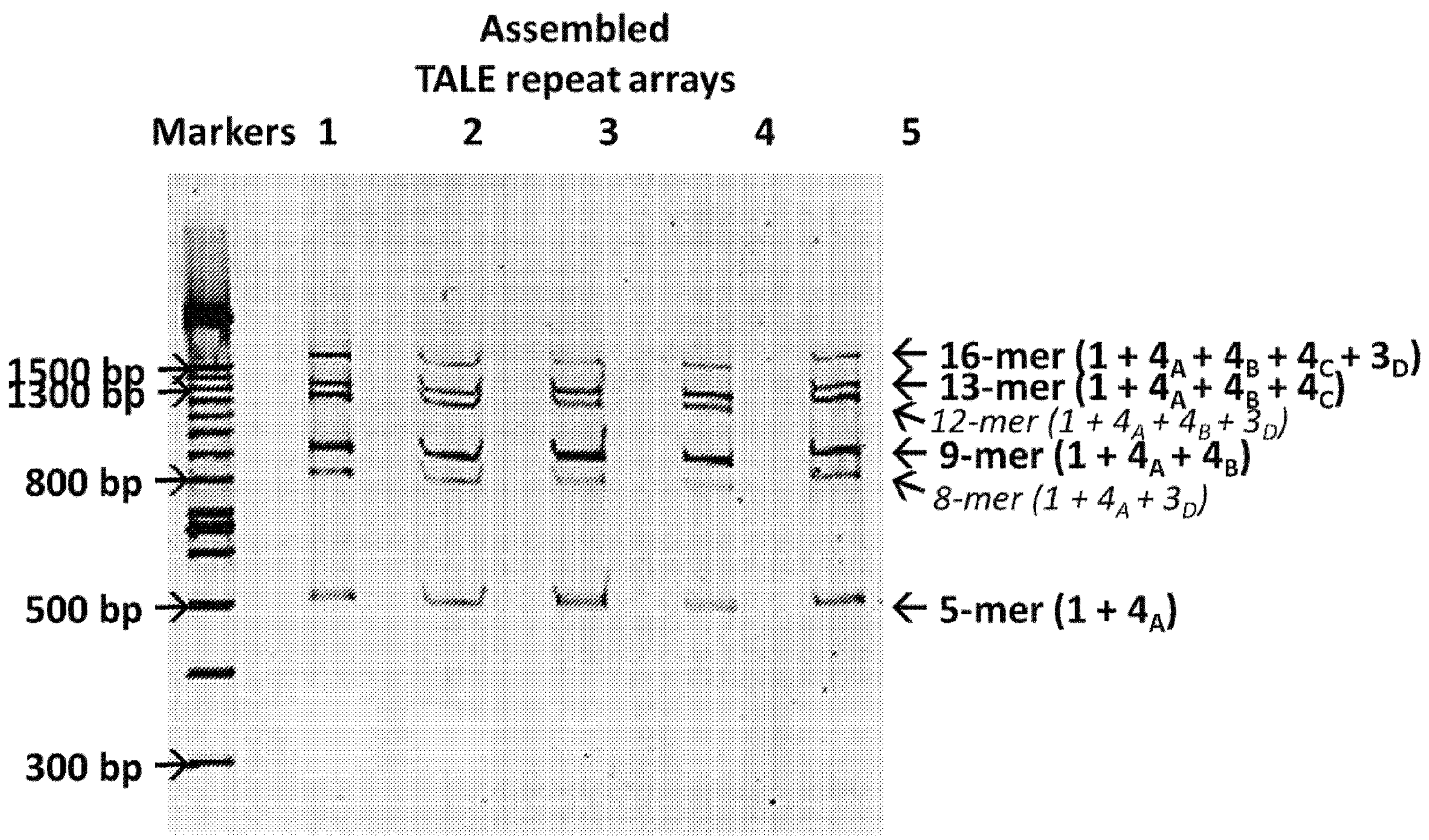

Assembled
TALE repeat arrays
Markers
1
2
3
4
5
1500 bp
1300 bp
800 bp
500 bp
300 bp
16-mer (1 + 4$_A$ + 4$_B$ + 4$_C$ + 3$_D$)
13-mer (1 + 4$_A$ + 4$_B$ + 4$_C$)
12-mer (1 + 4$_A$ + 4$_B$ + 3$_D$)
9-mer (1 + 4$_A$ + 4$_B$)
8-mer (1 + 4$_A$ + 3$_D$)
5-mer (1 + 4$_A$)

FIG. 10

FIG. 11A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGG
GCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCT
CCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAG
CAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTC
GCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA
CCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCA
GAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGA
GGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAA
GTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGC
CAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAAC
CGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCAC
GACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCG
ATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGT
TGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGG
AAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGT
CACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTA
CACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCC
CAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAG
CATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCAT
TGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCT
GCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGT
CTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGAT
CC
(SEQ ID NO:25)

FIG. 11B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGG
GKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDH
GLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS
(SEQ ID NO:26)

FIG. 12A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGG
GCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCT
CCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAG
CAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTC
GCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA
CCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCA
GAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGA
GGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAA
GTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGC
CAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAAC
CGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCAC
GACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCG
ATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGT
TGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGG
AAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGT
CACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTA
CACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCC
CAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAG
CATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCAT
CGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATG
GACTGACACCCGAACAGGTGGTCGCCATTGCTTCTAATGGGGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCC
AATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGAC
GACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTC
CCGAGAGAACTTCCCATCGAGTCGCGGGATCC
(SEQ ID NO:27)

FIG. 12B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGG
GKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDH
GLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAI
ASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPAL
DAVKKGLPHAPALIKRTNRRIPERTSHRVAGS
(SEQ ID NO:28)

FIG. 13A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGG
GCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCT
CCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAG
CAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTC
GCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGAC
CACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAG
AGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAG
GGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGT
GGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCA
GGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCG
TGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGA
CGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGAT
CAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTG
TGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAA
ACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAAC
AATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACA
CCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA
GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCA
TTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCG
CCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGAC
TGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAAT
TGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGAC
CCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCG
AGAGAACTTCCCATCGAGTCGCGGGATCC
(SEQ ID NO:29)

FIG. 13B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQ
DHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQV
VAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGK
QALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLL
PVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGL
TPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIAN
NNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDA
VKKGLPHAPALIKRTNRRIPERTSHRVAGS
(SEQ ID NO:30)

FIG. 14A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGG
GCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCT
CCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAG
CAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTC
GCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGAC
CACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAG
AGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAG
GGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGT
GGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCA
GGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCG
TGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAA
CGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGAT
CAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTG
TGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAA
ACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCA
CATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACA
CCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA
GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCA
TTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCG
CCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGAC
TGACACCCGAACAGGTGGTCGCCATTGCTTCTAATGGGGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAAT
TGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGAC
CCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCG
AGAGAACTTCCCATCGAGTCGCGGGATCC
(SEQ ID NO:31)

FIG. 14B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALET
VQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQ
DHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVV
AIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGK
QALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRL
LPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHG
LTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIA
SHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD
AVKKGLPHAPALIKRTNRRIPERTSHRVAGS
(SEQ ID NO:32)

FIG. 15A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGC
CCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATT
GCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGG
CTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTC
CTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGC
AGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCG
CAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACC
ACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAG
AGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAG
GGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGT
GGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCA
GGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCG
TGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAA
CGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGAT
CAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTG
TGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAA
ACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCA
CATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACA
CCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA
GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCA
TTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCATTG
CTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTG
CGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTC
TGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATC
C
(SEQ ID NO: 33)

FIG. 15B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIANNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGG
KQALETVQRLLPVLCQDHGLTPEQVVAIANNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNGGKQALETVQR
LLPVLCQAHGLTPAQVVAIANNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDH
GLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIA
SHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS
(SEQ ID NO:34)

FIG. 16A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGC
CCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATT
GCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGG
CTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTC
CTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGC
AGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCG
CAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACC
ACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAG
AGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAG
GGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGT
GGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCA
GGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCG
TGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAA
CGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGAT
CAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTG
TGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAA
ACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCA
CATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACA
CCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA
GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCA
TTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCG
CCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGAC
TGACACCCGAACAGGTGGTCGCCATTGCTAATAATAACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAAT
TGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGAC
CCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCG
AGAGAACTTCCCATCGAGTCGCGGGATCC
(SEQ ID NO:35)

FIG. 16B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGG
KQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQR
LLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDH
GLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIA
SHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD
AVKKGLPHAPALIKRTNRRIPERTSHRVAGS (SEQ ID NO:36)

FIG. 17A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGG
GCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCT
CCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAG
CAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTC
GCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGAC
CACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAG
AGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAG
GGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGT
GGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCA
GGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCG
TGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAA
CGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGAT
CAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTG
TGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAA
ACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCA
AACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAC
ACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCC
AGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGC
ATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATC
GCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGG
ACTGACACCCGAACAGGTGGTCGCCATTGCTAATAATAACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCA
ATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACG
ACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCC
GAGAGAACTTCCCATCGAGTCGCGGGATCC (SEQ ID NO:37)

FIG. 17B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGG
KQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQR
LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHG
LTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIA
SNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD
AVKKGLPHAPALIKRTNRRIPERTSHRVAGS (SEQ ID NO:38)

FIG. 18A

TCTAGAGCTAGCACCATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGAC
GATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGAC
ACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGG
CGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGC
TGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTG
GTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACA
CCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGC
GCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAG
CCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCA
TTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACG
GGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGC
TCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAA
GCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGT
CGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA
CCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCA
GAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGA
GGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAA
GTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGC
CAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAAC
CGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAAT
AACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCG
ATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGT
TGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGG
AAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGA
ACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTA
CACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCC
CAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAG
CATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCAT
CGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATG
GACTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCC
AATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGAC
GACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTC
CCGAGAGAACTTCCCATCGAGTCGCGGGATCC (SEQ ID NO:39)

FIG. 18B

MDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHG
FTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKR
GGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGG
KQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRL
LPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHG
LTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIA
NNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD
AVKKGLPHAPALIKRTNRRIPERTSHRVAGS (SEQ ID NO:40)

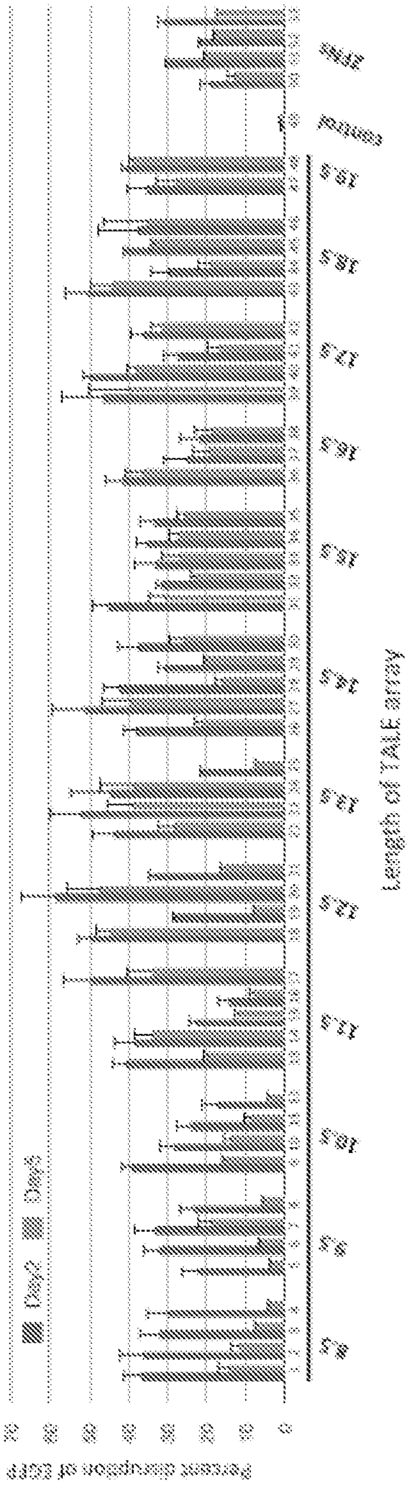


FIG. 19A

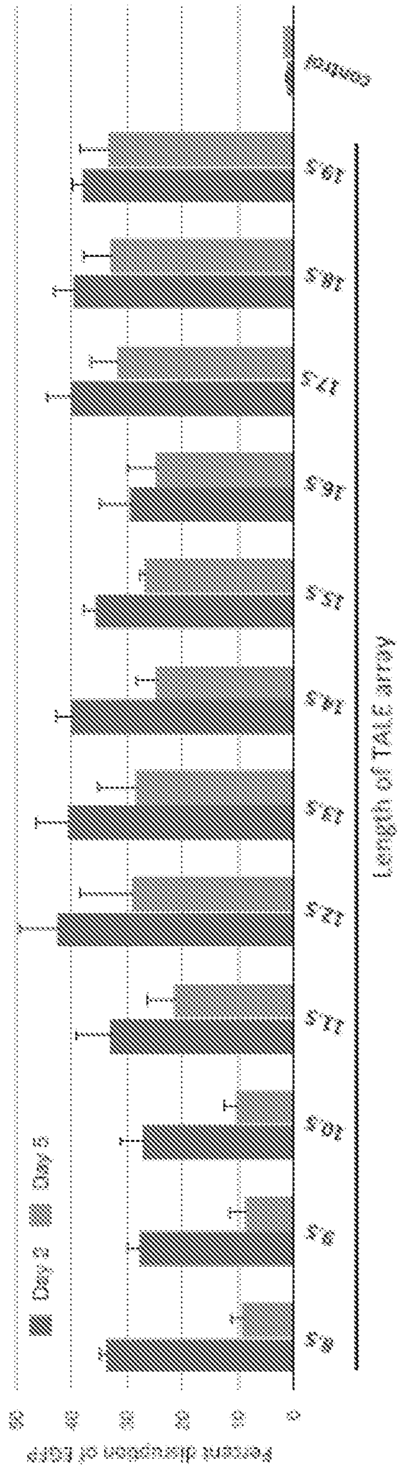


FIG. 19B

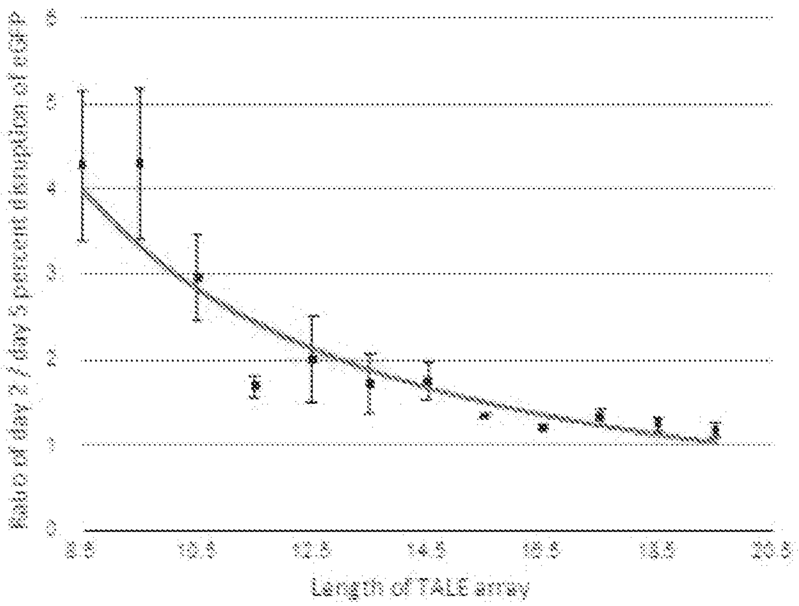


FIG. 20A

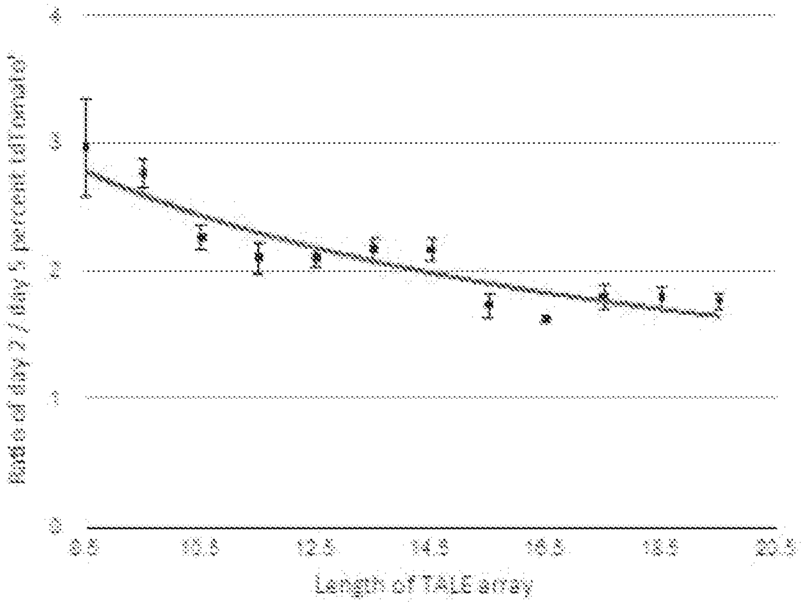


FIG. 20B

SEQUENCE	Δ SIZE	SEQ ID NO:
AXIN2 **TAL2200/TAL2201** **Mutations in 2 of 83 sequences ≈ 2.4%**		
TTCCCAGACTCAGTGGGAAGAGCTCCCTCACCATGAGTAGCGCTATGTTGGTGACTTGCCTCCCGGACCCCAGCAGCAGCTTCCGTGA	WT	301.
TTCCCAGACTCAGTGGGAAGAGCTCCCTCACCATGAGTAGCGCTATG--------TTGCCTCCCGGACCCCAGCAGCAGCTTCCGTGA	Δ8	302.
TTCCCAGACTCAGTGGGAAGAGCTCCCTCA-------------------------------CCCGGACCCCAGCAGCAGCTTCCGTGA	Δ31	303.
BRCA1 **TAL2384/TAL2385** **Mutations in 7 of 14 sequences ≈ 50.0%**		
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGATGGGTATTCTTTGACGGGGGTAGGGGCGGAACCTGAGAGGCGTAAGGCGTTGTG	WT	304.
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGAT-----------------GGGTAGGGGCGGAACCTGAGAGGCGTAAGGCGTTGTG	Δ17	305.
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGA-----------------------GGGGCGGAACCTGAGAGGCGTAAGGCGTTGTG	Δ23	306.
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGAT---------------------------GGAACCTGAGAGGCGTAAGGCGTTGTG	Δ27	307.
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGATG--------------------------------------GGGTAAGGCGTTGTG	Δ38	308.
GGCGTGGGAGAGTGGATTTCCGAAGCTGACAGATG---------------------------------------GGTAAGGCGTTGTG	Δ39	309.
AGTGGATTTCCGAAGCTGACAGATG-----------------/ /-------tggaagaagaGGCTGGTCATGAGGTCAGGAGTTCC	Δ183 (Δ193 +10)	310.
CGCTCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGG-----/ /-------------------AACTGGAATATGCCTTGAGGGGG	Δ235	311.
CHD7 **TAL2238/TAL2239** **Mutations in 4 of 81 sequences ≈ 4.9%**		
CCTGAGCTGTGGTTTGGAGGAGCCGTGTGTTGGAAGAAGATGGCAGATCCAGGAATGATGAGTCTTTTTGGCGAGGATGGAATATTT	WT	312.
CCTGAGCTGTGGTTTGGAGGAGCCGTGTGTTGGAAGAAGATca---------GAATGATGAGTCTTTTTGGCGAGGATGGAATATTT	Δ9 (Δ11 +2)	313.
CCTGAGCTGTGGTTTGGAGGAGCCGTGTGTTGGAAGAAGATG----------CAATCATCACTCTTTTTGGCGAGGATGGAATATTT	Δ10	314.
CCTGAGCTGTGGTTTGGAGGAGCCGTGTGTTGGAAGAAGAT----------------------------GGCGAGGATGGAATATTT	Δ28	315.
TAAAGAAATATGGAATGACAT---------------------/ /----------------------AAAATCCAGTAAATCCTATG	Δ199	316.

FIG. 21A

SEQUENCE	Δ SIZE	SEQ ID NO:
CDC73 **TAL2202/TAL2203** **Mutations in 9 of 37 sequences ≈ 24.3%**		
CAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAGTACAACATCCAGAAGAAGGAGATTGTGGTGAAGGGAGACGAAGTG	WT	317.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAGTACA-------GAAGAAGGAGATTGTGGTGAAGGGAGACGAAGTG	Δ7	318.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAGTACAAC--------GAAGGAGATTGTGGTGAAGGGAGACGAAGTG	Δ8	319.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACA--------TCCAGAAGAAGGAGATTGTGGTGAAGGGAGACGAAGTG	Δ8	320.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAG------------AAGAAGGAGATTGTGGTGAAGGGAGACGAAGTG	Δ12 (2x)	321.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAGT--------------------ATTGTGGTGAAGGGAGACGAAGTG	Δ20	322.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAG----------------------TTGTGGTGAAGGGAGACGAAGTG	Δ22	323.
GAGGGGGGGGAAGATGGCGGACGTGCTTAGCGTCCTGCGACAGTACAACAACATCCAGAAGAAGGAGATTGTGGTGAAGGGAGACGAA	+3	324.
AGGGCGAGGCGACAAGAGAAGAAGGAGGCAGG------------/ /-------------------ATTGTGGTGAAGGGAGACGAAGTG	Δ101	325.
CYLD **TAL2386/TAL2387** **Mutations in 10 of 44 ≈ 22.7%**		
TTAGTATTTTGAAGTTAATATCACAATGAGTTCAGGCTTATGGAGCCAAGAAAAAGTCACTTCACCCTACTGGGAAGAGCGGATTTTT	WT	326.
TTAGTATTTTGAAGTTAATATCACAATGAGTTCAGGCTTATGGA---------AAGTCACTTCACCCTACTGGGAAGAGCGGATTTTT	Δ9	327.
TTAGTATTTTGAAGTTAATATCACAA-----------------------------GTCACTTCACCCTACTGGGAAGAGCGGATTTTT	Δ29	328.
TTAGTATTTTGAAGTTAATA---TCACCCTACTGGGAAGAGCGGATTTTT	Δ41	329.
TTAGTATTTTGAAGTT--CCCTACTGGGAAGAGCGGATTTTT	Δ48	330.
T--AAGTCACTTCACCCTACTGGGAAGAGCGGATTTTT	Δ52	331.
TTAGTATTT---CCCTACTGGGAAGAGCGGATTTTT	Δ55	332.
TTAGTATTTTGAAGTT---GAAGAGCGGATTTTT	Δ57	333.
TTAGTATTTTGAA--CGGATTTTT	Δ66	334.
TTAG--	Δ84	335.
TAATATCACAATGAGTTCtcaggggcacaccaggccccagcggaacaccaggccctgggtaagcatccagtcccaggtggacatcagg tgccaggaggAAAAGTCACTTCACCCTA	+62 (Δ18 + 80)	336.

FIG. 21B

SEQUENCE	Λ SIZE	SEQ ID NO:
NCOR2 **TAL2284/TAL2285** **Mutations in 7 of 88 ≈ 8.0%**		
TCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCCGCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGA	WT	337.
TCCACACAGCCTGTGGCACAGACGTGCAGGGCCACTGAGCCCCGCTA-CCGCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGA	Δ1	338.
TCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGC-------CCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGA	Δ7	339.
TCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGC------------CCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGA	Δ12	340.
TCCACAC---AGATCGCCCGGA	Δ69	341.
CCCCCACCACC--------------------------------/ /---------------TTTCCTACCCAGTGCAGATCGCCCGGA	Δ70	342.
GCTTATTGCGGC-------------------------------/ /---------------------CTTTCTCCTGGGAGCCAGGCT	Δ213	343.
TCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCaccCGCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCC	+3	344.
JAK2 **TAL2406/TAL2407** **Mutations in 13 of 21 sequences ≈ 61.9%**		
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATGGGAATGGCCTGCCTTACGATGACAGAAATGGAGGGAACATCCACCTCT	WT	345.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATG----GGGCCTCCCTTACCATCACAGAAATGGAGGGAACATCCACCTCT	Δ4	346.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATG-----GGCCTGCCTTACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ5	347.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATGGGAATGG------TTACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ6	348.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCA--------GCCTGCCTTACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ8	349.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGC---------------CTTACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ15 (2x)	350.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATGGG------------------------AATGGAGGGAACATCCACCTCT	Δ24	351.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGAC-------------------------GATGACAGAAATGGAGGGAACATCCACCTCT	Δ25	352.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTG--------------------------CAGAAATGGAGGGAACATCCACCTCT	Δ26	353.
TTTCTCTTACAGGC---ATGGAGGGAACATCCACCTCT	Δ53	354.
T--ACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ54	355.
TTTCTCTTACAGGCAAATGTTCTGAAAAAGACTCTGCATGG----agtaagtCTTACGATGACAGAAATGGAGGGAACATCCACCTCT	Δ4 (Δ11 +7)	356.
CGGAGGTTTGCTGCAaacagagaaattt--------------/ /------------CGATGACAGAAATGGAGGGAACATCCACCTCT	Λ288 (Δ301 +13)	357.

FIG. 21C

SEQUENCE	Δ SIZE	SEQ ID NO:
MYCN TAL2280/TAL2281 Mutations in 12 of 35 sequences ≈ 34.3%		
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCACCATGCCGGGCATGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	WT	358.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCtCC------ccCATGATCTGCAGGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ6 (Δ8 +2)	359.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTC--------CGGGCATGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ8	360.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCACCAT----------ATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ10	361.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCACCATG-----------CTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ11	362.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCA------------TGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ12	363.
CGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCAC------------------CAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ18	364.
CGGGAGGCGAGCCGATGCCGAGCTGCTC-------------------ATGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACA	Δ19	365.
AAGGAAGCACCCCCGGTCTTAA--------------------/ /-------------------AGACCTCGAGTTTGACTCGCTACA	Δ100	366.
AGTGTTGGAGGTCGGCGCCGGCCCCCG---------------/ /----------GGCATGATCTGCAAGAACCCAGACCTCGAGTTT	Δ122	367.
AAGGAAGCACCCCCGGTATTAA--------------------/ /-------------------------------ACGAAGATGACT	Δ141	368.
GAGGCGAGCCGATGCCCGTGATCTGGGTCACGGCTGCTCCAGCTTGGAGGAGAGGCGGCTCTCCCGGCGACCCTCCTCGCGCGGCGC CCCTGCCATTCCCGGGAACAGGGGCTCAGCCCCCTTTGTTAGTGCTCGTATGTCTTGGCCTGGGGAGCATTTTGGAGGCAGTGCTAGG GGCAGAGAGGTCCTGTTTCCCCCAAGTCTTGATCTGCAAGAACCCA	+160(Δ29 +189)(2x)	369.
NBN TAL2408/TAL2409 Mutations in 12 of 20 sequences ≈ 60%		
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGGAAACTGCTGCCCGCCGCGGGCCCGGCAGGAGGTAAGGGCAGAAGGGAA	WT	370.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGG-----GCTGCCCGCCGCGGGCCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ5	371.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTG-------CTGCCCGCCGCGGGCCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ7	372.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGGAAACTG-------------GCCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ13	373.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGGAct-------------------CCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ17 (Δ19 and +2)	374.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGGA-------------------CCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ19	375.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATG----------------------------CAGGAGGTAAGGGCAGAAGGGAA	Δ28	376.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCGATGTGGAAA----------------------------GTAAGGGCAGAAGGGAA	Δ28	377.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGACCG------------------------------CCAGGAGGTAAGGGCAGAAGGGAA	Δ30	378.
TGCACGTCGGCCCCAGCCCTGAGGAGCCGGA-----------------------------------AGGAGGTAAGGGCAGAAGGGAA	Δ35	379.
TGCACGTCGGCCC---------------------------------------CGCGCGGGCCCGGCAGGAGGTAAGGGCAGAAGGGAA	Δ39	380.
TGCACGTCGGCCCCAGCC---GGCAGGAGGTAAGGGCAGAAGGGAA	Δ45	381.
GCTCCCGGGAGCGCGCACGTCCCGGAGCCCAT----------/ /-----------------------GCCTGCGGGTGATTCCTGCG	Δ183	382.

FIG. 21D

SEQUENCE	Δ SIZE	SEQ ID NO:
***XPC* - TAL2350/TAL2351** **Mutations in 10 of 36 ≈ 27.8%**		
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGCTCGGAAACGCGCGGCCGGCGGGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	WT	383.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGCTCGGAGG--AACGGCCGGCGGGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	Δ 2 (Δ6 and +4)	384.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGCTCGGAAA------------GGGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	Δ12	385.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGC---------------CGGCGGGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	Δ15	386.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGCTCG-----------------GGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	Δ17 (x2)	387.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGC-------------------GGGGAGCCGCGGGGACGCGAACTGCGCAGCCAG	Δ19	388.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGTT-----------------------------------GCGAACTGCGCAGCCAG	Δ35 (Δ37 and +2)	389.
TCGCGAAGTGGAATTTGCCCAGACAAGCAACATGGCTCG---------------------------------------GCGCAGCCAG	Δ39	390.
TCGCG--CAGCCAG	Δ76	391.
TCCCGAAGTGG-------------------------------/ /-----------------------AATCCAAGGCCAAGAGCAAG	Δ78	392.
***ERCC2* - TAL2306/TAL2307** **Mutations in 19 of 20 sequences ≈ 95.0%**		
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATGAAGTGAGAAGGGGGCTGGGGGTCGCGCTCGCTAGCGGGCGCGGGGGGTCTTGAA	WT	393.
CTCGACCCCCCTGCACAGTCCGGCCGGCGCCATGAAGT-------GGGCTGGGGGTCGCGCTCGCTAGCGGGCGCGGGGGGTCTTGAA	Δ7	394.
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATCAA-----------GCTGGGGGTCGCGCTCGCTAGCGGGCGCGGGGGGTCTTGAA	Δ11	395.
GTCGACCCCGCTGCACAGTCCGGCCGGCGC-------------------------------TCGCTAGCGGGCGCGGGGGGTCTTGAA	Δ31	396.
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATGAAGT---------------------------------------GGGGTCTTGAA	Δ39	397.
GGCCTCTCGCTGAATATTCATG--------------------/ /-----------------------ATGGGTCATCGGTGGGCGCG	Δ99	398.
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATGAAG-----/ /---------------------------GCTGAACCGCTCGCAC	Δ100	399.
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATGAAGTG---/ /-----------------CGTCCGGGGTGGGACGGGGGCAGCCG	Δ99 (Δ104 + 5)	400.
GTCGACCCCGCTGCACAGTCCGGCCGGCGCCATGAAGT----/ /---------------------GGCAGCCGCAGGGAGCAGCAGT	Δ118	401.
ATGGTCTCGTAATATAGGTGGAGCGACCCCTCCACG------/ /----------------------------GGGGTCTTGAAGATG	Δ122	402.
GTCGACCCCGCTG-----------------------------/ /-----------------------CTGAGGACCTGAGGGTTACC	Δ200	403.
GGCCTCTCGCTGAATATTCA----------------------/ /---------------------GCTCCTGAGGACCTGAGGGTTA	Δ221	404.
GTCGACCCCGCTGCACAGTCCGGC------------------/ /-----------------------CCGTCACCCTTCTCTGGGCT	Δ222 (2x)	405.
GTCGACCCCGCTGCACAGTCCGGCC-----------------/ /----------------------------GCTCGACGACCGGGC	Δ238	406.
GTCGACCCCGCTGCACAGTCCGGCCGGC--------------/ /-------------------------GACCGGGCACTGTGGAGG	Δ242	407.
GTCGACCCCGCTGCACAGTCCGGC------------------/ /----------------------------CGGGCACTGTGGAGG	Δ249	408.
GTCGAC------------------------------------/ /------------------------------CCAGCAGCCCCTG	Δ313	409.
GTCGACCC----------------------------------/ /--------------------------------CCCTGCCGCCA	Δ319	410.
GGCCTCTCGCTGAATATTCATGAG------------------/ /------------------------CCGCCAGGCTCAACGTGGA	Δ340	411.

FIG. 21E

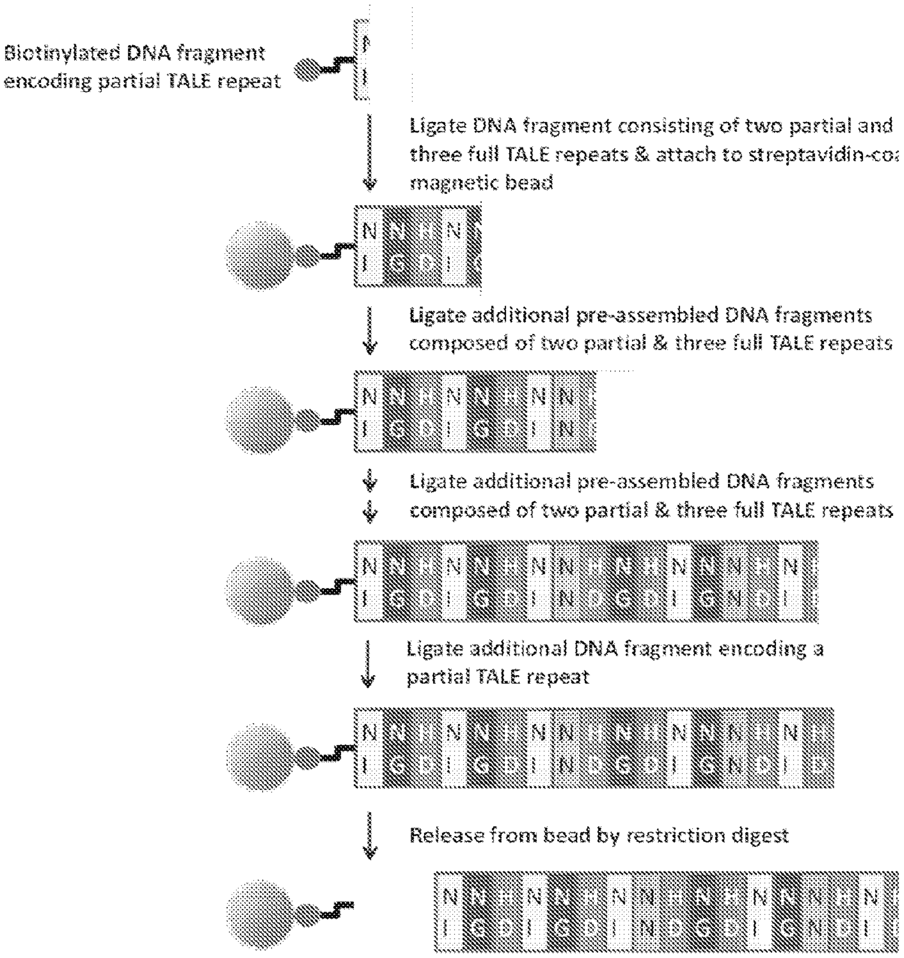

Biotinylated DNA fragment encoding partial TALE repeat
Ligate DNA fragment consisting of two partial and three full TALE repeats & attach to streptavidin-co
magnetic bead
Ligate additional pre-assembled DNA fragments composed of two partial & three full TALE repeats
Ligate additional pre-assembled DNA fragments composed of two partial & three full TALE repeats
Ligate additional DNA fragment encoding a partial TALE repeat
Release from bead by restriction digest

FIG. 22

METHODS OF TRANSCRIPTION ACTIVATOR LIKE EFFECTOR ASSEMBLY

CLAIM OF PRIORITY

[0001] This application claims the benefit of U.S. Provisional Patent Application Ser. No. 61/508,366, filed on Jul. 15, 2011, and 61/601,409, filed on Feb. 21, 2012, and 61/610,212, filed on Mar. 13, 2012, and the entire contents of each of the foregoing applications are hereby incorporated by reference.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under grant number DP1 OD006862 awarded by the National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jul. 11, 2012, is named 2953936W.txt and is 459,673 bytes in size.

TECHNICAL FIELD

[0004] This invention relates to methods of producing nucleic acids encoding peptides and polypeptides encoding multiple transcription-like activator effector (TALE) repeat domains and the proteins themselves.

BACKGROUND

[0005] TALE proteins of plant pathogenic bacteria in the genus *Xanthomonas* play important roles in disease, or trigger defense, by binding host DNA and activating effector-specific host genes (see, e.g., Gu et al., 2005, Nature 435:1122; Yang et al., 2006 Proc. Natl. Acad. Sci. USA 103:10503; Kay et al., 2007, Science 318:648; Sugio et al., 2007, Proc. Natl. Acad. Sci. USA 104:10720; and Romer et al., 2007, Science 318:645).

[0006] Specificity for nucleic acid sequences depends on an effector-variable number of imperfect, typically ~33-35 amino acid repeats (Schornack et al., 2006, J. Plant Physiol. 163:256). Each repeat binds to one nucleotide in the target sequence, and the specificity of each repeat for its nucleotide is largely context-independent, allowing for the development of custom sequence-specific TALE proteins (Moscou et al., 2009, Science 326:1501; Boch et al., 2009, Science 326:1509-1512).

SUMMARY

[0007] This application is based, at least in part, on the development of rapid, simple, and easily automatable methods for assembling nucleic acids encoding custom TALE repeat array proteins.

[0008] Accordingly, this disclosure features a process that includes: (a) providing a first nucleic acid having a sequence encoding a first set comprising one or more (e.g., two or more, three or more, four or more, five or more, six or more, one to six, two to six, three to six, four to six, five or six, one two to five, three to five, four or five, one to four, two to four, three or four, one, to three, two or three, one or two, one, two, three, four, five, or six) transcription activator-like effector (TALE) repeat domains and/or one or more portions of one or more TALE repeat domains; (b) contacting the first nucleic acid with a first enzyme, wherein the first enzyme creates a first ligatable end; (c) providing a second nucleic acid having a sequence encoding a second set comprising one or more (e.g., two or more, three or more, four or more, five or more, six or more, one to six, two to six, three to six, four to six, five or six, one two to five, three to five, four or five, one to four, two to four, three or four, one to three, two or three, one or two, one, two, three, four, five, or six) TALE repeat domains and/or one or more portions of one or more TALE repeat domains; (d) contacting the second nucleic acid with a second enzyme, wherein the second enzyme creates a second ligatable end, and wherein the first and second ligatable ends are compatible; and (e) ligating the first and second nucleic acids through the first and second ligatable ends to produce a first ligated nucleic acid, wherein the first ligated nucleic acid is linked to a solid support, and wherein the first ligated nucleic acid encodes a polypeptide comprising said first and second sets.

[0009] In some embodiments, the methods include linking the first nucleic acid to a solid support prior to (b) contacting the first nucleic acid with the first enzyme or prior to (e) ligating the first and second nucleic acids. In some embodiments, the methods include linking the first ligated nucleic acid to a solid support.

[0010] In some embodiments, the first set is N-terminal to the second set in the polypeptide. In some embodiments, the second set is N-terminal to the first set in the polypeptide.

[0011] In some embodiments, the first and second enzymes are a first and second restriction endonuclease, wherein the first restriction endonuclease cleaves at a site within the first nucleic acid and creates a first cut end, and the second restriction endonuclease cleaves at a site within the second nucleic acid and creates a second cut end, and wherein the first and second ligatable ends are the first and second cut ends. When restriction endonucleases are used, the first ligated nucleic acid cannot include a restriction site recognized by the first restriction endonuclease.

[0012] The process can further include: (f) contacting the first ligated nucleic acid with a third enzyme, wherein the third enzyme creates a third ligatable end; (g) providing a third nucleic acid comprising a sequence encoding a third set comprising one or more (e.g., two or more, three or more, four or more, five or more, six or more, one to six, two to six, three to six, four to six, five or six, one two to five, three to five, four or five, one to four, two to four, three or four, one to three, two or three, one or two, one, two, three, four, five, or six) TALE repeat domains and/or one or more portions of one or more TALE repeat domains; (h) contacting the third nucleic acid with a fourth enzyme, wherein the fourth enzyme creates a fourth ligatable end, and wherein the third and fourth ligatable ends are compatible; and (i) ligating the first ligated and third nucleic acids through the third and fourth ligatable ends to produce a second ligated nucleic acid linked to the solid support, wherein the second ligated nucleic acid encodes a polypeptide comprising said first, second, and third sets.

[0013] In some embodiments, the third and fourth enzymes are a third and fourth restriction endonuclease, wherein the third restriction endonuclease cleaves at a site within the first ligated nucleic acid and creates a third cut end, and the fourth restriction endonuclease cleaves at a site within the third nucleic acid and creates a fourth cut end, and wherein the third and fourth ligatable ends are the third and fourth cut ends.

[0014] In some embodiments, the ligated nucleic acid does not include a restriction site recognized by the first endonuclease, and the first and third restriction endonucleases are the same. In some embodiments, the second and fourth restriction endonucleases are the same.

[0015] The process can further include: (j) contacting the second ligated nucleic acid with a fifth enzyme, wherein the fifth enzyme creates a fifth ligatable end; (k) providing a fourth nucleic acid having a sequence encoding a fourth set comprising one or more (e.g., two or more, three or more, four or more, five or more, six or more, one to six, two to six, three to six, four to six, five or six, one two to five, three to five, four or five, one to four, two to four, three or four, one to three, two or three, one or two, one, two, three, four, five, or six) TALE repeat domains and/or one or more portions of one or more TALE repeat domains; (l) contacting the fourth nucleic acid with a sixth enzyme, wherein the sixth enzyme creates a sixth ligatable end, and wherein the fifth and sixth ligatable ends are compatible; and (m) ligating the second ligated and fourth nucleic acids through the fifth and sixth ligatable ends to produce a third ligated nucleic acid linked to the solid support, wherein the third ligated nucleic acid encodes a polypeptide comprising said first, second, third, and fourth sets. One of ordinary skill would recognize that the process can be repeated with similar additional steps. Such methods are included within this disclosure.

[0016] In some embodiments, the fifth and sixth enzymes are a fifth and sixth restriction endonuclease, wherein the fifth restriction endonuclease cleaves at a site within the second ligated nucleic acid and creates a fifth cut end, and the sixth restriction endonuclease cleaves at a site within the fourth nucleic acid and creates a sixth cut end, and wherein the fifth and sixth ligatable ends are the fifth and sixth cut ends.

[0017] In some embodiments, the second ligated nucleic acid does not include a restriction site recognized by the first endonuclease, and the first, third, and fifth restriction endonucleases are the same.

[0018] In some embodiments, the second, fourth, and sixth restriction endonucleases are the same.

[0019] In some embodiments, the solid support and linked nucleic acid are isolated, e.g., following any of the above steps (a)-(m).

[0020] In some embodiments, the second, third, or fourth set comprises one to four TALE repeat domains.

[0021] In some embodiments, the ligatable ends include an overhang of 1-10 nucleotides. In some embodiments, the ligatable ends are blunt ends. In some embodiments, an overhang can be generated using an exonuclease and polymerase in the presence of one or more nucleotides.

[0022] In some embodiments, an enzyme or restriction endonuclease used in the above processes is a type IIS restriction endonuclease.

[0023] The processes can further comprise unlinking a ligated nucleic acid from the solid support and inserting the ligated nucleic acid (or a processed derivative thereof comprising the TALE repeat array coding sequences) into a vector, e.g., an expression vector. The expression vector can include a sequence encoding an effector domain (e.g., a nuclease domain) configured to create a sequence encoding a fusion protein of the polypeptide and the effector domain. The expression vector can be inserted into a cell to affect the cell directly or for expression of the polypeptide or fusion protein. When the polypeptide or fusion protein is to be expressed, the processes can further include expressing and purifying the polypeptide or fusion protein.

[0024] In another aspect, this disclosure features TALE proteins that bind to a target nucleotide sequence (e.g., a "half site") disclosed herein (e.g., in Table 6 or 7), TALE nucleases that include the TALE proteins, pairs of TALE proteins (e.g., TALENs) that bind to the target sites disclosed herein (e.g., in Table 6 or 7), and nucleic acids that encode any of the above. In some embodiments, the TALE proteins, TALE nucleases, and pairs of TALE proteins (e.g., TALENs) are those disclosed in Example 7. The nucleic acids encoding the TALE proteins, TALE nucleases, and pairs of TALE proteins (e.g., TALENs) can be those disclosed in Example 7 or other sequences that encode the proteins disclosed in Example 7. The disclosure also includes vectors and cells that include the nucleic acids encoding the TALE proteins, TALE nucleases, or pairs of TALE proteins (e.g., TALENs) disclosed herein and methods of expressing the TALE proteins, TALE nucleases, or pairs of TALE proteins (e.g., TALENs) that include culturing the cells. The methods of expressing the TALE proteins, TALE nucleases, or pairs of TALE proteins (e.g., TALENs) can also include isolating the TALE proteins, TALE nucleases, or pairs of TALE proteins (e.g., TALENs) from the cell culture.

[0025] In another aspect, the invention features a set, archive, or library of nucleic acids (e.g., plasmids) that include sequences encoding one or more TALE domains. In some embodiments, the set, archive; or library includes sequences encoding one, two, three, and/or four (or more than four (e.g., five, six, or more)) TALE repeat domains. In some embodiments, the set, library, or archive of nucleic acids includes sequences encoding TALE repeat domains that bind to nucleotide sequences having one, two, three, four (or more than four (e.g., five, six, or more)) nucleotides. In some embodiments, the set, library, or archive includes restriction sites (e.g., sites for type IIS restriction endonucleases) surrounding the sequences encoding the TALE repeat domains.

[0026] The methods described herein provide several advantages, including avoiding extensive PCR amplification of the TALE repeats, thereby avoiding the introduction of mutations from PCR errors. Further, TALE repeat arrays of any desired length can be constructed, and the methods can be easily multiplexed and/or automated.

[0027] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

[0028] The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

[0029] FIG. **1** is a schematic depiction of an exemplary method of assembling a nucleic acid encoding a TALE protein.

[0030] FIG. **2** is a schematic depiction of exemplary archives of nucleic acids encoding single (one-mer), two-mer, three-mer, and four-mer TALE repeat domains.

[0031] FIG. **3** depicts the sequence of the pUC57-ΔBsaI plasmid. This plasmid is identical to plasmid pUC57 except for mutation of a single base (in bold, underlined and lowercase) that destroys a BsaI restriction site.

[0032] FIG. **4**A depicts the polypeptide sequences of exemplary TALE repeats of type α/ϵ, β, γ, and δ. Polymorphic residues characteristic of each type are indicated in bold and italic. The hypervariable triplet SNI for binding to A is indicated in underscore.

[0033] FIG. **4**B depicts the polynucleotide sequences of the exemplary TALE repeats of FIG. **4**A.

[0034] FIGS. **5**A-**5**B depict the common sequence of expression plasmids pJDS70, pJDS71, pJDS74, pJDS76, and pJDS78. The region of the variable sequences is depicted as XXXXXXXXX (underlined and bold).

[0035] FIG. **6** is a schematic diagram of the enhanced green fluorescent protein (eGFP) gene and the location of the binding sites for synthetic TALE proteins described herein.

[0036] FIG. **7** is a bar graph depicting the % of TALE nuclease-modified, eGFP-negative cells at 2 and 5 days following transfection with plasmids encoding TALE nucleases designed to bind and cleave the eGFP reporter gene.

[0037] FIG. **8** is a depiction of the sequences of insertion-deletion mutants of eGFP induced by TALE nucleases. Deleted bases are indicated by dashes and inserted bases indicated by double underlining; the TALEN target half-sites are single underlined. The net number of bases inserted or deleted is shown to the right.

[0038] FIG. **9** is a depiction of an electrophoresis gel of assembled DNA fragments encoding 17-mer TALE array preparations.

[0039] FIG. **10** is a depiction of an electrophoresis gel of 16-mer TALE array preparations.

[0040] FIGS. **11**A-**11**B depict the nucleotide (**11**A) and polypeptide (**11**B) sequence of engineered DR-TALE-0003.

[0041] FIGS. **12**A-**12**B depict the nucleotide (**12**A) and polypeptide (**12**B) sequence of engineered DR-TALE-0006.

[0042] FIGS. **13**A-**13**B depict the nucleotide (**13**A) and polypeptide (**13**B) sequence of engineered DR-TALE-0005.

[0043] FIGS. **14**A-**14**B depict the nucleotide (**14**A) and polypeptide (**14**B) sequence of engineered DR-TALE-0010.

[0044] FIGS. **15**A-**15**B depict the nucleotide (**15**A) and polypeptide (**15**B) sequence of engineered DR-TALE-0023.

[0045] FIGS. **16**A-**16**B depict the nucleotide (**16**A) and polypeptide (**16**B) sequence of engineered DR-TALE-0025.

[0046] FIGS. **17**A-**17**B depict the nucleotide (**17**A) and polypeptide (**17**B) sequence of engineered DR-TALE-0020.

[0047] FIGS. **18**A-**18**B depict the nucleotide (**18**A) and polypeptide (**18**B) sequence of engineered DR-TALE-0022.

[0048] FIG. **19**A is a bar graph depicting activities of 48 TALEN pairs and four ZFN pairs in the EGFP gene-disruption assay. Percentages of EGFP-negative cells as measured 2 and 5 days following transfection of U2OS cells bearing a chromosomally integrated EGFP reporter gene with nuclease-encoding plasmids are shown. Mean percent disruption of EGFP and standard error of the mean from three independent transfections are shown.

[0049] FIG. **19**B is a bar graph depicting mean EGFP-disruption activities from FIG. **19**A, grouped by length of the TALENs.

[0050] FIG. **20**A is a graph depicting the ratio of mean percent EGFP disruption values from day 2 to day 5. Ratios were calculated for groups of each length TALEN using the data from FIG. **19**B. Values greater than 1 indicate a decrease in the average of EGFP-disrupted cells at day 5 relative to day 2.

[0051] FIG. **20**B is a graph depicting the ratio of mean tdTomato-positive cells from day 2 to day 5 grouped by various lengths of TALENs. tdTomato-encoding control plasmids were transfected together with nuclease-encoding plasmids on day 0.

[0052] FIGS. **21**A-E depict DNA sequences and frequencies of assembled TALEN-induced mutations at endogenous human genes. For each endogenous gene target, the wild-type (WT) sequence is shown at the top with the TALEN target half-sites underlined and the translation start codon of the gene (ATG) indicated by a box. Deletions are indicated by dashes and insertions by lowercase letters and double underlining. The sizes of the insertions (+) or deletions (Δ) are indicated to the right of each mutated site. The number of times that each mutant was isolated is shown in parentheses. Mutation frequencies are calculated as the number of mutants identified divided by the total number of sequences analyzed. Note that for several of the genes, we also identified larger deletions that extend beyond the sequences of the TALEN target sites.

[0053] FIG. **22** is a schematic depiction of an exemplary method of assembling a nucleic acid encoding a TALE protein containing TALE repeat domains or portions of TALE repeat domains.

DETAILED DESCRIPTION

[0054] The methods described herein can be used to assemble engineered proteins containing TALE repeat domains for binding to specific sequences of interest. Assembling long arrays (e.g., 12 or more) of TALE repeat domain repeats can be challenging because the repeats differ only at a small number of amino acids within their highly conserved ~33-35 amino acid consensus sequence. PCR assembly can lead to the introduction of unwanted mutations. Hierarchical assembly methods that involve one or more passages of intermediate plasmid constructs in *E. coli* can also be problematic because the highly repetitive nature of these constructs can make them unstable and prone to recombination and because the need to passage these intermediate constructs makes these approaches difficult to automate.

TAL Effectors

[0055] TAL effectors of plant pathogenic bacteria in the genus *Xanthomonas* play important roles in disease, or trigger defense, by binding host DNA and activating effector-specific host genes. Specificity depends on an effector-variable number of imperfect, typically ~33-35 amino acid repeats. Polymorphisms are present primarily at repeat positions 12 and 13, which are referred to herein as the "repeat variable-diresidue" (RVD). The RVDs of TAL effectors correspond to the nucleotides in their target sites in a direct, linear fashion, one RVD to one nucleotide, with some degeneracy and no apparent context dependence. In some embodiments, the polymorphic region that grants nucleotide specificity may be expressed as a triresidue or triplet e.g., encompassing residues 11, 12, and 13.

[0056] Each DNA binding repeat can include an RVD that determines recognition of a base pair in the target DNA sequence, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA sequence, and wherein the RVD comprises, but is not limited to, one or more of the following: HA for recognizing C; ND for recognizing C; HI for recognizing C; HN for recognizing G; NA for recognizing G; SN for recognizing G or A; YG for recognizing T; and NK for recognizing G, and one or more of: HD for recognizing C; NG for recognizing T; NI for recognizing A; NN for recognizing G or A; NS for recognizing A or C or G or T; N* for recognizing C or T, wherein * represents a gap in the second position of the RVD; HG for recognizing T; H* for recognizing T, wherein * represents a gap in the second position of the RVD; and IG for recognizing T.

[0057] TALE proteins are useful in research and biotechnology as targeted chimeric nucleases that can facilitate homologous recombination in genome engineering (e.g., to add or enhance traits useful for biofuels or biorenewables in plants). These proteins also are useful as, for example, transcription factors, and especially for therapeutic applications requiring a very high level of specificity such as therapeutics against pathogens (e.g., viruses) as non-limiting examples.

Assembly Methods

[0058] An example of the methods described herein of assembling a TALE repeat domain array is shown in FIG. **1** and includes the following steps: (1) provision a single biotinylated PCR product encoding one single N-terminal TALE repeat domain (a one-mer) with a linker suitable for attachment to a solid support (in the example shown here, a magnetic streptavidin coated bead is used but other solid supports can also be utilized as well as other ways of tethering the initial DNA fragment to the solid support); (2) creation of an overhang at the 3' end of the one-mer DNA (e.g., using a Type IIS restriction enzyme); (3) ligation of a second fragment containing four TALE repeat domain (i.e., a pre-assembled four-mer), creating a five-mer; (4) attachment of the five-mer to the solid support; (5) ligation of additional pre-assembled TALE repeat domains to create a long array, e.g., a piece or pieces of DNA encoding one, two, three, or four TALE repeat domains depending upon the length of the desired final array, and (6) release of the extended DNA encoding the TALE repeats from the solid support (e.g., by using a Type IIS restriction enzyme whose site is built in at the 5' end of the initial biotinylated DNA product). The final fragment can then be prepared for ligation to an appropriate expression plasmid.

[0059] Alternatively, the method can proceed as follows: (1) attachment of a single biotinylated PCR product encoding one single N-terminal TALE repeat domains to a solid support (in the example shown here, a magnetic streptavidin coated bead is used but other solid supports such as the streptavidin-coated wells of a multi-well plate can also be utilized as well as other ways of tethering the initial DNA fragment to the solid support), (2) creation of an overhang at the 3' end of the anchored DNA (e.g., using a Type IIS restriction enzyme), (3) ligation of a second fragment containing four TALE repeat domain, (4) additional cycles of steps (2) and (3) to create a long array, (5) in the final cycle performing ligation of a piece of DNA encoding one, two, three, or four TALE repeat domains depending upon the length of the desired final array, and (6) release of the extended DNA encoding the TALE repeats from the solid support (e.g., by using a Type IIS restriction enzyme whose site is built in at the 5' end of the initial biotinylated DNA product).

[0060] Another example of a method of assembling a TALE repeat domain array based on the methods described herein is shown in FIG. **22** and includes the following steps: (1) provision a single biotinylated PCR product encoding a portion of one single N-terminal TALE repeat domain (a partial one-mer) with a linker suitable for attachment to a solid support (in the example shown here, a magnetic streptavidin coated bead is used but other solid supports can also be utilized as well as other ways of tethering the initial DNA fragment to the solid support); (2) creation of an overhang at the 3' end of the partial one-mer DNA (e.g., using a Type IIS restriction enzyme); (3) ligation of a second fragment containing consisting of two partial and three full TALE repeats; (4) attachment of the second fragment to the solid support; (5) ligation of additional pre-assembled TALE repeat domains or portions of TALE repeat domains to create a long array, e.g., a piece or pieces of DNA encoding one, two, three, or four TALE repeat domains (or portions of TALE repeat domains) depending upon the length of the desired final array, and (6) release of the extended DNA encoding the TALE repeats from the solid support (e.g., by using a Type IIS restriction enzyme whose site is built in at the 5' end of the initial biotinylated DNA product). The final fragment can then be prepared for ligation to an appropriate expression plasmid.

[0061] The initial nucleic acid encoding one or more TALE repeat domains (or portions) is linked to a solid support. The initial nucleic acid can be prepared by any means (e.g., chemical synthesis, PCR, or cleavage from a plasmid). Additionally, the nucleic acid can be linked to the solid support by any means, e.g., covalently or noncovalently.

[0062] In some embodiments, the nucleic acid is linked noncovalently by using a nucleic acid modified with one member of a binding pair and incorporating the other member of the binding pair on the solid support. A member of a binding pair is meant to be one of a first and a second moiety, wherein said first and said second moiety have a specific binding affinity for each other. Suitable binding pairs for use in the invention include, but are not limited to, antigens/antibodies (for example, digoxigenin/anti-digoxigenin, dinitrophenyl (DNP)/anti-DNP, dansyl-X/anti-dansyl, Fluorescein/anti-fluorescein, lucifer yellow/anti-lucifer yellow, peptide/anti-peptide, ligand/receptor and rhodamine/anti-rhodamine), biotin/avidin (or biotin/streptavidin) and calmodulin binding protein (CBP)/calmodulin. Other suitable binding pairs include polypeptides such as the FLAG-peptide (Hopp et al., 1988, BioTechnology, 6:1204 10); the KT3 epitope peptide (Martin et al., Science 255:192 194 (1992)); tubulin epitope peptide (Skinner et al., J. Biol. Chem. 266: 15163-66 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyerinuth et al., Proc. Natl. Acad. Sci. USA, 87:6393 97 (1990)) and the antibodies each thereto.

[0063] In some embodiments, the individual nucleic acids encoding one or more TALE repeat domains are present in an archive or library of plasmids (see FIG. **2**). Although nucleic acids encoding one to four TALE repeat domains are shown, the library of plasmids can contain nucleic acids encoding more than four (e.g., five, six, or more) TALE repeat domains. Alternatively, as shown FIG. **22**, the nucleic acids encoding parts or portions of one or more TALE repeat domains can also be joined together to create final DNA fragments encoding the desired full-length arrays of TALE repeat domains. Numerous TALE repeat domain sequences with binding specificity for specific nucleotides or sets of nucleotides are known in the art, and one of ordinary skill can design and prepare a library of plasmids based on these known sequences and the disclosures herein.

[0064] As used herein, a solid support refers to any solid or semisolid or insoluble support to which the nucleic acid can be linked. Such materials include any materials that are used as supports for chemical and biological molecule syntheses and analyses, such as, but not limited to: polystyrene, polycarbonate, polypropylene, nylon, glass, dextran, chitin, sand, pumice, agarose, polysaccharides, dendrimers, buckyballs, polyacryl-amide, silicon, rubber, and other materials used as supports for solid phase syntheses, affinity separations and purifications, hybridization reactions, immunoassays and other such applications. The solid support can be particulate or can be in the form of a continuous surface, such as a microtiter dish or well, a glass slide, a silicon chip, a nitrocellulose sheet, nylon mesh, or other such materials. When particulate, typically the particles have at least one dimension in the 5-10 mm range or smaller. Such particles, referred collectively herein as “beads,” are often, but not necessarily, spherical. Such reference, however, does not constrain the geometry of the matrix, which can be any shape, including random shapes, needles, fibers, and elongated. Roughly spherical “beads,” particularly microspheres that can be used in the liquid phase, also are contemplated. The “beads” can include additional components, such as magnetic or paramagnetic particles (see, e.g., Dynabeads (Dynal, Oslo, Norway)) for separation using magnets, as long as the additional components do not interfere with the methods described herein.

[0065] The ligatable ends can be produced by cutting with a restriction endonuclease (e.g., a type II or type IIS restriction endonuclease) or by “chewing back” the end using an enzyme (or enzymes) with exonuclease and polymerase activities in the presence of one or more nucleotides (see, Aslanidis et al., 1990, Nucl. Acids Res., 18:6069-74). Suitable enzymes are known to those of ordinary skill in the art. When restriction endonucleases are used, the nucleic acids can be designed to include restriction sites for the enzymes at suitable locations.

[0066] Following a ligation reaction, any unligated ends with 5' or 3' overhangs can be “blunted” by use of a polymerase, e.g., a DNA polymerase with both 3'→5' exonuclease activity and 5'→3' polymerase activity. This blunting step can reduce the appearance of undesired or partial assembly products. Alternatively, these ends can be capped using either a “hairpin” oligo bearing a compatible overhang (Briggs et al., 2012, Nucleic Acids Res, PMID: 22740649) or by short double-stranded DNAs bearing a compatible overhang on one end and a blunt end on the other.

[0067] To prepare the ligated nucleic acid for further downstream processing, it can be useful to select nucleic acids of the expected size, to reduce the presence of minor products created by incomplete ligations. Methods of selecting nucleic acids by size are known in the art, and include gel electrophoresis (e.g., slab gel electrophoresis or capillary gel electrophoresis (see, e.g., Caruso et al., 2003, Electrophoresis, 24:1-2:78-85)), liquid chromatography (e.g., size exclusion chromatography or reverse phase chromatography (see, e.g., Huber et al., 1995, Anal. Chem., 67:578-585)), and lab-on-a-chip systems (e.g., LabChip® XT system, Caliper Life Sciences, Hopkinton, Mass.). In some embodiments, a size exclusion step can be performed using an automated system, e.g., an automated gel electrophoresis system (e.g., a Pippin Prep™ automated DNA size selection system, Sage Science, Beverly, Mass.).

Automation

[0068] The methods disclosed herein can be performed manually or implemented in laboratory automation hardware (e.g., SciClone G3 Liquid Handling Workstation, Caliper Life, Sciences, Hopkinton, Mass.) controlled by a compatible software package (e.g., Maestro™ liquid handling software) programmed according to the new methods described herein or a new software package designed and implemented to carry out the specific method steps described herein. When performed by laboratory automation hardware, the methods can be implemented by computer programs using standard programming techniques following the method steps described herein.

[0069] Examples of automated laboratory system robots include the Sciclone™ G3 liquid handling workstation (Caliper Life Sciences, Hopkinton, Mass.), Biomek® FX liquid handling system (Beckman-Coulter, Fullerton, Calif.), TekBench™ automated liquid handling platform (TekCel, Hopkinton, Mass.), and Freedom EVO® automation platform (Tecan Trading AG, Switzerland).

[0070] The programs can be designed to execute on a programmable computer including at least one processor, at least one data storage system (including volatile and non-volatile memory and/or storage elements, e.g., RAM and ROM), at least one communications port that provides access for devices such as a computer keyboard, telephone, or a wireless, hand-held device, such as a PDA, and optionally at least one output device, such as a monitor, printer, or website. The central computer also includes a clock and a communications port that provides control of the lab automation hardware. These are all implemented using known techniques, software, and devices. The system also includes a database that includes data, e.g., data describing the procedure of one or more method steps described herein.

[0071] Program code is applied to data input by a user (e.g., location of samples to be processed, timing and frequency of manipulations, amounts of liquid dispensed or aspirated, transfer of samples from one location in the system to another) and data in the database, to perform the functions described herein. The system can also generate inquiries and provide messages to the user. The output information is applied to instruments, e.g., robots, that manipulate, heat, agitate, etc. the vessels that contain the reactants as described herein. In addition, the system can include one or more output devices such as a telephone, printer, or a monitor, or a web page on a computer monitor with access to a website to provide to the user information regarding the synthesis and/or its progress.

[0072] Each program embodying the new methods is preferably implemented in a high level procedural or object-oriented programming language to communicate with a computer system. However, the programs can also be implemented in assembly or machine language if desired. In any case, the language can be a compiled or interpreted language.

[0073] Each such computer program is preferably stored on a storage medium or device (e.g., RAM, ROM, optical, magnetic) readable by a general or special purpose programmable computer, for configuring and operating the computer when the storage media or device is read by the computer to perform the procedures described herein. The system can also be considered to be implemented as a computer- or machine-readable storage medium (electronic apparatus readable medium), configured with a program, whereby the storage medium so configured causes a computer or machine to operate in a specific and predefined manner to perform the functions described herein.

[0074] The new methods can be implemented using various means of data storage. The files can be transferred physically on recordable media or electronically, e.g., by email on a dedicated intranet, or on the Internet. The files can be encrypted using standard encryption software from such companies as RSA Security (Bedford, Mass.) and Baltimore®. The files can be stored in various formats, e.g., spreadsheets or databases.

[0075] As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; communications networks, including local area networks (LAN), wide area networks (WAN), Internet, Intranet, and Extranet; electronic appliances such as a personal digital assistants (PDAs), cellular telephones, "smartphones," pagers and the like; and local and distributed processing systems.

[0076] As used herein, "stored" refers to a process for encoding information on an electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising the sequence information.

[0077] A variety of software programs and formats can be used to store method data on an electronic apparatus readable medium. For example, the data and machine instructions can be incorporated in the system of the software provided with the automated system, represented in a word processing text file, formatted in commercially-available software such as WordPerfect® and Microsoft® Word®, or represented in the form of an ASCII file, stored in a database application, such as Microsoft Access®, Microsoft SQL Server®, Sybase®, Oracle®, or the like, as well as in other forms. Any number of data processor structuring formats (e.g., text file or database) can be employed to obtain or create a medium having recorded thereon the relevant data and machine instructions to implement the methods described herein.

[0078] By providing information in electronic apparatus readable form, the programmable computer can communicate with and control the lab automation hardware to perform the methods described herein. One skilled in the art can input data in electronic apparatus readable form (or a form that is converted to electronic apparatus readable form) to describe the completion of various method steps by the lab automation hardware.

Polypeptide Expression Systems

[0079] In order to use the engineered proteins of the present invention, it is typically necessary to express the engineered proteins from a nucleic acid that encodes them. This can be performed in a variety of ways. For example, the nucleic acid encoding the engineered TALE repeat protein is typically cloned into an intermediate vector for transformation into prokaryotic or eukaryotic cells for replication and/or expression. Intermediate vectors are typically prokaryote vectors, e.g., plasmids, or shuttle vectors, or insect vectors, for storage or manipulation of the nucleic acid encoding the engineered TALE protein or production of protein. The nucleic acid encoding the engineered TALE repeat protein is also typically cloned into an expression vector, for administration to a plant cell, animal cell, preferably a mammalian cell or a human cell, fungal cell, bacterial cell, or protozoan cell.

[0080] To obtain expression of a cloned gene or nucleic acid, the engineered TALE repeat protein is typically subcloned into an expression vector that contains a promoter to direct transcription. Suitable bacterial and eukaryotic promoters are well known in the art and described, e.g., in Sambrook et al., Molecular Cloning, A Laboratory Manual (3d ed. 2001); Kriegler, Gene Transfer and Expression: A Laboratory Manual (1990); and Current Protocols in Molecular Biology (Ausubel et al., eds., 2010). Bacterial expression systems for expressing the engineered TALE repeat protein are available in, e.g., *E. coli, Bacillus* sp., and *Salmonella* (Palva et al., 1983, Gene 22:229-235). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially available.

[0081] The promoter used to direct expression of the engineered TALE repeat protein nucleic acid depends on the particular application. For example, a strong constitutive promoter is typically used for expression and purification of the engineered TALE repeat protein. In contrast, when the engineered TALE repeat protein is to be administered in vivo for gene regulation, either a constitutive or an inducible promoter can be used, depending on the particular use of the engineered TALE repeat protein. In addition, a preferred promoter for administration of the engineered TALE repeat protein can be a weak promoter, such as HSV TK or a promoter having similar activity. The promoter typically can also include elements that are responsive to transactivation, e.g., hypoxia response elements, Gal4 response elements, lac repressor response element, and small molecule control systems such as tet-regulated systems and the RU-486 system (see, e.g., Gossen & Bujard, 1992, Proc. Natl. Acad. Sci. USA, 89:5547; Oligino et al., 1998, Gene Ther., 5:491-496; Wang et al., 1997, Gene Ther., 4:432-441; Neering et al., 1996, Blood, 88:1147-55; and Rendahl et al., 1998, Nat. Biotechnol., 16:757-761).

[0082] In addition to the promoter, the expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the nucleic acid in host cells, either prokaryotic or eukaryotic. A typical expression cassette thus contains a promoter operably linked, e.g., to the nucleic acid sequence encoding the TALE repeat protein signals required, e.g., for efficient polyadenylation of the transcript, transcriptional termination, ribosome binding sites, or translation termination. Additional elements of the cassette can include, e.g., enhancers, and heterologous spliced intronic signals.

[0083] The particular expression vector used to transport the genetic information into the cell is selected with regard to the intended use of the engineered TALE repeat protein, e.g., expression in plants, animals, bacteria, fungus, protozoa, etc. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and commercially available fusion expression systems such as GST and

LacZ. A preferred fusion protein is the maltose binding protein, "MBP." Such fusion proteins can be used for purification of the engineered TALE repeat protein. Epitope tags can also be added to recombinant proteins to provide convenient methods of isolation, for monitoring expression, and for monitoring cellular and subcellular localization, e.g., c-myc or FLAG.

[0084] Expression vectors containing regulatory elements from eukaryotic viruses are often used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, and vectors derived from Epstein-Barr virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A+, pMT010/A+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the SV40 early promoter, SV40 late promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

[0085] Some expression systems have markers for selection of stably transfected cell lines such as thymidine kinase, hygromycin B phosphotransferase, and dihydrofolate reductase. High yield expression systems are also suitable, such as using a baculovirus vector in insect cells, with the engineered TALE repeat protein encoding sequence under the direction of the polyhedrin promoter or other strong baculovirus promoters.

[0086] The elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of recombinant sequences.

[0087] Standard transfection methods are used to produce bacterial, mammalian, yeast or insect cell lines that express large quantities of protein, which are then purified using standard techniques (see, e.g., Colley et al., 1989, J. Biol. Chem., 264:17619-22; Guide to Protein Purification, in Methods in Enzymology, vol. 182 (Deutscher, ed., 1990)). Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (see, e.g., Morrison, 1977, J. Bacteriol. 132:349-351; Clark-Curtiss & Curtiss, Methods in Enzymology 101:347-362 (Wu et al., eds, 1983).

[0088] Any of the well-known procedures for introducing foreign nucleotide sequences into host cells can be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, naked DNA, plasmid vectors, viral vectors, both episomal and integrative, and any of the other well-known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Sambrook et al., supra). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the protein of choice.

Characterization of TALE Proteins

[0089] Engineered TALE repeat array proteins designed using methods of the present invention can be further characterized to ensure that they have the desired characteristics for their chosen use. For example, TALE repeat array protein can be assayed using a bacterial two-hybrid, bacterial promoter repression, phage-display, or ribosome display system or using an electrophoretic mobility shift assay or "EMSA" (Buratowski & Chodosh, in Current Protocols in Molecular Biology pp. 12.2.1-12.2.7). Equally, any other DNA binding assay known in the art could be used to verify the DNA binding properties of the selected protein.

[0090] In one embodiment, a bacterial "two-hybrid" system is used to express and test a TALE repeat protein of the present invention. The bacterial two-hybrid system has an additional advantage, in that the protein expression and the DNA binding "assay" occur within the same cells, thus there is no separate DNA binding assay to set up.

[0091] Methods for the use of the bacterial two-hybrid system to express and assay DNA binding proteins are described in Joung et al., 2000, Proc. Natl. Acad. Sci. USA, 97:7382, Wright et al., 2006, Nat. Protoc, 1:1637-52; Maeder et al., 2008, Mol. Cell, 31:294-301; Maeder et al., 2009, Nat. Protoc., 4:1471-1501; and US Patent Application No. 2002/0119498, the contents of which are incorporated herein by reference. Briefly, in a bacterial two-hybrid system, the DNA binding protein is expressed in a bacterial strain bearing the sequence of interest upstream of a weak promoter controlling expression of a reporter gene (e.g., histidine 3 (HIS3), the beta-lactamase antibiotic resistance gene, or the beta-galactosidase (lacZ) gene). Expression of the reporter gene occurs in cells in which the DNA binding protein expressed by the cell binds to the target site sequence. Thus, bacterial cells expressing DNA binding proteins that bind to their target site are identified by detection of an activity related to the reporter gene (e.g., growth on selective media, expression of beta-galactosidase).

[0092] In some embodiments, calculations of binding affinity and specificity are also made. This can be done by a variety of methods. The affinity with which the selected TALE repeat array protein binds to the sequence of interest can be measured and quantified in terms of its K_D. Any assay system can be used, as long as it gives an accurate measurement of the actual K_D of the TALE repeat array protein. In one embodiment, the K_D for the binding of a TALE repeat array protein to its target is measured using an EMSA

[0093] In one embodiment, EMSA is used to determine the K_r for binding of the selected TALE repeat array protein both to the sequence of interest (i.e., the specific K_D) and to non-specific DNA (i.e., the non-specific K_D). Any suitable non-specific or "competitor" double stranded DNA known in the art can be used. In some embodiments, calf thymus DNA or human placental DNA is used. The ratio of the non-specific K_D to the specific KD is the specificity ratio. TALE repeat array proteins that bind with high specificity have a high specificity ratio. This measurement is very useful in deciding which of a group of selected TALE should be used for a given purpose. For example, use of TALE repeat array protein in vivo requires not only high affinity binding but also high-specificity binding.

Construction of Chimeric TALE Proteins

[0094] Often, the aim of producing a custom-designed TALE repeat array DNA binding domain is to obtain a TALE repeat array protein that can be used to perform a function. The TALE repeat array DNA binding domain can be used alone, for example to bind to a specific site on a gene and thus block binding of other DNA-binding domains. However, in some embodiments, the TALE repeat array protein will be used in the construction of a chimeric TALE protein containing a TALE repeat array DNA binding domain and an additional domain having some desired specific function (e.g., gene activation) or enzymatic activity i.e., a "functional domain."

[0095] Chimeric TALE repeat array proteins designed and produced using the methods described herein can be used to perform any function where it is desired to target, for example, some specific enzymatic activity to a specific DNA sequence, as well as any of the functions already described for other types of synthetic or engineered DNA binding molecules. Engineered TALE repeat array DNA binding domains, can be used in the construction of chimeric proteins useful for the treatment of disease (see, for example, U.S. patent application 2002/0160940, and U.S. Pat. Nos. 6,511,808, 6,013,453 and 6,007,988, and International patent application WO 02/057308), or for otherwise altering the structure or function of a given gene in vivo. The engineered TALE repeat array proteins of the present invention are also useful as research tools, for example, in performing either in vivo or in vitro functional genomics studies (see, for example, U.S. Pat. No. 6,503,717 and U.S. patent application 2002/0164575).

[0096] To generate a functional recombinant protein, the engineered TALE repeat array DNA binding domain will typically be fused to at least one "functional" domain. Fusing functional domains to synthetic TALE repeat array proteins to form functional transcription factors involves only routine molecular biology techniques which are commonly practiced by those of skill in the art, see for example, U.S. Pat. Nos. 6,511,808, 6,013,453, 6,007,988, 6,503,717 and U.S. patent application 2002/0160940).

[0097] Functional domains can be associated with the engineered TALE repeat array domain at any suitable position, including the C- or N-terminus of the TALE protein. Suitable "functional" domains for addition to the engineered protein made using the methods of the invention are described in U.S. Pat. Nos. 6,511,808, 6,013,453, 6,007,988, and 6,503,717 and U.S. patent application 2002/0160940.

[0098] In one embodiment, the functional domain is a nuclear localization domain which provides for the protein to be translocated to the nucleus. Several nuclear localization sequences (NLS) are known, and any suitable NLS can be used. For example, many NLSs have a plurality of basic amino acids, referred to as a bipartite basic repeats (reviewed in Garcia-Bustos et al, 1991, Biochim. Biophys. Acta, 1071: 83-101). An NLS containing bipartite basic repeats can be placed in any portion of chimeric protein and results in the chimeric protein being localized inside the nucleus. It is preferred that a nuclear localization domain is routinely incorporated into the final chimeric protein, as the ultimate functions of the chimeric proteins of the present invention will typically require the proteins to be localized in the nucleus. However, it may not be necessary to add a separate nuclear localization domain in cases where the engineered TALE repeat array domain itself, or another functional domain within the final chimeric protein, has intrinsic nuclear translocation function.

[0099] In another embodiment, the functional domain is a transcriptional activation domain such that the chimeric protein can be used to activate transcription of the gene of interest. Any transcriptional activation domain known in the art can be used, such as for example, the VP16 domain form herpes simplex virus (Sadowski et al., 1988, Nature, 335:563-564) or the p65 domain from the cellular transcription factor NF-kappaB (Ruben et al., 1991, Science, 251:1490-93).

[0100] In yet another embodiment, the functional domain is a transcriptional repression domain such that the chimeric protein can be used to repress transcription of the gene of interest. Any transcriptional repression domain known in the art can be used, such as for example, the KRAB (Kruppel-associated box) domain found in many naturally occurring KRAB proteins (Thiesen et al., 1991, Nucleic Acids Res., 19:3996).

[0101] In a further embodiment, the functional domain is a DNA modification domain such as a methyltransferase (or methylase) domain, a de-methylation domain, a deaminase domain, a hydroxylase domain, an acetylation domain, or a deacetylation domain. Many such domains are known in the art and any such domain can be used, depending on the desired function of the resultant chimeric protein. For example, it has been shown that a DNA methylation domain can be fused to a TALE repeat array DNA binding protein and used for targeted methylation of a specific DNA sequence (Xu et al., 1997, Nat. Genet., 17:376-378). The state of methylation of a gene affects its expression and regulation, and furthermore, there are several diseases associated with defects in DNA methylation.

[0102] In a still further embodiment the functional domain is a chromatin modification domain such as a histone acetylase or histone de-acetylase (or HDAC) domain. Many such domains are known in the art and any such domain can be used, depending on the desired function of the resultant chimeric protein. Histone deacetylases (such as HDAC1 and HDAC2) are involved in gene repression. Therefore, by targeting HDAC activity to a specific gene of interest using an engineered TALE protein, the expression of the gene of interest can be repressed.

[0103] In an alternative embodiment, the functional domain is a nuclease domain, such as a restriction endonuclease (or restriction enzyme) domain. The DNA cleavage activity of a nuclease enzyme can be targeted to a specific target sequence by fusing it to an appropriate engineered TALE repeat array DNA binding domain. In this way, sequence specific chimeric restriction enzyme can be produced. Several nuclease domains are known in the art and any suitable nuclease domain can be used. For example, an endonuclease domain of a type IIS restriction endonuclease (e.g., FokI) can be used, as taught by Kim et al., 1996, Proc. Natl. Acad. Sci. USA, 6:1156-60). In some embodiments, the endonuclease is an engineered Fold variant as described in US 2008/0131962. Such chimeric endonucleases can be used in any situation where cleavage of a specific DNA sequence is desired, such as in laboratory procedures for the construction of recombinant DNA molecules, or in producing double-stranded DNA breaks in genomic DNA in order to promote homologous recombination (Kim et al., 1996, Proc. Natl. Acad. Sci. USA, 6:1156-60; Bibikova et al., 2001, Mol. Cell. Biol., 21:289-297; Porteus & Baltimore, 2003, Science, 300: 763; Miller et al., 2011, Nat. Biotechnol., 29:143-148; Cermak et al., 2011, Nucl. Acids Res., 39:e82). Repair of TALE nuclease-induced double-strand breaks (DSB) by error-prone non-homologous end-joining leads to efficient introduction of insertion or deletion mutations at the site of the DSB (Miller et al., 2011, Nat. Biotechnol., 29:143-148; Cermak et al., 2011, Nucl. Acids Res., 39:e82). Alternatively, repair of a DSB by homology-directed repair with an exogenously introduced "donor template" can lead to highly efficient introduction of precise base alterations or insertions at the break site (Bibikova et al., 2003, Science, 300:764; Urnov et al., 2005, Nature, 435:646-651; Porteus et al., 2003, Science, 300:763; Miller et al., 2011, Nat. Biotechnol., 29:143-148).

[0104] In some embodiments, the functional domain is an integrase domain, such that the chimeric protein can be used to insert exogenous DNA at a specific location in, for example, the human genome.

[0105] Other suitable functional domains include silencer domains, nuclear hormone receptors, resolvase domains oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.), kinases, phosphatases, and any other proteins that modify the structure of DNA and/or the expression of genes. Suitable kinase domains, from kinases involved in transcription regulation are reviewed in Davis, 1995, Mol. Reprod. Dev., 42:459-67. Suitable phosphatase domains are reviewed in, for example, Schonthal & Semin, 1995, Cancer Biol. 6:239-48.

[0106] Fusions of TALE repeat arrays to functional domains can be performed by standard recombinant DNA techniques well known to those skilled in the art, and as are described in, for example, basic laboratory texts such as Sambrook et al., Molecular Cloning; A Laboratory Manual 3d ed. (2001), and in U.S. Pat. Nos. 6,511,808, 6,013,453, 6,007, 988, and 6,503,717 and U.S. patent application 2002/0160940.

[0107] In some embodiments, two or more engineered TALE repeat array proteins are linked together to produce the final DNA binding domain. The linkage of two or more engineered proteins can be performed by covalent or non-covalent means. In the case of covalent linkage, engineered proteins can be covalently linked together using an amino acid linker (see, for example, U.S. patent application 2002/0160940, and International applications WO 02/099084 and WO 01/53480). This linker can be any string of amino acids desired. In one embodiment the linker is a canonical TGEKP linker. Whatever linkers are used, standard recombinant DNA techniques (such as described in, for example, Sambrook et al., Molecular Cloning; A Laboratory Manual 3d ed. (2001)) can be used to produce such linked proteins.

[0108] In embodiments where the engineered proteins are used in the generation of chimeric endonuclease, the chimeric protein can possess a dimerization domain as such endonucleases are believed to function as dimers. Any suitable dimerization domain can be used. In one embodiment the endonuclease domain itself possesses dimerization activity. For example, the nuclease domain of FokI which has intrinsic dimerization activity can be used (Kim et al., 1996, Proc. Natl. Acad. Sci., 93:1156-60).

Assays for Determining Regulation of Gene Expression by Engineered Proteins

[0109] A variety of assays can be used to determine the level of gene expression regulation by the engineered TALE repeat proteins, see for example U.S. Pat. No. 6,453,242. The activity of a particular engineered TALE repeat protein can be assessed using a variety of in vitro and in vivo assays, by measuring, e.g., protein or mRNA levels, product levels, enzyme activity, tumor growth; transcriptional activation or repression of a reporter gene; second messenger levels (e.g., cGMP, cAMP, IP3, DAG, Ca^{2+}); cytokine and hormone production levels; and neovascularization, using, e.g., immunoassays (e.g., ELISA and immunohistochemical assays with antibodies), hybridization assays (e.g., RNase protection, northerns, in situ hybridization, oligonucleotide array studies), colorimetric assays, amplification assays, enzyme activity assays, tumor growth assays, phenotypic assays, and the like.

[0110] TALE proteins can be first tested for activity in vitro using cultured cells; e.g., 293 cells, CHO cells, VERO cells, BHK cells, HeLa cells, COS cells, and the like. In some embodiments, human cells are used. The engineered TALE repeat array protein is often first tested using a transient expression system with a reporter gene, and then regulation of the target endogenous gene is tested in cells and in animals, both in vivo and ex vivo. The engineered TALE repeat array protein can be recombinantly expressed in a cell, recombinantly expressed in cells transplanted into an animal, or recombinantly expressed in a transgenic animal, as well as administered as a protein to an animal or cell using delivery vehicles described below. The cells can be immobilized, be in solution, be injected into an animal, or be naturally occurring in a transgenic or non-transgenic animal.

[0111] Modulation of gene expression is tested using one of the in vitro or in vivo assays described herein. Samples or assays are treated with the engineered TALE repeat array protein and compared to un-treated control samples, to examine the extent of modulation. For regulation of endogenous gene expression, the TALE repeat array protein ideally has a K_D of 200 nM or less, more preferably 100 nM or less, more preferably 50 nM, most preferably 25 nM or less. The effects of the engineered TALE repeat array protein can be measured by examining any of the parameters described above. Any suitable gene expression, phenotypic, or physiological change can be used to assess the influence of the engineered TALE repeat array protein. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as tumor growth, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots or oligonucleotide array studies), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP.

[0112] Preferred assays for regulation of endogenous gene expression can be performed in vitro. In one in vitro assay format, the engineered TALE repeat array protein regulation of endogenous gene expression in cultured cells is measured by examining protein production using an ELISA assay. The test sample is compared to control cells treated with an empty vector or an unrelated TALE repeat array protein that is targeted to another gene.

[0113] In another embodiment, regulation of endogenous gene expression is determined in vitro by measuring the level of target gene mRNA expression. The level of gene expression is measured using amplification, e.g., using RT-PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting. RNase protection is used in one embodiment. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

[0114] Alternatively, a reporter gene system can be devised using the target gene promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or beta-galactosidase. The reporter construct is typically co-transfected into a cultured cell. After treatment with the TALE repeat array protein, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

[0115] Another example of an assay format useful for monitoring regulation of endogenous gene expression is performed in vivo. This assay is particularly useful for examining TALE repeat array proteins that inhibit expression of tumor promoting genes, genes involved in tumor support, such as neovascularization (e.g., VEGF), or that activate tumor suppressor genes such as p53. In this assay, cultured tumor cells expressing the engineered TALE protein are injected subcutaneously into an immune compromised mouse such as an athymic mouse, an irradiated mouse, or a SCID mouse. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured, e.g., by volume or by its two largest dimensions, and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth. Alternatively, the extent of tumor neovascularization can also be measured. Immunoassays using endothelial cell specific antibodies are used to stain for vascularization of the tumor and the number of vessels in the tumor. Tumors that have a statistically significant reduction in the number of vessels (using, e.g., Student's T test) are said to have inhibited neovascularization.

[0116] Transgenic and non-transgenic animals can also be used for examining regulation of endogenous gene expression in vivo. Transgenic animals can express the engineered TALE repeat array protein. Alternatively, animals that transiently express the engineered TALE repeat array protein, or to which the engineered TALE repeat array protein has been administered in a delivery vehicle, can be used. Regulation of endogenous gene expression is tested using any one of the assays described herein.

Use of Engineered TALE Repeat-Containing Proteins in Gene Therapy

[0117] The engineered proteins of the present invention can be used to regulate gene expression or alter gene sequence in gene therapy applications in the same. Similar methods have been described for synthetic zinc finger proteins, see for example U.S. Pat. No. 6,511,808, U.S. Pat. No. 6,013,453, U.S. Pat. No. 6,007,988, U.S. Pat. No. 6,503,717, U.S. patent application 2002/0164575, and U.S. patent application 2002/0160940.

[0118] Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids encoding the engineered TALE repeat array protein into mammalian cells or target tissues. Such methods can be used to administer nucleic acids encoding engineered TALE repeat array proteins to cells in vitro. Preferably, the nucleic acids encoding the engineered TALE repeat array proteins are administered for in vivo or ex vivo gene therapy uses. Non-viral vector delivery systems include DNA plasmids, naked nucleic acid, and nucleic acid complexed with a delivery vehicle such as a liposome. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see Anderson, 1992, Science, 256:808-813; Nabel & Felgner, 1993, TIBTECH, 11:211-217; Mitani & Caskey, 1993, TIBTECH, 11:162-166; Dillon, 1993, TIBTECH, 11:167-175; Miller, 1992, Nature, 357:455-460; Van Brunt, 1988, Biotechnology, 6:1149-54; Vigne, 1995, Restorat. Neurol. Neurosci., 8:35-36; Kremer & Perricaudet, 1995, Br. Med. Bull., 51:31-44; Haddada et al., in Current Topics in Microbiology and Immunology Doerfler and Bohm (eds) (1995); and Yu et al., 1994, Gene Ther., 1:13-26.

[0119] Methods of non-viral delivery of nucleic acids encoding the engineered TALE repeat array proteins include lipofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA or RNA, artificial virions, and agent-enhanced uptake of DNA or RNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Felgner, WO 91/17424, WO 91/16024. Delivery can be to cells (ex vivo administration) or target tissues (in vivo administration).

[0120] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, 1995, Science, 270:404-410; Blaese et al., 1995, Cancer Gene Ther., 2:291-297; Behr et al., 1994, Bioconjugate Chem. 5:382-389; Remy et al., 1994, Bioconjugate Chem., 5:647-654; Gao et al., Gene Ther., 2:710-722; Ahmad et al., 1992, Cancer Res., 52:4817-20; U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

[0121] The use of RNA or DNA viral based systems for the delivery of nucleic acids encoding the engineered TALE repeat array proteins takes advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (in vivo) or they can be used, to treat cells in vitro and the modified cells are administered to patients (ex vivo). Conventional viral based systems for the delivery of TALE repeat array proteins could include retroviral, lentivirus, adenoviral, adeno-associated, Sendai, and herpes simplex virus vectors for gene transfer. Viral vectors are currently the most efficient and versatile method of gene transfer in target cells and tissues. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues.

[0122] The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system would therefore depend on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SW), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., 1992, J. Virol., 66:2731-39; Johann et al., 1992, J. Virol., 66:1635-40; Sommerfelt et al., 1990, Virology, 176:58-59; Wilson et al., 1989, J. Virol., 63:2374-78; Miller et al., 1991, J. Virol., 65:2220-24; WO 94/26877).

[0123] In applications where transient expression of the engineered TALE repeat array protein is preferred, adenoviral based systems can be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors are also used to transduce cells with target nucleic acids, e.g., in the in vitro production of nucleic acids and peptides, and for in vivo and ex vivo gene therapy procedures (see, e.g., West et al., 1987, Virology 160:38-47; U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, 1994, Hum. Gene Ther., 5:793-801; Muzyczka, 1994, J. Clin. Invest., 94:1351). Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin et al., 1985, Mol. Cell. Biol. 5:3251-60; Tratschin et al., 1984, Mol. Cell. Biol., 4:2072-81; Hermonat & Muzyczka, 1984, Proc. Natl. Acad. Sci. USA, 81:6466-70; and Samulski et al., 1989, J. Virol., 63:3822-28.

[0124] In particular, at least six viral vector approaches are currently available for gene transfer in clinical trials, with retroviral vectors by far the most frequently used system. All of these viral vectors utilize approaches that involve complementation of defective vectors by genes inserted into helper cell lines to generate the transducing agent.

[0125] pLASN and MFG-S are examples are retroviral vectors that have been used in clinical trials (Dunbar et al., 1995, Blood, 85:3048; Kohn et al., 1995, Nat. Med., 1:1017; Malech et al., 1997, Proc. Natl. Acad. Sci. USA, 94:12133-38). PA317/pLASN was the first therapeutic vector used in a gene therapy trial. (Blaese et al., 1995, Science, 270:475-480). Transduction efficiencies of 50% or greater have been observed for MFG-S packaged vectors (Ellem et al., 1997, Immunol Immunother., 44:10-20; Dranoffet al., 1997, Hum. Gene Ther., 1:111-112).

[0126] Recombinant adeno-associated virus vectors (rAAV) are a promising alternative gene delivery systems based on the defective and nonpathogenic parvovirus adeno-associated type 2 virus. Typically, the vectors are derived from a plasmid that retains only the AAV 145 bp inverted terminal repeats flanking the transgene expression cassette. Efficient gene transfer and stable transgene delivery due to integration into the genomes of the transduced cell are key features for this vector system (Wagner et al., 1998, Lancet, 351:1702-1703; Kearns et al., 1996, Gene Ther., 9:748-55).

[0127] Replication-deficient recombinant adenoviral vectors (Ad) are predominantly used for colon cancer gene therapy, because they can be produced at high titer and they readily infect a number of different cell types. Most adenovirus vectors are engineered such that a transgene replaces the Ad E1a, E1b, and E3 genes; subsequently the replication defector vector is propagated in human 293 cells that supply deleted gene function in trans. Ad vectors can transduce multiple types of tissues in vivo, including nondividing, differentiated cells such as those found in the liver, kidney and muscle system tissues. Conventional Ad vectors have a large carrying capacity. An example of the use of an Ad vector in a clinical trial involved polynucleotide therapy for antitumor immunization with intramuscular injection (Sterman et al., 1998, Hum. Gene Ther. 7:1083-89). Additional examples of the use of adenovirus vectors for gene transfer in clinical trials include Rosenecker et al., 1996, Infection, 24:15-10; Sterman et al., 1998, Hum. Gene Ther., 9:7 1083-89; Welsh et al., 1995, Hum. Gene Ther., 2:205-218; Alvarez et al., 1997, Hum. Gene Ther. 5:597-613; Topf et al., 1998, Gene Ther., 5:507-513; Sterman et al., 1998, Hum. Gene Ther., 7:1083-89.

[0128] Packaging cells are used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and T2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by producer cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host, other viral sequences being replaced by an expression cassette for the protein to be expressed. The missing viral functions are supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess ITR sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences. The cell line is also infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV.

[0129] In many gene therapy applications, it is desirable that the gene therapy vector be delivered with a high degree of specificity to a particular tissue type. A viral vector is typically modified to have specificity for a given cell type by expressing a ligand as a fusion protein with a viral coat protein on the viruses outer surface. The ligand is chosen to have affinity for a receptor known to be present on the cell type of interest. For example, Han et al., 1995, Proc. Natl. Acad. Sci. USA, 92:9747-51, reported that Moloney murine leukemia virus can be modified to express human heregulin fused to gp70, and the recombinant virus infects certain human breast cancer cells expressing human epidermal growth factor receptor. This principle can be extended to other pairs of virus expressing a ligand fusion protein and target cell expressing a receptor. For example, filamentous phage can be engineered to display antibody fragments (e.g., Fab or Fv) having specific binding affinity for virtually any chosen cellular receptor. Although the above description applies primarily to viral vectors, the same principles can be applied to nonviral vectors. Such vectors can be engineered to contain specific uptake sequences thought to favor uptake by specific target cells.

[0130] Gene therapy vectors can be delivered in vivo by administration to an individual patient, typically by systemic administration (e.g., intravenous, intraperitoneal, intramuscular, subdermal, or intracranial infusion) or topical application, as described below. Alternatively, vectors can be delivered to cells ex vivo, such as cells explanted from an individual patient (e.g., lymphocytes, bone marrow aspirates, tissue biopsy) or stem cells (e.g., universal donor hematopoietic stem cells, embryonic stem cells (ES), partially differentiated stem cells, non-pluripotent stem cells, pluripotent stem cells, induced pluripotent stem cells (iPS cells) (see e.g., Sipione et al., Diabetologia, 47:499-508, 2004)), followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector.

[0131] Ex vivo cell transfection for diagnostics, research, or for gene therapy (e.g., via re-infusion of the transfected cells into the host organism) is well known to those of skill in the art. In a preferred embodiment, cells are isolated from the subject organism, transfected with nucleic acid (gene or cDNA), encoding the engineered TALE repeat array protein, and re-infused back into the subject organism (e.g., patient). Various cell types suitable for ex vivo transfection are well known to those of skill in the art (see, e.g., Freshney et al., Culture of Animal Cells, A Manual of Basic Technique (5th ed. 2005)) and the references cited therein for a discussion of how to isolate and culture cells from patients).

[0132] In one embodiment, stem cells (e.g., universal donor hematopoietic stem cells, embryonic stem cells (ES), partially differentiated stem cells, non-pluripotent stem cells, pluripotent stem cells, induced pluripotent stem cells (iPS cells) (see e.g., Sipione et al., Diabetologia, 47:499-508, 2004)) are used in ex vivo procedures for cell transfection and gene therapy. The advantage to using stem cells is that they can be differentiated into other cell types in vitro, or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34+ cells in vitro into clinically important immune cell types using cytokines such a GM-CSF, IFN-gamma and TNF-alpha are known (see Inaba et al., 1992, J. Exp. Med., 176:1693-1702).

[0133] Stem cells can be isolated for transduction and differentiation using known methods. For example, stem cells can be isolated from bone marrow cells by panning the bone marrow cells with antibodies which bind unwanted cells, such as CD4+ and CD8+ (T cells), CD45+ (panB cells), GR-1 (granulocytes), and lad (differentiated antigen presenting cells) (see Inaba et al., 1992, J. Exp. Med., 176:1693-1702).

[0134] Vectors (e.g., retroviruses, adenoviruses, liposomes, etc.) containing nucleic acids encoding the engineered TALE repeat array protein can be also administered directly to the organism for transduction of cells in vivo. Alternatively, naked DNA can be administered. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Alternatively, stable formulations of the engineered TALE repeat array protein can also be administered.

[0135] Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions available, as described below (see, e.g., Remington: The Science and Practice of Pharmacy, 21st ed., 2005).

Delivery Vehicles

[0136] An important factor in the administration of polypeptide compounds, such as the engineered TALE repeat array proteins of the present invention, is ensuring that the polypeptide has the ability to traverse the plasma membrane of a cell, or the membrane of an intra-cellular compartment such as the nucleus. Cellular membranes are composed of lipid-protein bilayers that are freely permeable to small, nonionic lipophilic compounds and are inherently impermeable to polar compounds, macromolecules, and therapeutic or diagnostic agents. However, proteins and other compounds such as liposomes have been described, which have the ability to translocate polypeptides such as engineered TALE repeat array protein across a cell membrane.

[0137] For example, "membrane translocation polypeptides" have amphiphilic or hydrophobic amino acid subsequences that have the ability to act as membrane-translocating carriers. In one embodiment, homeodomain proteins have the ability to translocate across cell membranes. The shortest internalizable peptide of a homeodomain protein, Antennapedia, was found to be the third helix of the protein, from amino acid position 43 to 58 (see, e.g., Prochiantz, 1996, Curr. Opin. Neurobiol., 6:629-634). Another subsequence, the h (hydrophobic) domain of signal peptides, was found to have similar cell membrane translocation characteristics (see, e.g., Lin et al., 1995, J. Biol. Chem., 270:14255-58).

[0138] Examples of peptide sequences that can be linked to a protein, for facilitating uptake of the protein into cells, include, but are not limited to: peptide fragments of the tat protein of HIV (Endoh et al., 2010, Methods Mol. Biol., 623:271-281; Schmidt et al., 2010, FEBS Lett., 584:1806-13; Futaki, 2006, Biopolymers, 84:241-249); a 20 residue peptide sequence which corresponds to amino acids 84-103 of the p16 protein (see Fahraeus et al., 1996, Curr. Biol., 6:84); the third helix of the 60-amino acid long homeodomain of Antennapedia (Derossi et al., 1994, J. Biol. Chem., 269: 10444); the h region of a signal peptide, such as the Kaposi fibroblast growth factor (K-FGF) h region (Lin et al., supra); or the VP22 translocation domain from HSV (Elliot & O'Hare, 1997, Cell, 88:223-233). See also, e.g., Caron et al., 2001, Mol. Ther., 3:310-318; Langel, Cell-Penetrating Peptides Processes and Applications (CRC Press, Boca Raton Fla. 2002); El-Andaloussi et al., 2005, Curr. Pharm. Des., 11:3597-3611; and Deshayes et al., 2005, Cell. Mol. Life. Sci., 62:1839-49. Other suitable chemical moieties that provide enhanced cellular uptake can also be chemically linked to TALE repeat array proteins described herein.

[0139] Toxin molecules also have the ability to transport polypeptides across cell membranes. Often, such molecules are composed of at least two parts (called "binary toxins"): a translocation or binding domain or polypeptide and a separate toxin domain or polypeptide. Typically, the translocation domain or polypeptide binds to a cellular receptor, and then the toxin is transported into the cell. Several bacterial toxins, including *Clostridium perfringens* iota toxin, diphtheria toxin (DT), *Pseudomonas* exotoxin A (PE), pertussis toxin (PT), *Bacillus anthracis* toxin, and pertussis adenylate cyclase (CYA), have been used in attempts to deliver peptides to the cell cytosol as internal or amino-terminal fusions (Arora et al., 1993, J. Biol. Chem., 268:3334-41; Perelle et al., 1993, Infect. Immun., 61:5147-56; Stenmark et al., 1991, J. Cell Biol., 113:1025-32; Donnelly et al., 1993, Proc. Natl. Acad. Sci. USA, 90:3530-34; Carbonetti et al., 1995, Abstr. Annu. Meet. Am. Soc. Microbiol. 95:295; Sebo et al., 1995, Infect. Immun., 63:3851-57; Klimpel et al., 1992, Proc. Natl. Acad. Sci. USA, 89:10277-81; and Novak et al., 1992, J. Biol. Chem., 267:17186-93).

[0140] Such subsequences can be used to translocate engineered TALE repeat array proteins across a cell membrane. The engineered TALE repeat array proteins can be conveniently fused to or derivatized with such sequences. Typically, the translocation sequence is provided as part of a fusion protein. Optionally, a linker can be used to link the engineered

TALE repeat array protein and the translocation sequence. Any suitable linker can be used, e.g., a peptide linker.

[0141] The engineered TALE repeat array protein can also be introduced into an animal cell, preferably a mammalian cell, via liposomes and liposome derivatives such as immunoliposomes. The term "liposome" refers to vesicles comprised of one or more concentrically ordered lipid bilayers, which encapsulate an aqueous phase. The aqueous phase typically contains the compound to be delivered to the cell, i.e., the engineered TALE repeat array protein.

[0142] The liposome fuses with the plasma membrane, thereby releasing the compound into the cytosol. Alternatively, the liposome is phagocytosed or taken up by the cell in a transport vesicle. Once in the endosome or phagosome, the liposome either degrades or fuses with the membrane of the transport vesicle and releases its contents.

[0143] In current methods of drug delivery via liposomes, the liposome ultimately becomes permeable and releases the encapsulated compound (e.g., the engineered TALE repeat array protein or a nucleic acid encoding the same) at the target tissue or cell. For systemic or tissue specific delivery, this can be accomplished, for example, in a passive manner wherein the liposome bilayer degrades over time through the action of various agents in the body. Alternatively, active compound release involves using an agent to induce a permeability change in the liposome vesicle. Liposome membranes can be constructed so that they become destabilized when the environment becomes acidic near the liposome membrane (see, e.g., Proc. Natl. Acad. Sci. USA, 84:7851 (1987); Biochemistry, 28:908 (1989)). When liposomes are endocytosed by a target cell, for example, they become destabilized and release their contents. This destabilization is termed fusogenesis. Dioleoylphosphatidylethanolamine (DOPE) is the basis of many "fusogenic" systems.

[0144] Such liposomes typically comprise the engineered TALE repeat array protein and a lipid component, e.g., a neutral and/or cationic lipid, optionally including a receptor-recognition molecule such as an antibody that binds to a predetermined cell surface receptor or ligand (e.g., an antigen). A variety of methods are available for preparing liposomes as described in, e.g., Szoka et al., 1980, Annu. Rev. Biophys. Bioeng., 9:467, U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, 4,946,787, PCT Publication. No. WO 91/17424, Deamer & Bangham, 1976, Biochim. Biophys. Acta, 443:629-634; Fraley, et al., 1979, Proc. Natl. Acad. Sci. USA, 76:3348-52; Hope et al., 1985, Biochim. Biophys. Acta, 812:55-65; Mayer et al., 1986, Biochim Biophys. Acta, 858:161-168; Williams et al., 1988, Proc. Natl. Acad. Sci. USA, 85:242-246; Liposomes (Ostro (ed.), 1983, Chapter 1); Hope et al., 1986, Chem. Phys. Lip., 40:89; Gregoriadis, Liposome Technology (1984) and Lasic, Liposomes: from Physics to Applications (1993)). Suitable methods include, for example, sonication, extrusion, high pressure/homogenization, microfluidization, detergent dialysis, calcium-induced fusion of small liposome vesicles and ether-fusion methods, all of which are well known in the art.

[0145] In certain embodiments, it is desirable to target liposomes using targeting moieties that are specific to a particular cell type, tissue, and the like. Targeting of liposomes using a variety of targeting moieties (e.g., ligands, receptors, and monoclonal antibodies) has been previously described (see, e.g., U.S. Pat. Nos. 4,957,773 and 4,603,044).

[0146] Examples of targeting moieties include monoclonal antibodies specific to antigens associated with neoplasms, such as prostate cancer specific antigen and MAGE. Tumors can also be diagnosed by detecting gene products resulting from the activation or overexpression of oncogenes, such as ras or c-erbB2. In addition, many tumors express antigens normally expressed by fetal tissue, such as the alphafetoprotein (AFP) and carcinoembryonic antigen (CEA). Sites of viral infection can be diagnosed using various viral antigens such as hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV1) and papilloma virus antigens. Inflammation can be detected using molecules specifically recognized by surface molecules which are expressed at sites of inflammation such as integrins (e.g., VCAM-1), selectin receptors (e.g., ELAM-1) and the like.

[0147] Standard methods for coupling targeting agents to liposomes can be used. These methods generally involve incorporation into liposomes lipid components, e.g., phosphatidylethanolamine, which can be activated for attachment of targeting agents, or derivatized lipophilic compounds, such as lipid derivatized bleomycin. Antibody targeted liposomes can be constructed using, for instance, liposomes which incorporate protein A (see Renneisen et al., 1990, J. Biol. Chem., 265:16337-42 and Leonetti et al., 1990, Proc. Natl. Acad. Sci. USA, 87:2448-51).

Dosages

[0148] For therapeutic applications, the dose of the engineered TALE repeat array protein to be administered to a patient is calculated in a similar way as has been described for zinc finger proteins, see for example U.S. Pat. No. 6,511,808, U.S. Pat. No. 6,492,117, U.S. Pat. No. 6,453,242, U.S. patent application 2002/0164575, and U.S. patent application 2002/0160940. In the context of the present disclosure, the dose should be sufficient to effect a beneficial therapeutic response in the patient over time. In addition, particular dosage regimens can be useful for determining phenotypic changes in an experimental setting, e.g., in functional genomics studies, and in cell or animal models. The dose will be determined by the efficacy, specificity, and K_D of the particular engineered TALE repeat array protein employed, the nuclear volume of the target cell, and the condition of the patient, as well as the body weight or surface area of the patient to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular compound or vector in a particular patient.

Pharmaceutical Compositions and Administration

[0149] Appropriate pharmaceutical compositions for administration of the engineered TALE repeat array proteins of the present invention can be determined as described for zinc finger proteins, see for example U.S. Pat. Nos. 6,511,808, 6,492,117, 6,453,242, U.S. patent application 2002/0164575, and U.S. patent application 2002/0160940. Engineered TALE repeat array proteins, and expression vectors encoding engineered TALE repeat array proteins, can be administered directly to the patient for modulation of gene expression and for therapeutic or prophylactic applications, for example, cancer, ischemia, diabetic retinopathy, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's disease, muscular dystrophy, neurodegenerative diseases, vascular disease, cystic fibrosis, stroke, and the like. Examples of microorganisms that can be inhibited by TALE repeat array protein-mediated gene therapy include pathogenic bacteria, e.g., chlamydia, rickettsial bacteria, mycobacteria, staphylococci, streptococci, pneumococci, meningococci and conococci, *klebsiella, proteus, serratia, pseudomonas*, legionella, diphtheria, *salmonella*, bacilli, cholera, tetanus, botulism, anthrax, plague, leptospirosis, and Lyme disease bacteria; infectious fungus, e.g., *Aspergillus, Candida* species; protozoa such as sporozoa (e.g., *Plasmodia*), rhizopods (e.g., *Entamoeba*) and flagellates (*Trypanosoma, Leishmania, Trichomonas, Giardia*, etc.); viral diseases, e.g., hepatitis (A, B, or C), herpes virus (e.g., VZV, HSV-1, HSV-6, HSV-II, CMV, and EBV), HIV, Ebola, adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus, coxsackie virus, cornovirus, respiratory syncytial virus, mumps virus, rotavirus, measles virus, rubella virus, parvovirus, vaccinia virus, HTLV virus, dengue virus, papillomavirus, poliovirus, rabies virus, and arboviral encephalitis virus, etc.

[0150] Administration of therapeutically effective amounts is by any of the routes normally used for introducing TALE repeat array proteins into ultimate contact with the tissue to be treated. The TALE repeat array proteins are administered in any suitable manner, preferably with pharmaceutically acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

[0151] Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions that are available (see, e.g., Remington: The Science and Practice of Pharmacy, 21st ed., 2005).

[0152] The engineered TALE repeat array proteins, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

[0153] Formulations suitable for parenteral administration, such as, for example, by intravenous, intramuscular, intradermal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. The disclosed compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described.

Use of TALE Nucleases

[0154] TALE nucleases engineered using the methods described herein can be used to induce mutations in a genomic sequence, e.g., by cleaving at two sites and deleting sequences in between, by cleavage at a single site followed by non-homologous end joining, and/or by cleaving at a site so as to remove or replace one or two or a few nucleotides. In some embodiments, the TALE nuclease is used to induce mutation in an animal, plant, fungal, or bacterial genome. Targeted cleavage can also be used to create gene knock-outs (e.g., for functional genomics or target validation) and to facilitate targeted insertion of a sequence into a genome (i.e., gene knock-in); e.g., for purposes of cell engineering or protein overexpression. Insertion can be by means of replacements of chromosomal sequences through homologous recombination or by targeted integration, in which a new sequence (i.e., a sequence not present in the region of interest), flanked by sequences homologous to the region of interest in the chromosome, is used to insert the new sequence at a predetermined target site via homologous recombination. Exogenous DNA can also be inserted into TALE nuclease-induced double stranded breaks without the need for flanking homology sequences (see, Orlando et al., 2010, Nucl. Acids Res., 1-15, doi:10.1093/nar/gkq512).

[0155] As demonstrated in Example 3 below, the TALE nucleases produced by the methods described herein were capable of inducing site-specific mutagenesis in mammalian cells. A skilled practitioner will readily appreciate that TALE nucleases produced by the methods described herein would also function to induce efficient site-specific mutagenesis in other cell types and organisms (see, for example, Cade et al., 2012, Nucleic Acids Res., PMID: 22684503 and Moore et al., 2012, PLoS One, PMID: 22655075).

[0156] The same methods can also be used to replace a wild-type sequence with a mutant sequence, or to convert one allele to a different allele.

[0157] Targeted cleavage of infecting or integrated viral genomes can be used to treat viral infections in a host. Additionally, targeted cleavage of genes encoding receptors for viruses can be used to block expression of such receptors, thereby preventing viral infection and/or viral spread in a host organism. Targeted mutagenesis of genes encoding viral receptors (e.g., the CCR5 and CXCR4 receptors for HIV) can be used to render the receptors unable to bind to virus, thereby preventing new infection and blocking the spread of existing infections. Non-limiting examples of viruses or viral receptors that can be targeted include herpes simplex virus (HSV), such as HSV-1 and HSV-2, varicella zoster virus (VZV), Epstein-Barr virus (EBV) and cytomegalovirus (CMV), HHV6 and HHV7. The hepatitis family of viruses includes hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), the delta hepatitis virus (HDV), hepatitis E virus (HEV) and hepatitis G virus (HGV). Other viruses or their receptors can be targeted, including, but not limited to, Picornaviridae (e.g., polioviruses, etc.); Caliciviridae; Togaviridae (e.g., rubella virus, dengue virus, etc.); Flaviviridae; Coronaviridae; Reoviridae; Bimaviridae; Rhabodoviridae (e.g., rabies virus, etc.); Filoviridae; Paramyxoviridae (e.g., mumps virus, measles virus, respiratory syncytial virus, etc.); Orthomyxoviridae influenza virus types A, B and C, etc.); Bunyaviridae; Arenaviridae; Retroviradae; lentiviruses (e.g., HTLV-I; HTLV-II; HIV-1 (also known as HTLV-III, LAV, ARV, hTLR, etc.) HIV-II); simian immunodeficiency virus (SIV), human papillomavirus (HPV), influenza virus and the tick-borne encephalitis viruses. See, e.g., Virology, 3rd Edition (W. K. Joklik, ed. 1988); Fundamental Virology, 4th

Edition (Knipe and Howley, eds. 2001), for a description of these and other viruses. Receptors for HIV, for example, include CCR-5 and CXCR-4.

[0158] In similar fashion, the genome of an infecting bacterium can be mutagenized by targeted DNA cleavage followed by non-homologous end joining, to block or ameliorate bacterial infections.

[0159] The disclosed methods for targeted recombination can be used to replace any genomic sequence with a homologous, non-identical sequence. For example, a mutant genomic sequence can be replaced by its wild-type counterpart, thereby providing methods for treatment of e.g., genetic disease, inherited disorders, cancer, and autoimmune disease. In like fashion, one allele of a gene can be replaced by a different allele using the methods of targeted recombination disclosed herein.

[0160] Exemplary genetic diseases include, but are not limited to, achondroplasia, achromatopsia, acid maltase deficiency, adenosine deaminase deficiency (OMIM No. 102700), adrenoleukodystrophy, aicardi syndrome, alpha-1 antitrypsin deficiency, alpha-thalassemia, androgen insensitivity syndrome, apert syndrome, arrhythmogenic right ventricular, dysplasia, ataxia telangictasia, barth syndrome, beta-thalassemia, blue rubber bleb nevus syndrome, canavan disease, chronic granulomatous diseases (CGD), cri du chat syndrome, cystic fibrosis, dercum's disease, ectodermal dysplasia, Fanconi anemia, fibrodysplasia ossificans progressive, fragile X syndrome, galactosemis, Gaucher's disease, generalized gangliosidoses (e.g., GM1), hemochromatosis, the hemoglobin C mutation in the 6th codon of beta-globin (HbC), hemophilia, Huntington's disease, Hurler Syndrome, hypophosphatasia, Klinefelter's syndrome, Krabbes Disease, Langer-Giedion Syndrome, leukocyte adhesion deficiency (LAD, OMIM No. 116920), leukodystrophy, long QT syndrome, Marfan syndrome, Moebius syndrome, mucopolysaccharidosis (MPS), nail patella syndrome, nephrogenic diabetes insipdius, neurofibromatosis, Neimann-Pick disease, osteogenesis imperfecta, porphyria, Prader-Willi syndrome, progeria, Proteus syndrome, retinoblastoma, Rett syndrome, Rubinstein-Taybi syndrome, Sanfilippo syndrome, severe combined immunodeficiency (SCID), Shwachman syndrome, sickle cell disease (sickle cell anemia), Smith-Magenis syndrome, Stickler syndrome, Tay-Sachs disease, Thrombocytopenia Absent Radius (TAR) syndrome, Treacher Collins syndrome, trisomy, tuberous sclerosis, Turner's syndrome, urea cycle disorder, von Hippel-Landau disease, Waardenburg syndrome, Williams syndrome, Wilson's disease, Wiskott-Aldrich syndrome, X-linked lymphoproliferative syndrome (XLP, OMIM No. 308240).

[0161] Additional exemplary diseases that can be treated by targeted DNA cleavage and/or homologous recombination include acquired immunodeficiencies, lysosomal storage diseases (e.g., Gaucher's disease, GM1, Fabry disease and Tay-Sachs disease), mucopolysaccahidosis (e.g., Hunter's disease, Hurler's disease), hemoglobinopathies (e.g., sickle cell diseases, HbC, alpha-thalassemia, beta-thalassemia) and hemophilias.

[0162] In certain cases, alteration of a genomic sequence in a pluripotent cell (e.g., a hematopoietic stem cell) is desired. Methods for mobilization, enrichment and culture of hematopoietic stem cells are known in the art. See for example, U.S. Pat. Nos. 5,061,620; 5,681,559; 6,335,195; 6,645,489 and 6,667,064. Treated stem cells can be returned to a patient for treatment of various diseases including, but not limited to, SCID and sickle-cell anemia.

[0163] In many of these cases, a region of interest comprises a mutation, and the donor polynucleotide comprises the corresponding wild-type sequence. Similarly, a wild-type genomic sequence can be replaced by a mutant sequence, if such is desirable. For example, overexpression of an oncogene can be reversed either by mutating the gene or by replacing its control sequences with sequences that support a lower, non-pathologic level of expression. As another example, the wild-type allele of the ApoAI gene can be replaced by the ApoAI Milano allele, to treat atherosclerosis. Indeed, any pathology dependent upon a particular genomic sequence, in any fashion, can be corrected or alleviated using the methods and compositions disclosed herein.

[0164] Targeted cleavage and targeted recombination can also be used to alter non-coding sequences (e.g., sequences encoding microRNAs and long non-coding RNAs, and regulatory sequences such as promoters, enhancers, initiators, terminators, splice sites) to alter the levels of expression of a gene product. Such methods can be used, for example, for therapeutic purposes, functional genomics and/or target validation studies.

[0165] The compositions and methods described herein also allow for novel approaches and systems to address immune reactions of a host to allogeneic grafts. In particular, a major problem faced when allogeneic stem cells (or any type of allogeneic cell) are grafted into a host recipient is the high risk of rejection by the host's immune system, primarily mediated through recognition of the Major Histocompatibility Complex (MHC) on the surface of the engrafted cells. The MHC comprises the HLA class I protein(s) that function as heterodimers that are comprised of a common beta subunit and variable alpha subunits. It has been demonstrated that tissue grafts derived from stem cells that are devoid of HLA escape the host's immune response. See, e.g., Coffman et al., 1993, J. Immunol., 151:425-35; Markmann et al., 1992, Transplantation, 54:1085-89; Koller et al., 1990, Science, 248:1227-30. Using the compositions and methods described herein, genes encoding HLA proteins involved in graft rejection can be cleaved, mutagenized or altered by recombination, in either their coding or regulatory sequences, so that their expression is blocked or they express a non-functional product. For example, by inactivating the gene encoding the common beta subunit gene (beta2 microglobulin) using TALE nuclease fusion proteins as described herein, HLA class I can be removed from the cells to rapidly and reliably generate HLA class I null stem cells from any donor, thereby reducing the need for closely matched donor/recipient MHC haplotypes during stem cell grafting.

[0166] Inactivation of any gene (e.g., the beta2 microglobulin gene) can be achieved, for example, by a single cleavage event, by cleavage followed by non-homologous end joining, by cleavage at two sites followed by joining so as to delete the sequence between the two cleavage sites, by targeted recombination of a missense or nonsense codon into the coding region, or by targeted recombination of an irrelevant sequence (i.e., a "stuffer" sequence) into the gene or its regulatory region, so as to disrupt the gene or regulatory region.

[0167] Targeted modification of chromatin structure, as disclosed in WO 01/83793, can be used to facilitate the binding of fusion proteins to cellular chromatin.

[0168] In additional embodiments, one or more fusions between a TALE binding domain and a recombinase (or functional fragment thereof) can be used, in addition to or instead of the TALE-cleavage domain fusions disclosed herein, to facilitate targeted recombination. See, for example, co-owned U.S. Pat. No. 6,534,261 and Akopian et al. (2003) Proc. Natl. Acad. Sci. USA 100:8688-8691.

[0169] In additional embodiments, the disclosed methods and compositions are used to provide fusions of TALE repeat DNA-binding domains with transcriptional activation or repression domains that require dimerization (either homodimerization or heterodimerization) for their activity. In these cases, a fusion polypeptide comprises a TALE repeat DNA-binding domain and a functional domain monomer (e.g., a monomer from a dimeric transcriptional activation or repression domain). Binding of two such fusion polypeptides to properly situated target sites allows dimerization so as to reconstitute a functional transcription activation or repression domain.

Regulation of Gene Expression in Plants

[0170] Engineered TALE repeat array proteins can be used to engineer plants for traits such as increased disease resistance, modification of structural and storage polysaccharides, flavors, proteins, and fatty acids, fruit ripening, yield, color, nutritional characteristics, improved storage capability, and the like. In particular, the engineering of crop species for enhanced oil production, e.g., the modification of the fatty acids produced in oilseeds, is of interest.

[0171] Seed oils are composed primarily of triacylglycerols (TAGs), which are glycerol esters of fatty acids. Commercial production of these vegetable oils is accounted for primarily by six major oil crops (soybean, oil palm, rapeseed, sunflower, cotton seed, and peanut). Vegetable oils are used predominantly (90%) for human consumption as margarine, shortening, salad oils, and frying oil. The remaining 10% is used for non-food applications such as lubricants, oleochemicals, biofuels, detergents, and other industrial applications.

[0172] The desired characteristics of the oil used in each of these applications varies widely, particularly in terms of the chain length and number of double bonds present in the fatty acids making up the TAGs. These properties are manipulated by the plant in order to control membrane fluidity and temperature sensitivity. The same properties can be controlled using TALE repeat array proteins to produce oils with improved characteristics for food and industrial uses.

[0173] The primary fatty acids in the TAGs of oilseed crops are 16 to 18 carbons in length and contain 0 to 3 double bonds. Palmitic acid (16:0 [16 carbons: 0 double bonds]), oleic acid (18:1), linoleic acid (18:2), and linolenic acid (18:3) predominate. The number of double bonds, or degree of saturation, determines the melting temperature, reactivity, cooking performance, and health attributes of the resulting oil.

[0174] The enzyme responsible for the conversion of oleic acid (18:1) into linoleic acid (18:2) (which is then the precursor for 18:3 formation) is delta-12-oleate desaturase, also referred to as omega-6 desaturase: A block at this step in the fatty acid desaturation pathway should result in the accumulation of oleic acid at the expense of polyunsaturates.

[0175] In one embodiment engineered TALE repeat array proteins are used to regulate expression of the FAD2-1 gene in soybeans. Two genes encoding microsomal delta-6 desaturases have been cloned recently from soybean, and are referred to as FAD2-1 and FAD2-2 (Heppard et al., 1996, Plant Physiol. 110:311-319). FAD2-1 (delta-12 desaturase) appears to control the bulk of oleic acid desaturation in the soybean seed. Engineered TALE repeat array proteins can thus be used to modulate gene expression of FAD2-1 in plants. Specifically, engineered TALE repeat array proteins can be used to inhibit expression of the FAD2-1 gene in soybean in order to increase the accumulation of oleic acid (18:1) in the oil seed. Moreover, engineered TALE proteins can be used to modulate expression of any other plant gene, such as delta-9 desaturase, delta-12 desaturases from other plants, delta-15 desaturase, acetyl-CoA carboxylase, acyl-ACP-thioesterase, ADP-glucose pyrophosphorylase, starch synthase, cellulose synthase, sucrose synthase, senescence-associated genes, heavy metal chelators, fatty acid hydroperoxide lyase, polygalacturonase, EPSP synthase, plant viral genes, plant fungal pathogen genes, and plant bacterial pathogen genes.

[0176] Recombinant DNA vectors suitable for transformation of plant cells are also used to deliver protein (e.g., engineered TALE repeat array protein)-encoding nucleic acids to plant cells. Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature (see, e.g., Weising et al., 1988, Ann. Rev. Genet., 22:421-477). A DNA sequence coding for the desired TALE repeat array protein is combined with transcriptional and translational initiation regulatory sequences which will direct the transcription of the TALE protein in the intended tissues of the transformed plant.

[0177] For example, a plant promoter fragment can be employed which will direct expression of the engineered TALE repeat array protein in all tissues of a regenerated plant. Such promoters are referred to herein as “constitutive” promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35 S transcription initiation region, the 1'- or 2'-promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill.

[0178] Alternatively, the plant promoter can direct expression of the engineered TALE repeat array protein in a specific tissue or can be otherwise under more precise environmental or developmental control. Such promoters are referred to here as “inducible” promoters. Examples of environmental conditions that can affect transcription by inducible promoters include anaerobic conditions or the presence of light.

[0179] Examples of promoters under developmental control include promoters that initiate transcription only in certain tissues, such as fruit, seeds, or flowers. For example, the use of a polygalacturonase promoter can direct expression of the TALE repeat array protein in the fruit, a CHS-A (chalcone synthase A from petunia) promoter can direct expression of the TALE repeat array protein in the flower of a plant.

[0180] The vector comprising the TALE repeat array protein sequences will typically comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker can encode biocide resistance, particularly antibiotic resistance, such as resistance to kanarpycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

[0181] Such DNA constructs can be introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the DNA construct can be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA constructs can be introduced directly to plant tissue using biolistic methods, such as DNA particle bombardment. Alternatively, the DNA constructs can be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria.

[0182] Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al., 1984, EMBO J., 3:2717-22. Electroporation techniques are described in Fromm et al. 1985, Proc. Natl. Acad. Sci. USA, 82:5824. Biolistic transformation techniques are described in Klein et al., 1987, Nature, 327:70-73.

[0183] *Agrobacterium tumefaciens-meditated* transformation techniques are well described in the scientific literature (see, e.g., Horsch et al., 1984, Science, 233:496-498; and Fraley et al., 1983, Proc. Natl. Acad. Sci. USA, 80:4803).

[0184] Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired TALE repeat array protein-controlled phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the TALE repeat array protein nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., Protoplasts Isolation and Culture, Handbook of Plant Cell Culture, pp. 124-176 (1983); and Binding, Regeneration of Plants, Plant Protoplasts, pp. 21-73 (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al., 1987, Ann. Rev. Plant Phys., 38:467-486.

Functional Genomics Assays

[0185] Engineered TALE repeat array proteins also have use for assays to determine the phenotypic consequences and function of gene expression. Recent advances in analytical techniques, coupled with focused mass sequencing efforts have created the opportunity to identify and characterize many more molecular targets than were previously available. This new information about genes and their functions will improve basic biological understanding and present many new targets for therapeutic intervention. In some cases analytical tools have not kept pace with the generation of new data. An example is provided by recent advances in the measurement of global differential gene expression. These methods, typified by gene expression microarrays, differential cDNA cloning frequencies, subtractive hybridization and differential display methods, can very rapidly identify genes that are up or down-regulated in different tissues or in response to specific stimuli. Increasingly, such methods are being used to explore biological processes such as, transformation, tumor progression, the inflammatory response, neurological disorders etc. Many differentially expressed genes correlate with a given physiological phenomenon, but demonstrating a causative relationship between an individual differentially expressed gene and the phenomenon is labor intensive. Until now, simple methods for assigning function to differentially expressed genes have not kept pace with the ability to monitor differential gene expression.

[0186] The engineered TALE repeat array proteins described herein can be used to rapidly analyze the function of a differentially expressed gene. Engineered TALE proteins can be readily used to up or down-regulate or knockout any endogenous target gene, or to knock in an endogenous or endogenous gene. Very little sequence information is required to create a gene-specific DNA binding domain. This makes the engineered TALE repeat array technology ideal for analysis of long lists of poorly characterized differentially expressed genes. One can simply build a TALE repeat array protein-based DNA binding domain for each candidate gene, create chimeric up and down-regulating artificial transcription factors and test the consequence of up or down-regulation on the phenotype under study (e.g., transformation or response to a cytokine) by switching the candidate genes on or off one at a time in a model system.

[0187] Additionally, greater experimental control can be imparted by engineered TALE repeat array proteins than can be achieved by more conventional methods. This is because the production and/or function of engineered TALE repeat array proteins can be placed under small molecule control. Examples of this approach are provided by the Tet-On system, the ecdysone-regulated system and a system incorporating a chimeric factor including a mutant progesterone receptor. These systems are all capable of indirectly imparting small molecule control on any endogenous gene of interest or any transgene by placing the function and/or expression of a engineered TALE repeat array protein under small molecule control.

Transgenic Animals

[0188] A further application of engineered TALE repeat array proteins is manipulating gene expression in animal models. As with cell lines, the introduction of a heterologous gene into or knockout of an endogenous in a transgenic animal, such as a transgenic mouse or zebrafish, is a fairly straightforward process. Thus, transgenic or transient expression of an engineered TALE repeat array protein in an animal can be readily performed.

[0189] By transgenically or transiently expressing a suitable engineered TALE repeat array protein fused to an activation domain, a target gene of interest can be over-expressed. Similarly, by transgenically or transiently expressing a suitable engineered TALE repeat array protein fused to a repressor or silencer domain, the expression of a target gene of interest can be down-regulated, or even switched off to create "functional knockout". Knock-in or knockout mutations by insertion or deletion of a target gene of interest can be prepared using TALE nucleases.

[0190] Two common issues often prevent the successful application of the standard transgenic and knockout technology; embryonic lethality and developmental compensation. Embryonic lethality results when the gene plays an essential role in development. Developmental compensation is the substitution of a related gene product for the gene product being knocked out, and often results in a lack of a phenotype in a knockout mouse when the ablation of that gene's function would otherwise cause a physiological change.

[0191] Expression of transgenic engineered TALE repeat array proteins can be temporally controlled, for example using small molecule regulated systems as described in the previous section. Thus, by switching on expression of an engineered TALE repeat array protein at a desired stage in development, a gene can be over-expressed or "functionally knocked-out" in the adult (or at a late stage in development), thus avoiding the problems of embryonic lethality and developmental compensation.

EXAMPLES

Example 1

Assembly of TALE Repeat Arrays Using Streptavidin Coated Magnetic Beads

[0192] An archive of DNA plasmids (~850 different plasmids) encoding one, two, three, or four TALE repeat domains was created for assembly of nucleic acids encoding multiple TALE arrays of any desired length. The plasmids were created by cloning synthetic arrays of one, two, three or four TALE repeat domains into the pUC57-ΔBsaI backbone (FIG. **3**). The TALE repeats were of the arrangement α, βγδϵ, βγδ, βγ', βγ, δϵ', and β, and included hypervariable triplet residues at each position to bind to the nucleotides as shown in Table 1. Polypeptide and nucleotide sequences of the TALE repeat types are shown in FIGS. **4**A and **4**B, respectively. The polypeptide and polynucleotide sequences were varied slightly among the four types to reduce the possibility of recombination-mediated mutations due to long sequences of exact repeats.

TABLE 1

Nucleotide binding code of TALE triplets

Triplet	Bound Nucleotide
SNI	A
SHD	C
NNN	G
SNK	G
SNG	T

[0193] A 16-mer TALE repeat array targeted to the eGFP gene was created by in vitro assembly of 16 TALE repeats designed to bind the target sequence GCAGTGCTTCAGCCGC (SEQ ID NO: 41). In the first step, a plasmid carrying an α-type TALE repeat with an NNN triplet (G) was amplified by PCR using a biotinylated forward primer Biotin-TCTAGAGAAGACAAGAACCTGACC (SEQ ID NO: 42) and a reverse primer GGATCCGGTCTCTTAAGGCCGTGG (SEQ ID NO: 43). The amplified fragment (50 μl) was purified using a QIA Quick PCR purification kit (QIAGEN), eluted in 40 μl 0.1× elution buffer (as provided in the QIA Quick PCR purification kit), and digested with BsaI HF (New England Biolabs (NEB)) in NEB Buffer 4 for 15 minutes at 50° C. (40 μl elution, 5 μl NEBuffer 4, 5 μl BsaI HF). The digested fragment was purified using a QIA Quick PCR purification kit and eluted in 0.1× elution buffer (50 μA).

[0194] A plasmid containing a four TALE repeat domain sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids SHD, SNI, NNN, and SNG (designed to bind the sequence 5'-CAGY3') was digested with BbsI (NEB) in NEBuffer 2 for 2 hours at 37° C. in 100 μl (50 μl plasmid [~200 ng/μl], 10 μl NEBuffer 2, 10 μl BbsI, 30 μl water). To the 100 μl digest was added 25 μl NEBuffer 4, 2.5 μl 100×BSA (NEB), 107.5 μl water, and 5 μl XbaI (NEB), and the digest was incubated for 5 minutes at 37° C. To the mixture, 5 μl of BamHI HF was then added for a 5 minute digest at 37° C., and then 5 μl SalI HF (NEB) was added for an additional 5 minute digest at 37° C. The resulting fragment was purified using a QIA Quick PCR purification kit (QIAGEN) and eluted in 180 μl 0.1× elution buffer.

[0195] For the initial ligation, 2 μl of the alpha unit digest was mixed with 2.5 μl of T4 DNA ligase (400 U/μl; NEB) and 27 μl Quick Ligase Buffer (QLB) (NEB). To this 31.5 μl mixture was added 22.5 μl of the first digested subarray, and the mixture was ligated for 15 minutes at room temperature. Magnetic beads were prepared by washing 5 μl of Dynabeads MyOne Streptavidin Cl (Invitrogen) three times with 50 μl 1×B&W Buffer (5.0 mM Tris-HCl [pH 7.5], 0.5 mM EDTA, 1.0 M NaCl, 0.005% Tween 20) and resuspending in 54 μl B&W Buffer. The ligated mixture was added to the washed beads and incubated for 15 minutes at room temperature (with mixing every five minutes). The mixture was then placed on a SPRIplate 96-well Ring magnet for 3 minutes. The supernatant was then aspirated, and 100 μl 1×B&W Buffer was added to wash, with mixing by moving the beads 31 times from side to side within the tube using a DynaMag-96 Side magnet (Invitrogen). The B&W Buffer was then aspirated, and 100 μl 1×BSA was added, with mixing, then aspirated. The ligated, bead-bound nucleic acids (αβγδϵ) were resuspended in 50 μl BsaI HF mix (5 μl NEBuffer 4, 2 μl BsaI HF, 43 μl water).

[0196] The digest was incubated at 50° C. for 10 minutes, and 50 μl 1×B&W buffer was added. The digest was placed on a magnet for 3 minutes, and the supernatant was aspirated. The beads were washed with 100 μl 1×B&W Buffer and 100 μl 1×BSA as above. To the washed beads were added a digested plasmid containing a four TALE repeat domain sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids NNN, SHD, SNG, and SNG (designed to bind the DNA sequence 5'-GCTT-3') (22.5 μl) and 27.5 μl ligase mix (25 μl Quick Ligase Buffer, 2 μl DNA ligase). The beads were resuspended by pipetting up and down, and the mixture was incubated for 15 minutes at room temperature with mixing every five minutes. To the ligation was added 50 μl 1×B&W Buffer, and the mixture was placed on the magnet for 3 minutes. The supernatant was aspirated, and the beads were washed with 100 μl 1×B&W Buffer and 100 μl 1×BSA as above. The ligated, bead-bound nucleic acids (αβγδϵβγδϵ) were resuspended in 50 μl BsaI HF mix (5 μl NEBuffer 4, 2 μl BsaI HF, 43 μl water). Two more TALE repeat sub-array units were ligated sequentially as above, the first a four TALE repeat sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids SHD, SNI, NNN, and SHD (designed to bind the DNA sequence 5'-CAGC-3') and the second a three TALE repeat sub-array unit (βγδ) coding for repeats that each harbor one of the following variable amino acids SHD, NNN, and SHD (designed to bind the DNA sequence 5'-CGC-3'). The final TALE repeat array contained subunits of the format αβγδϵ-βγδϵβγδϵβγδ with individual TALE repeats designed to bind the target DNA sequence 5'-GCAGTGCTTCAGCCGC-3' (SEQ ID NO: 44).

[0197] Following the final ligation step, the construct was digested with BsaI HF for eventual cloning into an expression vector and the beads were washed with 1×B&W Buffer and 1×BSA. The washed beads were resuspended in 50 μl BbsI mix (5 μl NEBuffer 2, 5 μl BbsI, 40 μl water) and incubated at 37° C. for 2 hours with agitation at 1500 rpm to cleave the biotinylated 5' end and release the assembled TALE repeat array from the magnetic beads. The digested mixture was purified by MinElute column purified (QIAGEN) and ligated into a BsmBI-digested TALE expression vector. The ligated mixture was transformed into chemically competent XL1 Blue cells and plated on LB/Carb^{100} plates overnight.

[0198] The expression vectors each harbor the following elements: a T7 promoter, a nuclear localization signal, a FLAG tag, amino acids 153 to 288 from the TALE13 protein (numbering as defined by Miller et al., 2011, Nat. Biotechnol., 29:143-148), two adjacent BsmBI restriction sites into which a DNA fragment encoding a TALE repeat array can be cloned, a 0.5 TALE repeat, amino acids 715 to 777 from the C-terminal end of the TALE13 protein (numbering as defined by Miller et al., 2011, Nat. Biotechnol., 29:143-148), and the wild-type FokI cleavage domain.

[0199] The plasmids differ in the identity of the C-terminal 0.5 TALE repeat. Plasmid pJDS70 encodes a 0.5 TALE repeat with a SNI RVD (for recognition of an A nucleotide), plasmid pJDS71 encodes a 0.5 TALE repeat with a SHD RVD (for recognition of a C nucleotide), plasmid pJDS74 encodes a 0.5 TALE repeat with a NNN RVD (for recognition of a G nucleotide), plasmid pJDS76 encodes a 0.5 TALE repeat with a SNK RVD (for recognition of a G nucleotide), and plasmid pJDS78 encodes a 0.5 TALE repeat with a NG RVD (for recognition of a T nucleotide). All plasmids share the common sequence shown in FIGS. **5**A-**5**B and differ at just nine nucleotide positions marked as XXXXXXXXX (underlined and bold). The sequence of these 9 bps and plasmid names are also shown below in Table 2.

TABLE 2

DNA sequences of expression vectors

Plasmid name	Sequence of variable 9 bps	SEQ ID NO:	RVD of C-terminal 0.5 TALE repeat
pJDS70	TCTAACATC	45	SNI (for binding to an A nucleotide)
pJDS71	TCCCACGAC	46	SHD (for binding to a C nucleotide)
pJDS74	AATAATAAC	47	NNN (for binding to a G nucleotide)
pJDS76	TCCAATAAA	48	SNK (for binding to a G nucleotide)
pJDS78	TCTAATGGG	49	SNG (for binding to a T nucleotide)

[0200] This example demonstrates the construction of TALE repeat arrays on an immobilized substrate using preassembled TALE repeat sub-array units. The above method, up to the cloning step, can be performed in one day.

Example 2

Assembly of TALE Repeat Arrays Using a Streptavidin Coated Plate

[0201] TALE repeats are assembled using the archive of DNA plasmids (~850 different plasmids) as described in Example 1. A 16-mer TALE repeat array was created by in vitro assembly of 16 TALE repeats designed to bind a target sequence. In the first step, a plasmid carrying an α-type TALE repeat with an NNN triplet (G) was amplified by PCR using a biotinylated forward primer Biotin-TCTAGAGAAGACAAGAACCTGACC (SEQ ID NO: 42) and a reverse primer GGATCCGGTCTCTTAAGGCCGTGG (SEQ ID NO: 43). The amplified fragment (50 μl) was purified using a QIA Quick PCR purification kit (QIAGEN), eluted in 40 μl 0.1× elution buffer (as provided in the QIA Quick PCR purification kit), and digested with BsaI HF (New England Biolabs (NEB)) in NEB Buffer 4 for 15 minutes at 50° C. (40 μl elution, 5 μl NEBuffer 4, 5 μl BsaI HF). The digested fragment was purified using a QIA Quick PCR purification kit and eluted in 0.1× elution buffer (50 μl).

[0202] A plasmid containing a four TALE repeat domain sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids SHD, SNI, NNN, and SNG (designed to bind the sequence 5'-CAGY3') was digested with BbsI (NEB) in NEBuffer 2 for 2 hours at 37° C. in 100 μl (50 μl plasmid [~200 ng/μl], 10 μl NEBuffer 2, 10 μl BbsI, 30 μl water). To the 100 μl digest was added 25 μl NEBuffer 4, 2.5 μl 100×BSA (NEB), 107.5 μl water, and 5 μl XbaI (NEB), and the digest was incubated for 5 minutes at 37° C. To the mixture, 5 μl of BamHI HF was then added for a 5 minute digest at 37° C., and then 5 μl SalI HF (NEB) was added for an additional 5 minute digest at 37° C. The resulting fragment was purified using a QIA Quick PCR purification kit (QIAGEN) and eluted in 180 μl 0.1× elution buffer.

[0203] For the initial ligation, 2 μl of the alpha unit digest was mixed with 2.5 μl of T4 DNA ligase (400 U/μ1; NEB) and 27 μl Quick Ligase Buffer (QLB) (NEB). To this 31.5 μl mixture was added 22.5 μl of the first digested subarray, and the mixture was ligated for 15 minutes at room temperature. The ligation mixture was then mixed with 2×B&@ buffer (Invitrogen) and added to a well in a 96-well plate coated with streptavidin (Thermo Scientific) and incubated at room temperature for 15 min. The supernatant was aspirated. Each well in the 96 well plate was washed with 200 μl of 1× Bovine Serum Albumin (BSA) by pipetting up and down 10 times before discarding the 1×BSA. This was repeated for a total of two washes with 1×BSA. Then 50 μl BsaI HF mix (5 μl NEBuffer 4, 2 μl BsaI HF, 43 μl water) was added to the ligated, nucleic acids (αβγδϵ) bound to the streptavidin-coated well.

[0204] The digest was incubated at 50° C. for 10 minutes and then the supernatant was aspirated. The wells were then washed with 200 μl 1×B&W Buffer and 200 μl 1×BSA twice by pipetting up and down ten times before removal of each supernatant. 22.5 μl of digested plasmid encoding a four TALE repeat domain sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids NNN, SHD, SNG, and SNI and 27.5 μl ligase mix (25 μl Quick Ligase Buffer, 2 μl DNA ligase) were added to the well. The supernatant was mixed by pipetting up and down, and the mixture was incubated for 15 minutes at room temperature. The supernatant was removed and the well was washed with 1×B&W and 1×BSA as above. Then 50 μl BsaI HF mix (5 μl NEBuffer 4, 2 μl BsaI HF, 43 μl water) was added to the ligated nucleic acids (αβγδϵβγδϵ) bound to the well. Two more TALE repeat sub-array units were ligated sequentially as above, the first a four TALE repeat sub-array unit (βγδϵ) coding for repeats that each harbor one of the following variable amino acids SHD, SNI, NNN, and SNG and the second a three TALE repeat sub-array unit (βγδ) coding for repeats that each harbor one of the following variable amino acids SHD, SNI, NNN, and SHD. The final TALE repeat array contained subunits of the format αβγδϵβγδϵβγδϵβγδ with individual TALE repeats designed to bind a target DNA sequence.

[0205] Following the final ligation step, the fragments in the well were digested with BsaI HF for eventual cloning into an expression vector. The well was then washed with 1×B&W Buffer and twice with 1×BSA. Then 50 μl BbsI mix (5 μl NEBuffer 2, 5 μl BbsI, 40 μl water) was added to the well and incubated at 37° C. for 2 hours to cleave the biotinylated 5' end and release the assembled TALE repeat array from the well. The digested mixture was purified, ligated, and transformed as described in Example 1.

Example 3

Site-Specific Mutagenesis Using TALE Nucleases

[0206] To demonstrate the effectiveness of TALE repeat domains created by the methods described herein, TALE repeat arrays were constructed and cloned into TALE nuclease expression vectors (as described in Example 1) to produce plasmids encoding TALE nuclease monomers targeted to the eGFP coding sequences shown in FIG. **6** and Table 3. Nucleic acid and polypeptide sequences of the TALE nuclease monomers are shown in FIGS. **11**A-**18**B.

TABLE 3

TALE nuclease monomer target sequences

TALE Fragment	Target Sequence	Length of target sequence	SEQ ID NO:	Site	Position (half-site)	Plasmid name
DR-TALE-0003	TGCAGTGCTTCAGCCGC	17	50	eGFP223	left	SQT70
DR-TALE-0006	TGCAGTGCTTCAGCCGCT	18	51	eGFP223	left	SQT114
DR-TALE-0005	TTGAAGAAGTCGTGCTGC	18	52	eGFP223	right	SQT72
DR-TALE-0010	TGAAGAAGTCGTGCTGCT	18	53	eGFP223	right	SQT56
DR-TALE-0023	TCGAGCTGAAGGGCATC	17	54	eGFP382	left	SQT84
DR-TALE-0025	TCGAGCTGAAGGGCATCG	18	55	eGFP382	left	SQT120
DR-TALE-0020	TTGTGCCCCAGGATGTTG	18	56	eGFP382	right	SQT135
DR-TALE-0022	TGTGCCCCAGGATGTTGC	18	57	eGFP382	right	SQT118

[0207] 4E5 U2OS-eGFP cells were nucleofected with 400 ng plasmid DNA in solution SE with program DN-100 using Nucleofector™ non-viral transfection (Lonza, Walkersville, Md.). The cells were analyzed by flow cytometry at days 2 and 5 (FIG. **7**). Non-homologous end joining (NHEJ)-mediated mutagenic repair of TALE nuclease-induced double-stranded breaks led to disruption of eGFP expression (eGFP-negative cells). All eight TALE nuclease pairs tested induced a high percentage of eGFP-negative (eGFP−) cells (y-axis). The percentage of eGFP− cells declined only modestly between day 2 and 5 suggesting that the alterations were stably induced.

[0208] A subset of mutated eGFP genes were amplified from cells and sequenced. The resulting mutations are shown in FIG. **8**. Sequences targeted by the TALE nucleases encoded by expression plasmids SQT70/SQT56 in human USOS-eGFP cells are underlined in the wild-type (WT) sequence shown at the top of FIG. **8**. Insertion and deletion mutations induced by the TALE nuclease pair are shown below with deleted bases indicated by dashes and inserted bases indicated by double underlining. The net number of bases inserted or deleted is shown to the right. All mutations were isolated once unless otherwise indicated in brackets. The overall frequency of mutagenesis (46%) is also indicated.

Example 4

Automated Assembly of TALE Repeat Arrays

[0209] The assembly method described in Example 1 has been automated so as to be performed using a Sciclone™ G3 liquid handling workstation (Caliper Life Sciences, Hopkinton, Mass.) in 96-well plates. All of the steps were automated except digestion of the nucleic acids prior to ligation and linking to the beads and the steps following release of the assembled TALE repeat array from the magnetic beads. The automated steps were performed essentially as when done manually with minor variations in the number of resuspension and mixing motions. The results of assembly of two 17-mers are shown in FIG. **9**. A major product of the expected size can be seen, corresponding to the 17-mer. Additional minor 13-mer, 9-mer, and 5-mer products can also be seen, likely produced by carry forward of incompletely ligated products. A similar result can be seen in FIG. **10**, which shows the results of assembly of 16-mers from an N-terminal 1-mer sub-array (1), three 4-mer subarrays (4_A, 4_B, 4_C), and a C-terminal 3-mer subarray (3_D).

[0210] This example demonstrates that the methods described herein can be automated for rapid and reproducible synthesis of nucleic acids encoding TALE repeat arrays.

Example 5

Assembly Methods

[0211] TALE repeat arrays were created using an architecture in which four distinct TALE repeat backbones that differ slightly in their amino acid and DNA sequences occur in a repeated pattern. The first, amino-terminal TALE repeat in an array was designated as the α unit. This was followed by β, γ, and δ units and then an c unit that is essentially identical to the α unit except for the different positioning of a Type IIS restriction site on the 5' end (required to enable creation of a unique overhang on the α unit needed for cloning). The ϵ unit was then followed again by repeats of β, γ, δ, and ϵ units. Due to constraints related to creation of a 3' end required for cloning, slightly modified DNA sequences were required for TALE repeat arrays that end with a carboxy-terminal γ or ϵ unit. We designated these variant units as γ* and ϵ*.

[0212] For each type of TALE repeat unit (i.e.—α, β, γ, δ, ϵ, γ*, and ϵ*), we commercially synthesized (Genscript) a series of four plasmids, each harboring one of the five repeat variable di-residues (RVDs) that specifies one of the four DNA bases (NI=A; HD=C; NN=G; NG=T, NK=G). Full DNA sequences of these plasmids are provided in Table 4 and FIG. **3**. For all 35 of these plasmids, the sequence encoding the TALE repeat domain is flanked on the 5' end by unique XbaI and BbsI restriction sites and on the 3' end by unique BsaI and BamHI restriction sites. Additionally, the overhangs generated by digestion of any plasmids encoding units designed to be adjacent to one another (e.g.—β and γ, or δ and ϵ) with BsaI and BbsI are complementary. Using these 35 different plasmids and serial ligation via the BsaI and BbsI restriction sites, we assembled an archive of all possible combinations of βγ, βγδϵ, βγδ, βγ*, and δϵ* repeats. In total, this archive consisted of 825 different plasmids encoding 5 α's, 5 β's, 25 βγ combinations, 625 βγδϵ combinations, 125 βγδ combinations, 25 βγ* combinations, and 25 δϵ* combinations (Table 5). These 825 plasmids plus ten of the original 35 plasmids encoding single TALE repeats (five α and five β plasmids) are required to practice the methods. With this archive of 835 plasmids listed in Table 5, the methods can be used to construct TALE repeat arrays of any desired length and composition.

TABLE 4

DNA sequences encoding individual TALE repeats

TAL ID#	Unit Architecture	RVD	Target Base	DNA Sequence (Cloned between Xbal/BamHI in pUC57-ΔBsal)	SEQ ID NO:
6	α	NI	A	TCTAGAGAAGACAAGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAAGAGACCGGATCC	58
7	α	HD	C	TCTAGAGAAGACAAGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAAGAGACCGGATCC	59
8	α	NK	G	TCTAGAGAAGACAAGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACAAAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAAGAGACCGGATCC	60
9	α	NN	G	TCTAGAGAAGACAAGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAAGAGACCGGATCC	61
10	α	NG	T	TCTAGAGAAGACAAGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTAAGAGACCGGATCC	62

TABLE 4-continued

DNA sequences encoding individual TALE repeats

TAL ID#	Unit Architecture	RVD	Target Base	DNA Sequence (Cloned between Xbal/BamHI in pUC57-ΔBsal)	SEQ ID NO:
11	β	NI	A	TCTAGAGAAGACAACTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGAAGAGACCGGATCC	63
12	β	HD	C	TCTAGAGAAGACAACTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGAAGAGACCGGATCC	64
13	β	NK	G	TCTAGAGAAGACAACTTACACCGGAGCAAGTCGTGGCCATTGCATCAAATAAAGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGAAGAGACCGGATCC	65
14	β	NN	G	TCTAGAGAAGACAACTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGAAGAGACCGGATCC	66
15	β	NG	T	TCTAGAGAAGACAACTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGAAGAGACCGGATCC	67
16	γ	NI	A	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAAGAGACCGGATCC	68
17	γ	HD	C	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAAGAGACCGGATCC	69
18	γ	NK	G	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACAAGGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAAGAGACCGGATCC	70
19	γ	NN	G	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAAGAGACCGGATCC	71
20	γ	NG	T	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAAGAGACCGGATCC	72

TABLE 4-continued

DNA sequences encoding individual TALE repeats

TAL Unit ID#	Architecture	RVD	Target Base	DNA Sequence (Cloned between Xbal/BamHI in pUC57-ΔBsal)	SEQ ID NO:
21	δ	NI	A	TCTAGAGAAGACAATTGACGCCTG CACAAGTGGTCGCCATCGCCTCCA ATATTGGCGGTAAGCAGGCGCTGG AAACAGTACAGCGCCTGCTGCCTG TACTGTGCCAGGATCATGGACTGA AGAGACCGGATCC	73
22	δ	HD	C	TCTAGAGAAGACAATTGACGCCTG CACAAGTGGTCGCCATCGCCAGCC ATGATGGCGGTAAGCAGGCGCTGG AAACAGTACAGCGCCTGCTGCCTG TACTGTGCCAGGATCATGGACTGA AGAGACCGGATCC	74
23	δ	NK	G	TCTAGAGAAGACAATTGACGCCTG CACAAGTGGTCGCCATCGCCAGCA ATAAGGGCGGTAAGCAGGCGCTGG AAACAGTACAGCGCCTGCTGCCTG TACTGTGCCAGGATCATGGACTGA AGAGACCGGATCC	75
24	δ	NN	G	TCTAGAGAAGACAATTGACGCCTG CACAAGTGGTCGCCATCGCCAACA ACAACGGCGGTAAGCAGGCGCTGG AAACAGTACAGCGCCTGCTGCCTG TACTGTGCCAGGATCATGGACTGA AGAGACCGGATCC	76
25	δ	NG	T	TCTAGAGAAGACAATTGACGCCTG CACAAGTGGTCGCCATCGCCTCGA ATGGCGGCGGTAAGCAGGCGCTGG AAACAGTACAGCGCCTGCTGCCTG TACTGTGCCAGGATCATGGACTGA AGAGACCGGATCC	77
26	ϵ	NI	A	TCTAGAGAAGACAACTGACCCCAG ACCAGGTAGTCGCAATCGCGTCGA ACATTGGGGGAAAGCAAGCCCTGG AAACCGTGCAAAGGTTGTTGCCGG TCCTTTGTCAAGACCACGGCCTTA AGAGACCGGATCC	78
27	ϵ	HD	C	TCTAGAGAAGACAACTGACCCCAG ACCAGGTAGTCGCAATCGCGTCAC ATGACGGGGGAAAGCAAGCCCTGG AAACCGTGCAAAGGTTGTTGCCGG TCCTTTGTCAAGACCACGGCCTTA AGAGACCGGATCC	79
28	ϵ	NK	G	TCTAGAGAAGACAACTGACCCCAG ACCAGGTAGTCGCAATCGCGTCGA ACAAAGGGGGAAAGCAAGCCCTGG AAACCGTGCAAAGGTTGTTGCCGG TCCTTTGTCAAGACCACGGCCTTA AGAGACCGGATCC	80
29	ϵ	NN	G	TCTAGAGAAGACAACTGACCCCAG ACCAGGTAGTCGCAATCGCGAACA ATAATGGGGGAAAGCAAGCCCTGG AAACCGTGCAAAGGTTGTTGCCGG TCCTTTGTCAAGACCACGGCCTTA AGAGACCGGATCC	81
30	ϵ	NG	T	TCTAGAGAAGACAACTGACCCCAG ACCAGGTAGTCGCAATCGCGTCAA ACGGAGGGGGAAAGCAAGCCCTGG AAACCGTGCAAAGGTTGTTGCCGG TCCTTTGTCAAGACCACGGCCTTA AGAGACCGGATCC	82

TABLE 4-continued

DNA sequences encoding individual TALE repeats

TALUnit ID#	Architecture	RVD	Target Base	DNA Sequence (Cloned between Xbal/BamHI in pUC57-ΔBsal)	SEQ ID NO:
31	γ'	NI	A	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGAAGAGACCGGATCC	83
32	γ'	HD	C	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGAAGAGACCGGATCC	84
33	γ'	NK	G	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACAAGGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGAAGAGACCGGATCC	85
34	γ'	NN	G	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGAAGAGACCGGATCC	86
35	γ'	NG	T	TCTAGAGAAGACAACTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGAAGAGACCGGATCC	87
36	ϵ'	NI	A	TCTAGAGAAGACAACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTGAAGAGACCGGATCC	88
37	ϵ'	HD	C	TCTAGAGAAGACAACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTGAAGAGACCGGATCC	89
38	ϵ'	NK	G	TCTAGAGAAGACAACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACAAAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTGAAGAGACCGGATCC	90
39	ϵ'	NN	G	TCTAGAGAAGACAACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTGAAGAGACCGGATCC	91
40	ϵ'	NG	T	TCTAGAGAAGACAACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTGAAGAGACCGGATCC	92

TABLE 5

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL006	A	NI	α
TAL007	C	HD	α
TAL008	G	NK	α
TAL009	G	NN	α
TAL010	T	NG	α
TAL011/016/021/026	AAAA	NI/NI/NI/NI	βγδϵ
TAL011/016/021/027	AAAC	NI/NI/NI/HD	βγδϵ
TAL011/016/021/028	AAAG	NI/NI/NI/NK	βγδϵ
TAL011/016/021/029	AAAG	NI/NI/NI/NN	βγδϵ
TAL011/016/021/030	AAAT	NI/NI/NI/NG	βγδϵ
TAL011/016/022/026	AACA	NI/NI/HD/NI	βγδϵ
TAL011/016/022/027	AACC	NI/NI/HD/HD	βγδϵ
TAL011/016/022/028	AACG	NI/NI/HD/NK	βγδϵ
TAL011/016/022/029	AACG	NI/NI/HD/NN	βγδϵ
TAL011/016/022/030	AACT	NI/NI/HD/NG	βγδϵ
TAL011/016/023/026	AAGA	NI/NI/NK/NI	βγδϵ
TAL011/016/023/027	AAGC	NI/NI/NK/HD	βγδϵ
TAL011/016/023/028	AAGG	NI/NI/NK/NK	βγδϵ
TAL011/016/023/029	AAGG	NI/NI/NK/NN	βγδϵ
TAL011/016/023/030	AAGT	NI/NI/NK/NG	βγδϵ
TAL011/016/024/026	AAGA	NI/NI/NN/NI	βγδϵ
TAL011/016/024/027	AAGC	NI/NI/NN/HD	βγδϵ
TAL011/016/024/028	AAGG	NI/NI/NN/NK	βγδϵ
TAL011/016/024/029	AAGG	NI/NI/NN/NN	βγδϵ
TAL011/016/024/030	AAGT	NI/NI/NN/NG	βγδϵ
TAL011/016/025/026	AATA	NI/NI/NG/NI	βγδϵ
TAL011/016/025/027	AATC	NI/NI/NG/HD	βγδϵ
TAL011/016/025/028	AATG	NI/NI/NG/NK	βγδϵ
TAL011/016/025/029	AATG	NI/NI/NG/NN	βγδϵ
TAL011/016/025/030	AATT	NI/NI/NG/NG	βγδϵ
TAL011/017/021/026	ACAA	NI/HD/NI/NI	βγδϵ
TAL011/017/021/027	ACAC	NI/HD/NI/HD	βγδϵ
TAL011/017/021/028	ACAG	NI/HD/NI/NK	βγδϵ
TAL011/017/021/029	ACAG	NI/HD/NI/NN	βγδϵ
TAL011/017/021/030	ACAT	NI/HD/NI/NG	βγδϵ
TAL011/017/022/026	ACCA	NI/HD/HD/NI	βγδϵ
TAL011/017/022/027	ACCC	NI/HD/HD/HD	βγδϵ
TAL011/017/022/028	ACCG	NI/HD/HD/NK	βγδϵ
TAL011/017/022/029	ACCG	NI/HD/HD/NN	βγδϵ
TAL011/017/022/030	ACCT	NI/HD/HD/NG	βγδϵ
TAL011/017/023/026	ACGA	NI/HD/NK/NI	βγδϵ
TAL011/017/023/027	ACGC	NI/HD/NK/HD	βγδϵ
TAL011/017/023/028	ACGG	NI/HD/NK/NK	βγδϵ
TAL011/017/023/029	ACGG	NI/HD/NK/NN	βγδϵ
TAL011/017/023/030	ACGT	NI/HD/NK/NG	βγδϵ
TAL011/017/024/026	ACGA	NI/HD/NN/NI	βγδϵ
TAL011/017/024/027	ACGC	NI/HD/NN/HD	βγδϵ
TAL011/017/024/028	ACGG	NI/HD/NN/NK	βγδϵ
TAL011/017/024/029	ACGG	NI/HD/NN/NN	βγδϵ
TAL011/017/024/030	ACGT	NI/HD/NN/NG	βγδϵ
TAL011/017/025/026	ACTA	NI/HD/NG/NI	βγδϵ
TAL011/017/025/027	ACTC	NI/HD/NG/HD	βγδϵ
TAL011/017/025/028	ACTG	NI/HD/NG/NK	βγδϵ
TAL011/017/025/029	ACTG	NI/HD/NG/NN	βγδϵ
TAL011/017/025/030	ACTT	NI/HD/NG/NG	βγδϵ
TAL011/018/021/026	AGAA	NI/NK/NI/NI	βγδϵ
TAL011/018/021/027	AGAC	NI/NK/NI/HD	βγδϵ
TAL011/018/021/028	AGAG	NI/NK/NI/NK	βγδϵ
TAL011/018/021/029	AGAG	NI/NK/NI/NN	βγδϵ
TAL011/018/021/030	AGAT	NI/NK/NI/NG	βγδϵ
TAL011/018/022/026	AGCA	NI/NK/HD/NI	βγδϵ
TAL011/018/022/027	AGCC	NI/NK/HD/HD	βγδϵ
TAL011/018/022/028	AGCG	NI/NK/HD/NK	βγδϵ
TAL011/018/022/029	AGCG	NI/NK/HD/NN	βγδϵ
TAL011/018/022/030	AGCT	NI/NK/HD/NG	βγδϵ
TAL011/018/023/026	AGGA	NI/NK/NK/NI	βγδϵ
TAL011/018/023/027	AGGC	NI/NK/NK/HD	βγδϵ
TAL011/018/023/028	AGGG	NI/NK/NK/NK	βγδϵ
TAL011/018/023/029	AGGG	NI/NK/NK/NN	βγδϵ
TAL011/018/023/030	AGGT	NI/NK/NK/NG	βγδϵ
TAL011/018/024/026	AGGA	NI/NK/NN/NI	βγδϵ
TAL011/018/024/027	AGGC	NI/NK/NN/HD	βγδϵ
TAL011/018/024/028	AGGG	NI/NK/NN/NK	βγδϵ
TAL011/018/024/029	AGGG	NI/NK/NN/NN	βγδϵ
TAL011/018/024/030	AGGT	NI/NK/NN/NG	βγδϵ
TAL011/018/025/026	AGTA	NI/NK/NG/NI	βγδϵ
TAL011/018/025/027	AGTC	NI/NK/NG/HD	βγδϵ
TAL011/018/025/028	AGTG	NI/NK/NG/NK	βγδϵ
TAL011/018/025/029	AGTG	NI/NK/NG/NN	βγδϵ
TAL011/018/025/030	AGTT	NI/NK/NG/NG	βγδϵ
TAL011/019/021/026	AGAA	NI/NN/NI/NI	βγδϵ
TAL011/019/021/027	AGAC	NI/NN/NI/HD	βγδϵ
TAL011/019/021/028	AGAG	NI/NN/NI/NK	βγδϵ
TAL011/019/021/029	AGAG	NI/NN/NI/NN	βγδϵ
TAL011/019/021/030	AGAT	NI/NN/NI/NG	βγδϵ
TAL011/019/022/026	AGCA	NI/NN/HD/NI	βγδϵ
TAL011/019/022/027	AGCC	NI/NN/HD/HD	βγδϵ
TAL011/019/022/028	AGCG	NI/NN/HD/NK	βγδϵ
TAL011/019/022/029	AGCG	NI/NN/HD/NN	βγδϵ
TAL011/019/022/030	AGCT	NI/NN/HD/NG	βγδϵ
TAL011/019/023/026	AGGA	NI/NN/NK/NI	βγδϵ
TAL011/019/023/027	AGGC	NI/NN/NK/HD	βγδϵ
TAL011/019/023/028	AGGG	NI/NN/NK/NK	βγδϵ
TAL011/019/023/029	AGGG	NI/NN/NK/NN	βγδϵ
TAL011/019/023/030	AGGT	NI/NN/NK/NG	βγδϵ
TAL011/019/024/026	AGGA	NI/NN/NN/NI	βγδϵ
TAL011/019/024/027	AGGC	NI/NN/NN/HD	βγδϵ
TAL011/019/024/028	AGGG	NI/NN/NN/NK	βγδϵ
TAL011/019/024/029	AGGG	NI/NN/NN/NN	βγδϵ
TAL011/019/024/030	AGGT	NI/NN/NN/NG	βγδϵ
TAL011/019/025/026	AGTA	NI/NN/NG/NI	βγδϵ
TAL011/019/025/027	AGTC	NI/NN/NG/HD	βγδϵ
TAL011/019/025/028	AGTG	NI/NN/NG/NK	βγδϵ
TAL011/019/025/029	AGTG	NI/NN/NG/NN	βγδϵ
TAL011/019/025/030	AGTT	NI/NN/NG/NG	βγδϵ
TAL011/020/021/026	ATAA	NI/NG/NI/NI	βγδϵ
TAL011/020/021/027	ATAC	NI/NG/NI/HD	βγδϵ
TAL011/020/021/028	ATAG	NI/NG/NI/NK	βγδϵ
TAL011/020/021/029	ATAG	NI/NG/NI/NN	βγδϵ
TAL011/020/021/030	ATAT	NI/NG/NI/NG	βγδϵ
TAL011/020/022/026	ATCA	NI/NG/HD/NI	βγδϵ
TAL011/020/022/027	ATCC	NI/NG/HD/HD	βγδϵ
TAL011/020/022/028	ATCG	NI/NG/HD/NK	βγδϵ
TAL011/020/022/029	ATCG	NI/NG/HD/NN	βγδϵ
TAL011/020/022/030	ATCT	NI/NG/HD/NG	βγδϵ
TAL011/020/023/026	ATGA	NI/NG/NK/NI	βγδϵ
TAL011/020/023/027	ATGC	NI/NG/NK/HD	βγδϵ
TAL011/020/023/028	ATGG	NI/NG/NK/NK	βγδϵ
TAL011/020/023/029	ATGG	NI/NG/NK/NN	βγδϵ
TAL011/020/023/030	ATGT	NI/NG/NK/NG	βγδϵ
TAL011/020/024/026	ATGA	NI/NG/NN/NI	βγδϵ
TAL011/020/024/027	ATGC	NI/NG/NN/HD	βγδϵ
TAL011/020/024/028	ATGG	NI/NG/NN/NK	βγδϵ
TAL011/020/024/029	ATGG	NI/NG/NN/NN	βγδϵ
TAL011/020/024/030	ATGT	NI/NG/NN/NG	βγδϵ
TAL011/020/025/026	ATTA	NI/NG/NG/NI	βγδϵ
TAL011/020/025/027	ATTC	NI/NG/NG/HD	βγδϵ
TAL011/020/025/028	ATTG	NI/NG/NG/NK	βγδϵ
TAL011/020/025/029	ATTG	NI/NG/NG/NN	βγδϵ
TAL011/020/025/030	ATTT	NI/NG/NG/NG	βγδϵ
TAL012/016/021/026	CAAA	HD/NI/NI/NI	βγδϵ
TAL012/016/021/027	CAAC	HD/NI/NI/HD	βγδϵ
TAL012/016/021/028	CAAG	HD/NI/NI/NK	βγδϵ
TAL012/016/021/029	CAAG	HD/NI/NI/NN	βγδϵ
TAL012/016/021/030	CAAT	HD/NI/NI/NG	βγδϵ
TAL012/016/022/026	CACA	HD/NI/HD/NI	βγδϵ
TAL012/016/022/027	CACC	HD/NI/HD/HD	βγδϵ
TAL012/016/022/028	CACG	HD/NI/HD/NK	βγδϵ
TAL012/016/022/029	CACG	HD/NI/HD/NN	βγδϵ
TAL012/016/022/030	CACT	HD/NI/HD/NG	βγδϵ
TAL012/016/023/026	CAGA	HD/NI/NK/NI	βγδϵ
TAL012/016/023/027	CAGC	HD/NI/NK/HD	βγδϵ
TAL012/016/023/028	CAGG	HD/NI/NK/NK	βγδϵ
TAL012/016/023/029	CAGG	HD/NI/NK/NN	βγδϵ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL012/016/023/030	CAGT	HD/NI/NK/NG	βγδϵ
TAL012/016/024/026	CAGA	HD/NI/NN/NI	βγδϵ
TAL012/016/024/027	CAGC	HD/NI/NN/HD	βγδϵ
TAL012/016/024/028	CAGG	HD/NI/NN/NK	βγδϵ
TAL012/016/024/029	CAGG	HD/NI/NN/NN	βγδϵ
TAL012/016/024/030	CAGT	HD/NI/NN/NG	βγδϵ
TAL012/016/025/026	CATA	HD/NI/NG/NI	βγδϵ
TAL012/016/025/027	CATC	HD/NI/NG/HD	βγδϵ
TAL012/016/025/028	CATG	HD/NI/NG/NK	βγδϵ
TAL012/016/025/029	CATG	HD/NI/NG/NN	βγδϵ
TAL012/016/025/030	CATT	HD/NI/NG/NG	βγδϵ
TAL012/017/021/026	CCAA	HD/HD/NI/NI	βγδϵ
TAL012/017/021/027	CCAC	HD/HD/NI/HD	βγδϵ
TAL012/017/021/028	CCAG	HD/HD/NI/NK	βγδϵ
TAL012/017/021/029	CCAG	HD/HD/NI/NN	βγδϵ
TAL012/017/021/030	CCAT	HD/HD/NI/NG	βγδϵ
TAL012/017/022/026	CCCA	HD/HD/HD/NI	βγδϵ
TAL012/017/022/027	CCCC	HD/HD/HD/HD	βγδϵ
TAL012/017/022/028	CCCG	HD/HD/HD/NK	βγδϵ
TAL012/017/022/029	CCCG	HD/HD/HD/NN	βγδϵ
TAL012/017/022/030	CCCT	HD/HD/HD/NG	βγδϵ
TAL012/017/023/026	CCGA	HD/HD/NK/NI	βγδϵ
TAL012/017/023/027	CCGC	HD/HD/NK/HD	βγδϵ
TAL012/017/023/028	CCGG	HD/HD/NK/NK	βγδϵ
TAL012/017/023/029	CCGG	HD/HD/NK/NN	βγδϵ
TAL012/017/023/030	CCGT	HD/HD/NK/NG	βγδϵ
TAL012/017/024/026	CCGA	HD/HD/NN/NI	βγδϵ
TAL012/017/024/027	CCGC	HD/HD/NN/HD	βγδϵ
TAL012/017/024/028	CCGG	HD/HD/NN/NK	βγδϵ
TAL012/017/024/029	CCGG	HD/HD/NN/NN	βγδϵ
TAL012/017/024/030	CCGT	HD/HD/NN/NG	βγδϵ
TAL012/017/025/026	CCTA	HD/HD/NG/NI	βγδϵ
TAL012/017/025/027	CCTC	HD/HD/NG/HD	βγδϵ
TAL012/017/025/028	CCTG	HD/HD/NG/NK	βγδϵ
TAL012/017/025/029	CCTG	HD/HD/NG/NN	βγδϵ
TAL012/017/025/030	CCTT	HD/HD/NG/NG	βγδϵ
TAL012/018/021/026	CGAA	HD/NK/NI/NI	βγδϵ
TAL012/018/021/027	CGAC	HD/NK/NI/HD	βγδϵ
TAL012/018/021/028	CGAG	HD/NK/NI/NK	βγδϵ
TAL012/018/021/029	CGAG	HD/NK/NI/NN	βγδϵ
TAL012/018/021/030	CGAT	HD/NK/NI/NG	βγδϵ
TAL012/018/022/026	CGCA	HD/NK/HD/NI	βγδϵ
TAL012/018/022/027	CGCC	HD/NK/HD/HD	βγδϵ
TAL012/018/022/028	CGCG	HD/NK/HD/NK	βγδϵ
TAL012/018/022/029	CGCG	HD/NK/HD/NN	βγδϵ
TAL012/018/022/030	CGCT	HD/NK/HD/NG	βγδϵ
TAL012/018/023/026	CGGA	HD/NK/NK/NI	βγδϵ
TAL012/018/023/027	CGGC	HD/NK/NK/HD	βγδϵ
TAL012/018/023/028	CGGG	HD/NK/NK/NK	βγδϵ
TAL012/018/023/029	CGGG	HD/NK/NK/NN	βγδϵ
TAL012/018/023/030	CGGT	HD/NK/NK/NG	βγδϵ
TAL012/018/024/026	CGGA	HD/NK/NN/NI	βγδϵ
TAL012/018/024/027	CGGC	HD/NK/NN/HD	βγδϵ
TAL012/018/024/028	CGGG	HD/NK/NN/NK	βγδϵ
TAL012/018/024/029	CGGG	HD/NK/NN/NN	βγδϵ
TAL012/018/024/030	CGGT	HD/NK/NN/NG	βγδϵ
TAL012/018/025/026	CGTA	HD/NK/NG/NI	βγδϵ
TAL012/018/025/027	CGTC	HD/NK/NG/HD	βγδϵ
TAL012/018/025/028	CGTG	HD/NK/NG/NK	βγδϵ
TAL012/018/025/029	CGTG	HD/NK/NG/NN	βγδϵ
TAL012/018/025/030	CGTT	HD/NK/NG/NG	βγδϵ
TAL012/019/021/026	CGAA	HD/NN/NI/NI	βγδϵ
TAL012/019/021/027	CGAC	HD/NN/NI/HD	βγδϵ
TAL012/019/021/028	CGAG	HD/NN/NI/NK	βγδϵ
TAL012/019/021/029	CGAG	HD/NN/NI/NN	βγδϵ
TAL012/019/021/030	CGAT	HD/NN/NI/NG	βγδϵ
TAL012/019/022/026	CGCA	HD/NN/HD/NI	βγδϵ
TAL012/019/022/027	CGCC	HD/NN/HD/HD	βγδϵ
TAL012/019/022/028	CGCG	HD/NN/HD/NK	βγδϵ
TAL012/019/022/029	CGCG	HD/NN/HD/NN	βγδϵ
TAL012/019/022/030	CGCT	HD/NN/HD/NG	βγδϵ
TAL012/019/023/026	CGGA	HD/NN/NK/NI	βγδϵ
TAL012/019/023/027	CGGC	HD/NN/NK/HD	βγδϵ
TAL012/019/023/028	CGGG	HD/NN/NK/NK	βγδϵ
TAL012/019/023/029	CGGG	HD/NN/NK/NN	βγδϵ
TAL012/019/023/030	CGGT	HD/NN/NK/NG	βγδϵ
TAL012/019/024/026	CGGA	HD/NN/NN/NI	βγδϵ
TAL012/019/024/027	CGGC	HD/NN/NN/HD	βγδϵ
TAL012/019/024/028	CGGG	HD/NN/NN/NK	βγδϵ
TAL012/019/024/029	CGGG	HD/NN/NN/NN	βγδϵ
TAL012/019/024/030	CGGT	HD/NN/NN/NG	βγδϵ
TAL012/019/025/026	CGTA	HD/NN/NG/NI	βγδϵ
TAL012/019/025/027	CGTC	HD/NN/NG/HD	βγδϵ
TAL012/019/025/028	CGTG	HD/NN/NG/NK	βγδϵ
TAL012/019/025/029	CGTG	HD/NN/NG/NN	βγδϵ
TAL012/019/025/030	CGTT	HD/NN/NG/NG	βγδϵ
TAL012/020/021/026	CTAA	HD/NG/NI/NI	βγδϵ
TAL012/020/021/027	CTAC	HD/NG/NI/HD	βγδϵ
TAL012/020/021/028	CTAG	HD/NG/NI/NK	βγδϵ
TAL012/020/021/029	CTAG	HD/NG/NI/NN	βγδϵ
TAL012/020/021/030	CTAT	HD/NG/NI/NG	βγδϵ
TAL012/020/022/026	CTCA	HD/NG/HD/NI	βγδϵ
TAL012/020/022/027	CTCC	HD/NG/HD/HD	βγδϵ
TAL012/020/022/028	CTCG	HD/NG/HD/NK	βγδϵ
TAL012/020/022/029	CTCG	HD/NG/HD/NN	βγδϵ
TAL012/020/022/030	CTCT	HD/NG/HD/NG	βγδϵ
TAL012/020/023/026	CTGA	HD/NG/NK/NI	βγδϵ
TAL012/020/023/027	CTGC	HD/NG/NK/HD	βγδϵ
TAL012/020/023/028	CTGG	HD/NG/NK/NK	βγδϵ
TAL012/020/023/029	CTGG	HD/NG/NK/NN	βγδϵ
TAL012/020/023/030	CTGT	HD/NG/NK/NG	βγδϵ
TAL012/020/024/026	CTGA	HD/NG/NN/NI	βγδϵ
TAL012/020/024/027	CTGC	HD/NG/NN/HD	βγδϵ
TAL012/020/024/028	CTGG	HD/NG/NN/NK	βγδϵ
TAL012/020/024/029	CTGG	HD/NG/NN/NN	βγδϵ
TAL012/020/024/030	CTGT	HD/NG/NN/NG	βγδϵ
TAL012/020/025/026	CTTA	HD/NG/NG/NI	βγδϵ
TAL012/020/025/027	CTTC	HD/NG/NG/HD	βγδϵ
TAL012/020/025/028	CTTG	HD/NG/NG/NK	βγδϵ
TAL012/020/025/029	CTTG	HD/NG/NG/NN	βγδϵ
TAL012/020/025/030	CTTT	HD/NG/NG/NG	βγδϵ
TAL013/016/021/026	GAAA	NK/NI/NI/NI	βγδϵ
TAL013/016/021/027	GAAC	NK/NI/NI/HD	βγδϵ
TAL013/016/021/028	GAAG	NK/NI/NI/NK	βγδϵ
TAL013/016/021/029	GAAG	NK/NI/NI/NN	βγδϵ
TAL013/016/021/030	GAAT	NK/NI/NI/NG	βγδϵ
TAL013/016/022/026	GACA	NK/NI/HD/NI	βγδϵ
TAL013/016/022/027	GACC	NK/NI/HD/HD	βγδϵ
TAL013/016/022/028	GACG	NK/NI/HD/NK	βγδϵ
TAL013/016/022/029	GACG	NK/NI/HD/NN	βγδϵ
TAL013/016/022/030	GACT	NK/NI/HD/NG	βγδϵ
TAL013/016/023/026	GAGA	NK/NI/NK/NI	βγδϵ
TAL013/016/023/027	GAGC	NK/NI/NK/HD	βγδϵ
TAL013/016/023/028	GAGG	NK/NI/NK/NK	βγδϵ
TAL013/016/023/029	GAGG	NK/NI/NK/NN	βγδϵ
TAL013/016/023/030	GAGT	NK/NI/NK/NG	βγδϵ
TAL013/016/024/026	GAGA	NK/NI/NN/NI	βγδϵ
TAL013/016/024/027	GAGC	NK/NI/NN/HD	βγδϵ
TAL013/016/024/028	GAGG	NK/NI/NN/NK	βγδϵ
TAL013/016/024/029	GAGG	NK/NI/NN/NN	βγδϵ
TAL013/016/024/030	GAGT	NK/NI/NN/NG	βγδϵ
TAL013/016/025/026	GATA	NK/NI/NG/NI	βγδϵ
TAL013/016/025/027	GATC	NK/NI/NG/HD	βγδϵ
TAL013/016/025/028	GATG	NK/NI/NG/NK	βγδϵ
TAL013/016/025/029	GATG	NK/NI/NG/NN	βγδϵ
TAL013/016/025/030	GATT	NK/NI/NG/NG	βγδϵ
TAL013/017/021/026	GCAA	NK/HD/NI/NI	βγδϵ
TAL013/017/021/027	GCAC	NK/HD/NI/HD	βγδϵ
TAL013/017/021/028	GCAG	NK/HD/NI/NK	βγδϵ
TAL013/017/021/029	GCAG	NK/HD/NI/NN	βγδϵ
TAL013/017/021/030	GCAT	NK/HD/NI/NG	βγδϵ
TAL013/017/022/026	GCCA	NK/HD/HD/NI	βγδϵ
TAL013/017/022/027	GCCC	NK/HD/HD/HD	βγδϵ
TAL013/017/022/028	GCCG	NK/HD/HD/NK	βγδϵ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL013/017/022/029	GCCG	NK/HD/HD/NN	βγδε
TAL013/017/022/030	GCCT	NK/HD/HD/NG	βγδε
TAL013/017/023/026	GCGA	NK/HD/NK/NI	βγδε
TAL013/017/023/027	GCGC	NK/HD/NK/HD	βγδε
TAL013/017/023/028	GCGG	NK/HD/NK/NK	βγδε
TAL013/017/023/029	GCGG	NK/HD/NK/NN	βγδε
TAL013/017/023/030	GCGT	NK/HD/NK/NG	βγδε
TAL013/017/024/026	GCGA	NK/HD/NN/NI	βγδε
TAL013/017/024/027	GCGC	NK/HD/NN/HD	βγδε
TAL013/017/024/028	GCGG	NK/HD/NN/NK	βγδε
TAL013/017/024/029	GCGG	NK/HD/NN/NN	βγδε
TAL013/017/024/030	GCGT	NK/HD/NN/NG	βγδε
TAL013/017/025/026	GCTA	NK/HD/NG/NI	βγδε
TAL013/017/025/027	GCTC	NK/HD/NG/HD	βγδε
TAL013/017/025/028	GCTG	NK/HD/NG/NK	βγδε
TAL013/017/025/029	GCTG	NK/HD/NG/NN	βγδε
TAL013/017/025/030	GCTT	NK/HD/NG/NG	βγδε
TAL013/018/021/026	GGAA	NK/NK/NI/NI	βγδε
TAL013/018/021/027	GGAC	NK/NK/NI/HD	βγδε
TAL013/018/021/028	GGAG	NK/NK/NI/NK	βγδε
TAL013/018/021/029	GGAG	NK/NK/NI/NN	βγδε
TAL013/018/021/030	GGAT	NK/NK/NI/NG	βγδε
TAL013/018/022/026	GGCA	NK/NK/HD/NI	βγδε
TAL013/018/022/027	GGCC	NK/NK/HD/HD	βγδε
TAL013/018/022/028	GGCG	NK/NK/HD/NK	βγδε
TAL013/018/022/029	GGCG	NK/NK/HD/NN	βγδε
TAL013/018/022/030	GGCT	NK/NK/HD/NG	βγδε
TAL013/018/023/026	GGGA	NK/NK/NK/NI	βγδε
TAL013/018/023/027	GGGC	NK/NK/NK/HD	βγδε
TAL013/018/023/028	GGGG	NK/NK/NK/NK	βγδε
TAL013/018/023/029	GGGG	NK/NK/NK/NN	βγδε
TAL013/018/023/030	GGGT	NK/NK/NK/NG	βγδε
TAL013/018/024/026	GGGA	NK/NK/NN/NI	βγδε
TAL013/018/024/027	GGGC	NK/NK/NN/HD	βγδε
TAL013/018/024/028	GGGG	NK/NK/NN/NK	βγδε
TAL013/018/024/029	GGGG	NK/NK/NN/NN	βγδε
TAL013/018/024/030	GGGT	NK/NK/NN/NG	βγδε
TAL013/018/025/026	GGTA	NK/NK/NG/NI	βγδε
TAL013/018/025/027	GGTC	NK/NK/NG/HD	βγδε
TAL013/018/025/028	GGTG	NK/NK/NG/NK	βγδε
TAL013/018/025/029	GGTG	NK/NK/NG/NN	βγδε
TAL013/018/025/030	GGTT	NK/NK/NG/NG	βγδε
TAL013/019/021/026	GGAA	NK/NN/NI/NI	βγδε
TAL013/019/021/027	GGAC	NK/NN/NI/HD	βγδε
TAL013/019/021/028	GGAG	NK/NN/NI/NK	βγδε
TAL013/019/021/029	GGAG	NK/NN/NI/NN	βγδε
TAL013/019/021/030	GGAT	NK/NN/NI/NG	βγδε
TAL013/019/022/026	GGCA	NK/NN/HD/NI	βγδε
TAL013/019/022/027	GGCC	NK/NN/HD/HD	βγδε
TAL013/019/022/028	GGCG	NK/NN/HD/NK	βγδε
TAL013/019/022/029	GGCG	NK/NN/HD/NN	βγδε
TAL013/019/022/030	GGCT	NK/NN/HD/NG	βγδε
TAL013/019/023/026	GGGA	NK/NN/NK/NI	βγδε
TAL013/019/023/027	GGGC	NK/NN/NK/HD	βγδε
TAL013/019/023/028	GGGG	NK/NN/NK/NK	βγδε
TAL013/019/023/029	GGGG	NK/NN/NK/NN	βγδε
TAL013/019/023/030	GGGT	NK/NN/NK/NG	βγδε
TAL013/019/024/026	GGGA	NK/NN/NN/NI	βγδε
TAL013/019/024/027	GGGC	NK/NN/NN/HD	βγδε
TAL013/019/024/028	GGGG	NK/NN/NN/NK	βγδε
TAL013/019/024/029	GGGG	NK/NN/NN/NN	βγδε
TAL013/019/024/030	GGGT	NK/NN/NN/NG	βγδε
TAL013/019/025/026	GGTA	NK/NN/NG/NI	βγδε
TAL013/019/025/027	GGTC	NK/NN/NG/HD	βγδε
TAL013/019/025/028	GGTG	NK/NN/NG/NK	βγδε
TAL013/019/025/029	GGTG	NK/NN/NG/NN	βγδε
TAL013/019/025/030	GGTT	NK/NN/NG/NG	βγδε
TAL013/020/021/026	GTAA	NK/NG/NI/NI	βγδε
TAL013/020/021/027	GTAC	NK/NG/NI/HD	βγδε
TAL013/020/021/028	GTAG	NK/NG/NI/NK	βγδε
TAL013/020/021/029	GTAG	NK/NG/NI/NN	βγδε
TAL013/020/021/030	GTAT	NK/NG/NI/NG	βγδε
TAL013/020/022/026	GTCA	NK/NG/HD/NI	βγδε
TAL013/020/022/027	GTCC	NK/NG/HD/HD	βγδε
TAL013/020/022/028	GTCG	NK/NG/HD/NK	βγδε
TAL013/020/022/029	GTCG	NK/NG/HD/NN	βγδε
TAL013/020/022/030	GTCT	NK/NG/HD/NG	βγδε
TAL013/020/023/026	GTGA	NK/NG/NK/NI	βγδε
TAL013/020/023/027	GTGC	NK/NG/NK/HD	βγδε
TAL013/020/023/028	GTGG	NK/NG/NK/NK	βγδε
TAL013/020/023/029	GTGG	NK/NG/NK/NN	βγδε
TAL013/020/023/030	GTGT	NK/NG/NK/NG	βγδε
TAL013/020/024/026	GTGA	NK/NG/NN/NI	βγδε
TAL013/020/024/027	GTGC	NK/NG/NN/HD	βγδε
TAL013/020/024/028	GTGG	NK/NG/NN/NK	βγδε
TAL013/020/024/029	GTGG	NK/NG/NN/NN	βγδε
TAL013/020/024/030	GTGT	NK/NG/NN/NG	βγδε
TAL013/020/025/026	GTTA	NK/NG/NG/NI	βγδε
TAL013/020/025/027	GTTC	NK/NG/NG/HD	βγδε
TAL013/020/025/028	GTTG	NK/NG/NG/NK	βγδε
TAL013/020/025/029	GTTG	NK/NG/NG/NN	βγδε
TAL013/020/025/030	GTTT	NK/NG/NG/NG	βγδε
TAL014/016/021/026	GAAA	NN/NI/NI/NI	βγδε
TAL014/016/021/027	GAAC	NN/NI/NI/HD	βγδε
TAL014/016/021/028	GAAG	NN/NI/NI/NK	βγδε
TAL014/016/021/029	GAAG	NN/NI/NI/NN	βγδε
TAL014/016/021/030	GAAT	NN/NI/NI/NG	βγδε
TAL014/016/022/026	GACA	NN/NI/HD/NI	βγδε
TAL014/016/022/027	GACC	NN/NI/HD/HD	βγδε
TAL014/016/022/028	GACG	NN/NI/HD/NK	βγδε
TAL014/016/022/029	GACG	NN/NI/HD/NN	βγδε
TAL014/016/022/030	GACT	NN/NI/HD/NG	βγδε
TAL014/016/023/026	GAGA	NN/NI/NK/NI	βγδε
TAL014/016/023/027	GAGC	NN/NI/NK/HD	βγδε
TAL014/016/023/028	GAGG	NN/NI/NK/NK	βγδε
TAL014/016/023/029	GAGG	NN/NI/NK/NN	βγδε
TAL014/016/023/030	GAGT	NN/NI/NK/NG	βγδε
TAL014/016/024/026	GAGA	NN/NI/NN/NI	βγδε
TAL014/016/024/027	GAGC	NN/NI/NN/HD	βγδε
TAL014/016/024/028	GAGG	NN/NI/NN/NK	βγδε
TAL014/016/024/029	GAGG	NN/NI/NN/NN	βγδε
TAL014/016/024/030	GAGT	NN/NI/NN/NG	βγδε
TAL014/016/025/026	GATA	NN/NI/NG/NI	βγδε
TAL014/016/025/027	GATC	NN/NI/NG/HD	βγδε
TAL014/016/025/028	GATG	NN/NI/NG/NK	βγδε
TAL014/016/025/029	GATG	NN/NI/NG/NN	βγδε
TAL014/016/025/030	GATT	NN/NI/NG/NG	βγδε
TAL014/017/021/026	GCAA	NN/HD/NI/NI	βγδε
TAL014/017/021/027	GCAC	NN/HD/NI/HD	βγδε
TAL014/017/021/028	GCAG	NN/HD/NI/NK	βγδε
TAL014/017/021/029	GCAG	NN/HD/NI/NN	βγδε
TAL014/017/021/030	GCAT	NN/HD/NI/NG	βγδε
TAL014/017/022/026	GCCA	NN/HD/HD/NI	βγδε
TAL014/017/022/027	GCCC	NN/HD/HD/HD	βγδε
TAL014/017/022/028	GCCG	NN/HD/HD/NK	βγδε
TAL014/017/022/029	GCCG	NN/HD/HD/NN	βγδε
TAL014/017/022/030	GCCT	NN/HD/HD/NG	βγδε
TAL014/017/023/026	GCGA	NN/HD/NK/NI	βγδε
TAL014/017/023/027	GCGC	NN/HD/NK/HD	βγδε
TAL014/017/023/028	GCGG	NN/HD/NK/NK	βγδε
TAL014/017/023/029	GCGG	NN/HD/NK/NN	βγδε
TAL014/017/023/030	GCGT	NN/HD/NK/NG	βγδε
TAL014/017/024/026	GCGA	NN/HD/NN/NI	βγδε
TAL014/017/024/027	GCGC	NN/HD/NN/HD	βγδε
TAL014/017/024/028	GCGG	NN/HD/NN/NK	βγδε
TAL014/017/024/029	GCGG	NN/HD/NN/NN	βγδε
TAL014/017/024/030	GCGT	NN/HD/NN/NG	βγδε
TAL014/017/025/026	GCTA	NN/HD/NG/NI	βγδε
TAL014/017/025/027	GCTC	NN/HD/NG/HD	βγδε
TAL014/017/025/028	GCTG	NN/HD/NG/NK	βγδε
TAL014/017/025/029	GCTG	NN/HD/NG/NN	βγδε
TAL014/017/025/030	GCTT	NN/HD/NG/NG	βγδε
TAL014/018/021/026	GGAA	NN/NK/NI/NI	βγδε
TAL014/018/021/027	GGAC	NN/NK/NI/HD	βγδε

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL014/018/021/028	GGAG	NN/NK/NI/NK	βγδϵ
TAL014/018/021/029	GGAG	NN/NK/NI/NN	βγδϵ
TAL014/018/021/030	GGAT	NN/NK/NI/NG	βγδϵ
TAL014/018/022/026	GGCA	NN/NK/HD/NI	βγδϵ
TAL014/018/022/027	GGCC	NN/NK/HD/HD	βγδϵ
TAL014/018/022/028	GGCG	NN/NK/HD/NK	βγδϵ
TAL014/018/022/029	GGCG	NN/NK/HD/NN	βγδϵ
TAL014/018/022/030	GGCT	NN/NK/HD/NG	βγδϵ
TAL014/018/023/026	GGGA	NN/NK/NK/NI	βγδϵ
TAL014/018/023/027	GGGC	NN/NK/NK/HD	βγδϵ
TAL014/018/023/028	GGGG	NN/NK/NK/NK	βγδϵ
TAL014/018/023/029	GGGG	NN/NK/NK/NN	βγδϵ
TAL014/018/023/030	GGGT	NN/NK/NK/NG	βγδϵ
TAL014/018/024/026	GGGA	NN/NK/NN/NI	βγδϵ
TAL014/018/024/027	GGGC	NN/NK/NN/HD	βγδϵ
TAL014/018/024/028	GGGG	NN/NK/NN/NK	βγδϵ
TAL014/018/024/029	GGGG	NN/NK/NN/NN	βγδϵ
TAL014/018/024/030	GGGT	NN/NK/NN/NG	βγδϵ
TAL014/018/025/026	GGTA	NN/NK/NG/NI	βγδϵ
TAL014/018/025/027	GGTC	NN/NK/NG/HD	βγδϵ
TAL014/018/025/028	GGTG	NN/NK/NG/NK	βγδϵ
TAL014/018/025/029	GGTG	NN/NK/NG/NN	βγδϵ
TAL014/018/025/030	GGTT	NN/NK/NG/NG	βγδϵ
TAL014/019/021/026	GGAA	NN/NN/NI/NI	βγδϵ
TAL014/019/021/027	GGAC	NN/NN/NI/HD	βγδϵ
TAL014/019/021/028	GGAG	NN/NN/NI/NK	βγδϵ
TAL014/019/021/029	GGAG	NN/NN/NI/NN	βγδϵ
TAL014/019/021/030	GGAT	NN/NN/NI/NG	βγδϵ
TAL014/019/022/026	GGCA	NN/NN/HD/NI	βγδϵ
TAL014/019/022/027	GGCC	NN/NN/HD/HD	βγδϵ
TAL014/019/022/028	GGCG	NN/NN/HD/NK	βγδϵ
TAL014/019/022/029	GGCG	NN/NN/HD/NN	βγδϵ
TAL014/019/022/030	GGCT	NN/NN/HD/NG	βγδϵ
TAL014/019/023/026	GGGA	NN/NN/NK/NI	βγδϵ
TAL014/019/023/027	GGGC	NN/NN/NK/HD	βγδϵ
TAL014/019/023/028	GGGG	NN/NN/NK/NK	βγδϵ
TAL014/019/023/029	GGGG	NN/NN/NK/NN	βγδϵ
TAL014/019/023/030	GGGT	NN/NN/NK/NG	βγδϵ
TAL014/019/024/026	GGGA	NN/NN/NN/NI	βγδϵ
TAL014/019/024/027	GGGC	NN/NN/NN/HD	βγδϵ
TAL014/019/024/028	GGGG	NN/NN/NN/NK	βγδϵ
TAL014/019/024/029	GGGG	NN/NN/NN/NN	βγδϵ
TAL014/019/024/030	GGGT	NN/NN/NN/NG	βγδϵ
TAL014/019/025/026	GGTA	NN/NN/NG/NI	βγδϵ
TAL014/019/025/027	GGTC	NN/NN/NG/HD	βγδϵ
TAL014/019/025/028	GGTG	NN/NN/NG/NK	βγδϵ
TAL014/019/025/029	GGTG	NN/NN/NG/NN	βγδϵ
TAL014/019/025/030	GGTT	NN/NN/NG/NG	βγδϵ
TAL014/020/021/026	GTAA	NN/NG/NI/NI	βγδϵ
TAL014/020/021/027	GTAC	NN/NG/NI/HD	βγδϵ
TAL014/020/021/028	GTAG	NN/NG/NI/NK	βγδϵ
TAL014/020/021/029	GTAG	NN/NG/NI/NN	βγδϵ
TAL014/020/021/030	GTAT	NN/NG/NI/NG	βγδϵ
TAL014/020/022/026	GTCA	NN/NG/HD/NI	βγδϵ
TAL014/020/022/027	GTCC	NN/NG/HD/HD	βγδϵ
TAL014/020/022/028	GTCG	NN/NG/HD/NK	βγδϵ
TAL014/020/022/029	GTCG	NN/NG/HD/NN	βγδϵ
TAL014/020/022/030	GTCT	NN/NG/HD/NG	βγδϵ
TAL014/020/023/026	GTGA	NN/NG/NK/NI	βγδϵ
TAL014/020/023/027	GTGC	NN/NG/NK/HD	βγδϵ
TAL014/020/023/028	GTGG	NN/NG/NK/NK	βγδϵ
TAL014/020/023/029	GTGG	NN/NG/NK/NN	βγδϵ
TAL014/020/023/030	GTGT	NN/NG/NK/NG	βγδϵ
TAL014/020/024/026	GTGA	NN/NG/NN/NI	βγδϵ
TAL014/020/024/027	GTGC	NN/NG/NN/HD	βγδϵ
TAL014/020/024/028	GTGG	NN/NG/NN/NK	βγδϵ
TAL014/020/024/029	GTGG	NN/NG/NN/NN	βγδϵ
TAL014/020/024/030	GTGT	NN/NG/NN/NG	βγδϵ
TAL014/020/025/026	GTTA	NN/NG/NG/NI	βγδϵ
TAL014/020/025/027	GTTC	NN/NG/NG/HD	βγδϵ
TAL014/020/025/028	GTTG	NN/NG/NG/NK	βγδϵ
TAL014/020/025/029	GTTG	NN/NG/NG/NN	βγδϵ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL014/020/025/030	GTTT	NN/NG/NG/NG	βγδϵ
TAL015/016/021/026	TAAA	NG/NI/NI/NI	βγδϵ
TAL015/016/021/027	TAAC	NG/NI/NI/HD	βγδϵ
TAL015/016/021/028	TAAG	NG/NI/NI/NK	βγδϵ
TAL015/016/021/029	TAAG	NG/NI/NI/NN	βγδϵ
TAL015/016/021/030	TAAT	NG/NI/NI/NG	βγδϵ
TAL015/016/022/026	TACA	NG/NI/HD/NI	βγδϵ
TAL015/016/022/027	TACC	NG/NI/HD/HD	βγδϵ
TAL015/016/022/028	TACG	NG/NI/HD/NK	βγδϵ
TAL015/016/022/029	TACG	NG/NI/HD/NN	βγδϵ
TAL015/016/022/030	TACT	NG/NI/HD/NG	βγδϵ
TAL015/016/023/026	TAGA	NG/NI/NK/NI	βγδϵ
TAL015/016/023/027	TAGC	NG/NI/NK/HD	βγδϵ
TAL015/016/023/028	TAGG	NG/NI/NK/NK	βγδϵ
TAL015/016/023/029	TAGG	NG/NI/NK/NN	βγδϵ
TAL015/016/023/030	TAGT	NG/NI/NK/NG	βγδϵ
TAL015/016/024/026	TAGA	NG/NI/NN/NI	βγδϵ
TAL015/016/024/027	TAGC	NG/NI/NN/HD	βγδϵ
TAL015/016/024/028	TAGG	NG/NI/NN/NK	βγδϵ
TAL015/016/024/029	TAGG	NG/NI/NN/NN	βγδϵ
TAL015/016/024/030	TAGT	NG/NI/NN/NG	βγδϵ
TAL015/016/025/026	TATA	NG/NI/NG/NI	βγδϵ
TAL015/016/025/027	TATC	NG/NI/NG/HD	βγδϵ
TAL015/016/025/028	TATG	NG/NI/NG/NK	βγδϵ
TAL015/016/025/029	TATG	NG/NI/NG/NN	βγδϵ
TAL015/016/025/030	TATT	NG/NI/NG/NG	βγδϵ
TAL015/017/021/026	TCAA	NG/HD/NI/NI	βγδϵ
TAL015/017/021/027	TCAC	NG/HD/NI/HD	βγδϵ
TAL015/017/021/028	TCAG	NG/HD/NI/NK	βγδϵ
TAL015/017/021/029	TCAG	NG/HD/NI/NN	βγδϵ
TAL015/017/021/030	TCAT	NG/HD/NI/NG	βγδϵ
TAL015/017/022/026	TCCA	NG/HD/HD/NI	βγδϵ
TAL015/017/022/027	TCCC	NG/HD/HD/HD	βγδϵ
TAL015/017/022/028	TCCG	NG/HD/HD/NK	βγδϵ
TAL015/017/022/029	TCCG	NG/HD/HD/NN	βγδϵ
TAL015/017/022/030	TCCT	NG/HD/HD/NG	βγδϵ
TAL015/017/023/026	TCGA	NG/HD/NK/NI	βγδϵ
TAL015/017/023/027	TCGC	NG/HD/NK/HD	βγδϵ
TAL015/017/023/028	TCGG	NG/HD/NK/NK	βγδϵ
TAL015/017/023/029	TCGG	NG/HD/NK/NN	βγδϵ
TAL015/017/023/030	TCGT	NG/HD/NK/NG	βγδϵ
TAL015/017/024/026	TCGA	NG/HD/NN/NI	βγδϵ
TAL015/017/024/027	TCGC	NG/HD/NN/HD	βγδϵ
TAL015/017/024/028	TCGG	NG/HD/NN/NK	βγδϵ
TAL015/017/024/029	TCGG	NG/HD/NN/NN	βγδϵ
TAL015/017/024/030	TCGT	NG/HD/NN/NG	βγδϵ
TAL015/017/025/026	TCTA	NG/HD/NG/NI	βγδϵ
TAL015/017/025/027	TCTC	NG/HD/NG/HD	βγδϵ
TAL015/017/025/028	TCTG	NG/HD/NG/NK	βγδϵ
TAL015/017/025/029	TCTG	NG/HD/NG/NN	βγδϵ
TAL015/017/025/030	TCTT	NG/HD/NG/NG	βγδϵ
TAL015/018/021/026	TGAA	NG/NK/NI/NI	βγδϵ
TAL015/018/021/027	TGAC	NG/NK/NI/HD	βγδϵ
TAL015/018/021/028	TGAG	NG/NK/NI/NK	βγδϵ
TAL015/018/021/029	TGAG	NG/NK/NI/NN	βγδϵ
TAL015/018/021/030	TGAT	NG/NK/NI/NG	βγδϵ
TAL015/018/022/026	TGCA	NG/NK/HD/NI	βγδϵ
TAL015/018/022/027	TGCC	NG/NK/HD/HD	βγδϵ
TAL015/018/022/028	TGCG	NG/NK/HD/NK	βγδϵ
TAL015/018/022/029	TGCG	NG/NK/HD/NN	βγδϵ
TAL015/018/022/030	TGCT	NG/NK/HD/NG	βγδϵ
TAL015/018/023/026	TGGA	NG/NK/NK/NI	βγδϵ
TAL015/018/023/027	TGGC	NG/NK/NK/HD	βγδϵ
TAL015/018/023/028	TGGG	NG/NK/NK/NK	βγδϵ
TAL015/018/023/029	TGGG	NG/NK/NK/NN	βγδϵ
TAL015/018/023/030	TGGT	NG/NK/NK/NG	βγδϵ
TAL015/018/024/026	TGGA	NG/NK/NN/NI	βγδϵ
TAL015/018/024/027	TGGC	NG/NK/NN/HD	βγδϵ
TAL015/018/024/028	TGGG	NG/NK/NN/NK	βγδϵ
TAL015/018/024/029	TGGG	NG/NK/NN/NN	βγδϵ
TAL015/018/024/030	TGGT	NG/NK/NN/NG	βγδϵ
TAL015/018/025/026	TGTA	NG/NK/NG/NI	βγδϵ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL015/018/025/027	TGTC	NG/NK/NG/HD	βγδϵ
TAL015/018/025/028	TGTG	NG/NK/NG/NK	βγδϵ
TAL015/018/025/029	TGTG	NG/NK/NG/NN	βγδϵ
TAL015/018/025/030	TGTT	NG/NK/NG/NG	βγδϵ
TAL015/019/021/026	TGAA	NG/NN/NI/NI	βγδϵ
TAL015/019/021/027	TGAC	NG/NN/NI/HD	βγδϵ
TAL015/019/021/028	TGAG	NG/NN/NI/NK	βγδϵ
TAL015/019/021/029	TGAG	NG/NN/NI/NN	βγδϵ
TAL015/019/021/030	TGAT	NG/NN/NI/NG	βγδϵ
TAL015/019/022/026	TGCA	NG/NN/HD/NI	βγδϵ
TAL015/019/022/027	TGCC	NG/NN/HD/HD	βγδϵ
TAL015/019/022/028	TGCG	NG/NN/HD/NK	βγδϵ
TAL015/019/022/029	TGCG	NG/NN/HD/NN	βγδϵ
TAL015/019/022/030	TGCT	NG/NN/HD/NG	βγδϵ
TAL015/019/023/026	TGGA	NG/NN/NK/NI	βγδϵ
TAL015/019/023/027	TGGC	NG/NN/NK/HD	βγδϵ
TAL015/019/023/028	TGGG	NG/NN/NK/NK	βγδϵ
TAL015/019/023/029	TGGG	NG/NN/NK/NN	βγδϵ
TAL015/019/023/030	TGGT	NG/NN/NK/NG	βγδϵ
TAL015/019/024/026	TGGA	NG/NN/NN/NI	βγδϵ
TAL015/019/024/027	TGGC	NG/NN/NN/HD	βγδϵ
TAL015/019/024/028	TGGG	NG/NN/NN/NK	βγδϵ
TAL015/019/024/029	TGGG	NG/NN/NN/NN	βγδϵ
TAL015/019/024/030	TGGT	NG/NN/NN/NG	βγδϵ
TAL015/019/025/026	TGTA	NG/NN/NG/NI	βγδϵ
TAL015/019/025/027	TGTC	NG/NN/NG/HD	βγδϵ
TAL015/019/025/028	TGTG	NG/NN/NG/NK	βγδϵ
TAL015/019/025/029	TGTG	NG/NN/NG/NN	βγδϵ
TAL015/019/025/030	TGTT	NG/NN/NG/NG	βγδϵ
TAL015/020/021/026	TTAA	NG/NG/NI/NI	βγδϵ
TAL015/020/021/027	TTAC	NG/NG/NI/HD	βγδϵ
TAL015/020/021/028	TTAG	NG/NG/NI/NK	βγδϵ
TAL015/020/021/029	TTAG	NG/NG/NI/NN	βγδϵ
TAL015/020/021/030	TTAT	NG/NG/NI/NG	βγδϵ
TAL015/020/022/026	TTCA	NG/NG/HD/NI	βγδϵ
TAL015/020/022/027	TTCC	NG/NG/HD/HD	βγδϵ
TAL015/020/022/028	TTCG	NG/NG/HD/NK	βγδϵ
TAL015/020/022/029	TTCG	NG/NG/HD/NN	βγδϵ
TAL015/020/022/030	TTCT	NG/NG/HD/NG	βγδϵ
TAL015/020/023/026	TTGA	NG/NG/NK/NI	βγδϵ
TAL015/020/023/027	TTGC	NG/NG/NK/HD	βγδϵ
TAL015/020/023/028	TTGG	NG/NG/NK/NK	βγδϵ
TAL015/020/023/029	TTGG	NG/NG/NK/NN	βγδϵ
TAL015/020/023/030	TTGT	NG/NG/NK/NG	βγδϵ
TAL015/020/024/026	TTGA	NG/NG/NN/NI	βγδϵ
TAL015/020/024/027	TTGC	NG/NG/NN/HD	βγδϵ
TAL015/020/024/028	TTGG	NG/NG/NN/NK	βγδϵ
TAL015/020/024/029	TTGG	NG/NG/NN/NN	βγδϵ
TAL015/020/024/030	TTGT	NG/NG/NN/NG	βγδϵ
TAL015/020/025/026	TTTA	NG/NG/NG/NI	βγδϵ
TAL015/020/025/027	TTTC	NG/NG/NG/HD	βγδϵ
TAL015/020/025/028	TTTG	NG/NG/NG/NK	βγδϵ
TAL015/020/025/029	TTTG	NG/NG/NG/NN	βγδϵ
TAL015/020/025/030	TTTT	NG/NG/NG/NG	βγδϵ
TAL011/016	AA	NI/NI	βγ
TAL011/017	AC	NI/HD	βγ
TAL011/018	AG	NI/NK	βγ
TAL011/019	AG	NI/NN	βγ
TAL011/020	AT	NI/NG	βγ
TAL012/016	CA	HD/NI	βγ
TAL012/017	CC	HD/HD	βγ
TAL012/018	CG	HD/NK	βγ
TAL012/019	CG	HD/NN	βγ
TAL012/020	CT	HD/NG	βγ
TAL013/016	GA	NK/NI	βγ
TAL013/017	GC	NK/HD	βγ
TAL013/018	GG	NK/NK	βγ
TAL013/019	GG	NK/NN	βγ
TAL013/020	GT	NK/NG	βγ
TAL014/016	GA	NN/NI	βγ
TAL014/017	GC	NN/HD	βγ
TAL014/018	GG	NN/NK	βγ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL014/019	GG	NN/NN	βγ
TAL014/020	GT	NN/NG	βγ
TAL015/016	TA	NG/NI	βγ
TAL015/017	TC	NG/HD	βγ
TAL015/018	TG	NG/NK	βγ
TAL015/019	TG	NG/NN	βγ
TAL015/020	TT	NG/NG	βγ
TAL011/016/021	AAA	NI/NI/NI	βγδ
TAL011/016/022	AAC	NI/NI/HD	βγδ
TAL011/016/023	AAG	NI/NI/NK	βγδ
TAL011/016/024	AAG	NI/NI/NN	βγδ
TAL011/016/025	AAT	NI/NI/NG	βγδ
TAL011/017/021	ACA	NI/HD/NI	βγδ
TAL011/017/022	ACC	NI/HD/HD	βγδ
TAL011/017/023	ACG	NI/HD/NK	βγδ
TAL011/017/024	ACG	NI/HD/NN	βγδ
TAL011/017/025	ACT	NI/HD/NG	βγδ
TAL011/018/021	AGA	NI/NK/NI	βγδ
TAL011/018/022	AGC	NI/NK/HD	βγδ
TAL011/018/023	AGG	NI/NK/NK	βγδ
TAL011/018/024	AGG	NI/NK/NN	βγδ
TAL011/018/025	AGT	NI/NK/NG	βγδ
TAL011/019/021	AGA	NI/NN/NI	βγδ
TAL011/019/022	AGC	NI/NN/HD	βγδ
TAL011/019/023	AGG	NI/NN/NK	βγδ
TAL011/019/024	AGG	NI/NN/NN	βγδ
TAL011/019/025	AGT	NI/NN/NG	βγδ
TAL011/020/021	ATA	NI/NG/NI	βγδ
TAL011/020/022	ATC	NI/NG/HD	βγδ
TAL011/020/023	ATG	NI/NG/NK	βγδ
TAL011/020/024	ATG	NI/NG/NN	βγδ
TAL011/020/025	ATT	NI/NG/NG	βγδ
TAL012/016/021	CAA	HD/NI/NI	βγδ
TAL012/016/022	CAC	HD/NI/HD	βγδ
TAL012/016/023	CAG	HD/NI/NK	βγδ
TAL012/016/024	CAG	HD/NI/NN	βγδ
TAL012/016/025	CAT	HD/NI/NG	βγδ
TAL012/017/021	CCA	HD/HD/NI	βγδ
TAL012/017/022	CCC	HD/HD/HD	βγδ
TAL012/017/023	CCG	HD/HD/NK	βγδ
TAL012/017/024	CCG	HD/HD/NN	βγδ
TAL012/017/025	CCT	HD/HD/NG	βγδ
TAL012/018/021	CGA	HD/NK/NI	βγδ
TAL012/018/022	CGC	HD/NK/HD	βγδ
TAL012/018/023	CGG	HD/NK/NK	βγδ
TAL012/018/024	CGG	HD/NK/NN	βγδ
TAL012/018/025	CGT	HD/NK/NG	βγδ
TAL012/019/021	CGA	HD/NN/NI	βγδ
TAL012/019/022	CGC	HD/NN/HD	βγδ
TAL012/019/023	CGG	HD/NN/NK	βγδ
TAL012/019/024	CGG	HD/NN/NN	βγδ
TAL012/019/025	CGT	HD/NN/NG	βγδ
TAL012/020/021	CTA	HD/NG/NI	βγδ
TAL012/020/022	CTC	HD/NG/HD	βγδ
TAL012/020/023	CTG	HD/NG/NK	βγδ
TAL012/020/024	CTG	HD/NG/NN	βγδ
TAL012/020/025	CTT	HD/NG/NG	βγδ
TAL013/016/021	GAA	NK/NI/NI	βγδ
TAL013/016/022	GAC	NK/NI/HD	βγδ
TAL013/016/023	GAG	NK/NI/NK	βγδ
TAL013/016/024	GAG	NK/NI/NN	βγδ
TAL013/016/025	GAT	NK/NI/NG	βγδ
TAL013/017/021	GCA	NK/HD/NI	βγδ
TAL013/017/022	GCC	NK/HD/HD	βγδ
TAL013/017/023	GCG	NK/HD/NK	βγδ
TAL013/017/024	GCG	NK/HD/NN	βγδ
TAL013/017/025	GCT	NK/HD/NG	βγδ
TAL013/018/021	GGA	NK/NK/NI	βγδ
TAL013/018/022	GGC	NK/NK/HD	βγδ
TAL013/018/023	GGG	NK/NK/NK	βγδ
TAL013/018/024	GGG	NK/NK/NN	βγδ
TAL013/018/025	GGT	NK/NK/NG	βγδ

TABLE 5-continued

Archive of 835 plasmids encoding pre-assembled TALE repeat units

Plasmid ID	DNA Target	RVDs	Unit Architecture
TAL013/019/021	GGA	NK/NN/NI	βγδ
TAL013/019/022	GGC	NK/NN/HD	βγδ
TAL013/019/023	GGG	NK/NN/NK	βγδ
TAL013/019/024	GGG	NK/NN/NN	βγδ
TAL013/019/025	GGT	NK/NN/NG	βγδ
TAL013/020/021	GTA	NK/NG/NI	βγδ
TAL013/020/022	GTC	NK/NG/HD	βγδ
TAL013/020/023	GTG	NK/NG/NK	βγδ
TAL013/020/024	GTG	NK/NG/NN	βγδ
TAL013/020/025	GTT	NK/NG/NG	βγδ
TAL014/016/021	GAA	NN/NI/NI	βγδ
TAL014/016/022	GAC	NN/NI/HD	βγδ
TAL014/016/023	GAG	NN/NI/NK	βγδ
TAL014/016/024	GAG	NN/NI/NN	βγδ
TAL014/016/025	GAT	NN/NI/NG	βγδ
TAL014/017/021	GCA	NN/HD/NI	βγδ
TAL014/017/022	GCC	NN/HD/HD	βγδ
TAL014/017/023	GCG	NN/HD/NK	βγδ
TAL014/017/024	GCG	NN/HD/NN	βγδ
TAL014/017/025	GCT	NN/HD/NG	βγδ
TAL014/018/021	GGA	NN/NK/NI	βγδ
TAL014/018/022	GGC	NN/NK/HD	βγδ
TAL014/018/023	GGG	NN/NK/NK	βγδ
TAL014/018/024	GGG	NN/NK/NN	βγδ
TAL014/018/025	GGT	NN/NK/NG	βγδ
TAL014/019/021	GGA	NN/NN/NI	βγδ
TAL014/019/022	GGC	NN/NN/HD	βγδ
TAL014/019/023	GGG	NN/NN/NK	βγδ
TAL014/019/024	GGG	NN/NN/NN	βγδ
TAL014/019/025	GGT	NN/NN/NG	βγδ
TAL014/020/021	GTA	NN/NG/NI	βγδ
TAL014/020/022	GTC	NN/NG/HD	βγδ
TAL014/020/023	GTG	NN/NG/NK	βγδ
TAL014/020/024	GTG	NN/NG/NN	βγδ
TAL014/020/025	GTT	NN/NG/NG	βγδ
TAL015/016/021	TAA	NG/NI/NI	βγδ
TAL015/016/022	TAC	NG/NI/HD	βγδ
TAL015/016/023	TAG	NG/NI/NK	βγδ
TAL015/016/024	TAG	NG/NI/NN	βγδ
TAL015/016/025	TAT	NG/NI/NG	βγδ
TAL015/017/021	TCA	NG/HD/NI	βγδ
TAL015/017/022	TCC	NG/HD/HD	βγδ
TAL015/017/023	TCG	NG/HD/NK	βγδ
TAL015/017/024	TCG	NG/HD/NN	βγδ
TAL015/017/025	TCT	NG/HD/NG	βγδ
TAL015/018/021	TGA	NG/NK/NI	βγδ
TAL015/018/022	TGC	NG/NK/HD	βγδ
TAL015/018/023	TGG	NG/NK/NK	βγδ
TAL015/018/024	TGG	NG/NK/NN	βγδ
TAL015/018/025	TGT	NG/NK/NG	βγδ
TAL015/019/021	TGA	NG/NN/NI	βγδ
TAL015/019/022	TGC	NG/NN/HD	βγδ
TAL015/019/023	TGG	NG/NN/NK	βγδ
TAL015/019/024	TGG	NG/NN/NN	βγδ
TAL015/019/025	TGT	NG/NN/NG	βγδ
TAL015/020/021	TTA	NG/NG/NI	βγδ
TAL015/020/022	TTC	NG/NG/HD	βγδ
TAL015/020/023	TTG	NG/NG/NK	βγδ
TAL015/020/024	TTG	NG/NG/NN	βγδ
TAL015/020/025	TTT	NG/NG/NG	βγδ
TAL011/031	AA	NI/NI	βγ'
TAL011/032	AC	NI/HD	βγ'
TAL011/033	AG	NI/NK	βγ'
TAL011/034	AG	NI/NN	βγ'
TAL011/035	AT	NI/NG	βγ'
TAL012/031	CA	HD/NI	βγ'
TAL012/032	CC	HD/HD	βγ'
TAL012/033	CG	HD/NK	βγ'
TAL012/034	CG	HD/NN	βγ'
TAL012/035	CT	HD/NG	βγ'
TAL013/031	GA	NK/NI	βγ'
TAL013/032	GC	NK/HD	βγ'
TAL013/033	GG	NK/NK	βγ'
TAL013/034	GG	NK/NN	βγ'
TAL013/035	GT	NK/NG	βγ'
TAL014/031	GA	NN/NI	βγ'
TAL014/032	GC	NN/HD	βγ'
TAL014/033	GG	NN/NK	βγ'
TAL014/034	GG	NN/NN	βγ'
TAL014/035	GT	NN/NG	βγ'
TAL015/031	TA	NG/NI	βγ'
TAL015/032	TC	NG/HD	βγ'
TAL015/033	TG	NG/NK	βγ'
TAL015/034	TG	NG/NN	βγ'
TAL015/035	TT	NG/NG	βγ'
TAL021/036	AA	NI/NI	δϵ'
TAL021/037	AC	NI/HD	δϵ'
TAL021/038	AG	NI/NK	δϵ'
TAL021/039	AG	NI/NN	δϵ'
TAL021/040	AT	NI/NG	δϵ'
TAL022/036	CA	HD/NI	δϵ'
TAL022/037	CC	HD/HD	δϵ'
TAL022/038	CG	HD/NK	δϵ'
TAL022/039	CG	HD/NN	δϵ'
TAL022/040	CT	HD/NG	δϵ'
TAL023/036	GA	NK/NI	δϵ'
TAL023/037	GC	NK/HD	δϵ'
TAL023/038	GG	NK/NK	δϵ'
TAL023/039	GG	NK/NN	δϵ'
TAL023/040	GT	NK/NG	δϵ'
TAL024/036	GA	NN/NI	δϵ'
TAL024/037	GC	NN/HD	δϵ'
TAL024/038	GG	NN/NK	δϵ'
TAL024/039	GG	NN/NN	δϵ'
TAL024/040	GT	NN/NG	δϵ'
TAL025/036	TA	NG/NI	δϵ'
TAL025/037	TC	NG/HD	δϵ'
TAL025/038	TG	NG/NK	δϵ'
TAL025/039	TG	NG/NN	δϵ'
TAL025/040	TT	NG/NG	δϵ'
TAL011	A	NI	β
TAL012	C	HD	β
TAL013	G	NK	β
TAL014	G	NN	β
TAL015	T	NG	β

[0213] To prepare DNA fragments encoding a units for use in assembly, 20 rounds of PCR were performed with each a unit plasmid as a template using primers oJS2581 (5'-Biotin-TCTAGAGAAGACAAGAACCTGACC-3' (SEQ ID NO:237)) and oJS2582 (5'-GGATCCGGTCTCTTAAGGC-CGTGG-3' (SEQ ID NO:238)). The resulting PCR products were biotinylated on the 5' end. Each a PCR product was then digested with 40 units of BsaI-HF restriction enzyme to generate 4 bp overhangs, purified using the QIAquick PCR purification kit (QIAGEN) according to manufacturer's instructions except that the final product was eluted in 50 μl of 0.1×EB.

[0214] To prepare DNA fragments encoding β, βγδϵ, βγδ, βγ, βγ*, and δϵ* repeats, 10 μg of each of these plasmids was digested with 50 units of BbsI restriction enzyme in NEBuffer 2 for 2 hours at 37° C. followed by serial restriction digests performed in NEBuffer 4 at 37° C. using 100 units each of XbaI, BamHI-HF, and SalI-HF enzymes that were added at 5 minute intervals. The latter set of restriction digestions were designed to cleave the plasmid backbone to ensure that this larger DNA fragment does not interfere with subsequent ligations performed during the assembly process. These restriction to digest reactions were then purified using the QIAquick PCR purification kit (QIAGEN) according to manufacturer's instructions except that the final product was eluted in 180 μl of 0.1×EB.

[0215] All assembly steps were performed using a Sciclone G3 liquid handling workstation (Caliper) in 96-well plates and using a SPRIplate 96-ring magnet (Beckman Coulter Genomics) and a DynaMag-96 Side magnet (Life Technologies). In the first assembly step, a biotinylated α unit fragment was ligated to the first βγδϵ fragment and then the resulting αβγδϵ fragments are bound to Dynabeads MyOne Cl streptavidin-coated magnetic beads (Life Technologies) in 2×B&W Buffer (Life Technologies). Beads were then drawn to the side of the well by placing the plate on the magnet and then washed with 100 μl B&W buffer with 0.005% Tween 20 (Sigma) and again with 100 μl 0.1 mg/ml bovine serum albumin (BSA) (New England Biolabs). Additional βγδϵ fragments were ligated by removing the plate from the magnet, resuspending the beads in solution in each well, digesting the bead bound fragment with BsaI-HF restriction enzyme, placing the plate on the magnet, washing with 100 μl B&W/Tween20 followed by 100 μl of 0.1 mg/ml BSA, and then ligating the next fragment. This process was repeated multiple times with additional βγδϵ units to extend the bead-bound fragment. The last fragment to be ligated was always a β, βγ*, βγδ, or δϵ* unit to enable cloning of the full-length fragment into expression vectors (note that fragments that end with a δϵ* unit are always preceded by ligation of a βγ unit).

[0216] The final full-length bead-bound fragment was digested with 40 units of BsaI-HF restriction enzyme followed by 25 units of BbsI restriction enzyme (New England Biolabs). Digestion with BbsI releaseed the fragment from the beads and generated a unique 5' overhang for cloning of the fragment. Digestion with BsaI-HF resulted in creation of a unique 3' overhang for cloning.

[0217] DNA fragments encoding the assembled TALE repeat arrays were subcloned into one of four TALEN expression vectors. Each of these vectors included a CMV promoter, a translational start codon optimized for mammalian cell expression, a triple FLAG epitope tag, a nuclear localization signal, amino acids 153 to 288 from the TALE13 protein (Miller et al., 2011, Nat. Biotechnol., 29:143-148), two unique and closely positioned Type IIS BsmBI restriction sites, a 0.5 TALE repeat domain encoding one of four possible RVDs (NI, HD, NN, or NG for recognition of an A, C, G, or T nucleotide, respectively), amino acids 715 to 777 from the TALE13 protein, and the wild-type FokI cleavage domain. All DNA fragments possessed overhangs that enable directional cloning into any of the four TALEN expression vectors that has been digested with BsmBI.

[0218] To prepare a TALEN expression vector for subcloning, 5 μg of plasmid DNA were digested with 50 units of BsmBI restriction enzyme (New England Biolabs) in NEBuffer 3 for 8 hours at 55 degrees C. Digested DNA was purified using 90 μl of Ampure XP beads (Agencourt) according to manufacturer's instructions and diluted to a final concentration of 5 ng/μl in 1 mM TrisHCl. The assembled TALE repeat arrays were ligated into TALEN expression vectors using 400 U of T4 DNA Ligase (New England Biolabs). Ligation products were transformed into chemically competent XL-1 Blue cells. Six colonies were picked for each ligation and plasmid DNA isolated by an alkaline lysis miniprep procedure. Simultaneously, the same six colonies were screened by PCR using primers oSQT34 (5'-GACGGTGGCTGTCAAATACCAAGATATG-3' (SEQ ID NO:239)) and oSQT35 (5'-TCTCCTCCAGTTCACTTTTGACTAGTTGGG-3' (SEQ ID NO:240)). PCR products were analyzed on a QIAxcel capillary electrophoresis system (Qiagen). Miniprep DNA from clones that contained correctly sized PCR products were sent for DNA sequence confirmation with primers oSQT1 (5'-AGTAACAGCGGTAGAGGCAG-3' (SEQ ID NO:241)), oSQT3 (5'-ATTGGGCTACGATGGACTCC-3' (SEQ ID NO:242)), and oJS2980 (5-TTAATTCAATATATTCATGAGGCAC-3' (SEQ ID NO:243)).

[0219] Because the final fragment ligated can encode one, two, or three TALE repeats, the methods disclosed herein can be used to assemble arrays consisting of any desired number of TALE repeats. Assembled DNA fragments encoding the final full-length TALE repeat array are released from the beads by restriction enzyme digestion and can be directly cloned into a desired expression vector of choice.

[0220] The methods can be efficiently practiced in 96-well format using a robotic liquid handling workstation. With automation, DNA fragments encoding 96 different TALE repeat arrays of variable lengths can be assembled in less than one day. Medium-throughput assembly of fragments can be performed in one to two days using multi-channel pipets and 96-well plates. Fragments assembled using either approach can then be cloned into expression vectors (e.g., for expression as a TALEN) to generate sequence-verified plasmids in less than one week. Using the automated assembly approach, sequence-verified TALE repeat array expression plasmids can be made quickly and inexpensively.

Example 6

Large-Scale Testing of Assembled TALENs Using a Human Cell-Based Reporter Assay

[0221] To perform a large-scale test of the robustness of TALENs for genome editing in human cells, the method described in Example 5 was used to construct a series of plasmids encoding 48 TALEN pairs targeted to different sites scattered throughout the EGFP reporter gene. Monomers in each of the TALEN pairs contained the same number of repeats (ranging from 8.5 to 19.5 in number), and these pairs were targeted to sites possessing a fixed length "spacer" sequence (16 bps) between the "half-sites" bound by each TALEN monomer (Table 6).

TABLE 6

EGFP reporter gene sequences targeted by 48 pairs of TALENs

TALEN pair #	Position within EGFP of the first nucleotide in the binding site	Target site (half-sites in CAPS, spacer in lowercase)	SEQ ID NO:	# of repeat domains in Left TALEN	# of repeat domains in Right TALEN
1	-8	TCGCCACCATggtgagcaagggcgagGAGCTGTTCA	93	8.5	8.5
2	35	TGGTGCCCATcctggtcgagctggacGGCGACGTAA	94	8.5	8.5
3	143	TCTGCACCACcggcaagctgcccgtgCCCTGGCCCA	95	8.5	8.5
4	425	TGGAGTACAActacaacagccacaacGTCTATATCA	96	8.5	8.5
5	82	TTCAGCGTGTCcggcgagggcgagggcGATGCCACCTA	97	9.5	9.5
6	111	TGCCACCTACGgcaagctgaccctgaaGTTCATCTGCA	98	9.5	9.5
7	172	TGGCCCACCCTcgtgaccaccctgaccTACGGCGTGCA	99	9.5	9.5
8	496	TTCAAGATCCGccacaacatcgaggacGGCAGCGTGCA	100	9.5	9.5
9	-23	TAGAGGATCCACcggtcgccaccatggtGAGCAAGGGCGA	101	10.5	10.5
10	91	TCCGGCGAGGGCgagggcgatgccacctACGGCAAGCTGA	102	10.5	10.5
11	194	TGACCTACGGCGtgcagtgcttcagccgCTACCCCGACCA	103	10.5	10.5
12	503	TCCGCCACAACAt cgaggacggcagcgtGCAGCTCGCCGA	104	10.5	10.5
13	44	TCCTGGTCGAGCTggacggcgacgtaaacGGCCACAAGTTCA	105	11.5	11.5
14	215	TCAGCCGCTACCCcgaccacatgaagcagCACGACTTCTTCA	106	11.5	11.5
15	251	TCTTCAAGTCCGCcatgcccgaaggctacGTCCAGGAGCGCA	107	11.5	11.5
16	392	TCAAGGAGGACGGcaacatcctggggcacAAGCTGGAGTACA	108	11.5	11.5
17	485	TCAAGGTGAACTTcaagatccgccacaacATCGAGGACGGCA	109	11.5	11.5
18	-16	TCCACCGGTCGCCAccatggtgagcaagggCGAGGAGCTGTTCA	110	12.5	12.5
19	82	TTCAGCGTGTCCGGcgagggcgagggcgatGCCACCTACGGCAA	111	12.5	12.5
20	214	TTCAGCCGCTACCCcgaccacatgaagcagCACGACTTCTTCAA	112	12.5	12.5
21	436	TACAACAGCCACAAcgtctatatcatggccGACAAGCAGAAGAA	113	12.5	12.5
22	35	TGGTGCCCATCCTGGtcgagctggacggcgaCGTAAACGGCCACAA	114	13.5	13.5

TABLE 6-continued

EGFP reporter gene sequences targeted by 48 pairs of TALENs

TALEN pair #	Position within EGFP of the first nucleotide in the binding site	Target site (half-sites in CAPS, spacer in lowercase)	SEQ ID NO:	# of repeat domains in Left TALEN	# of repeat domains in Right TALEN
23	266	TGCCCGAAGGCTACGtccaggagcgcaccatCTTCTTCAAGGACGA	115	13.5	13.5
24	362	TGAACCGCATCGAGCtgaagggcatcgacttCAAGGAGGACGGCAA	116	13.5	13.5
25	497	TCAAGATCCGCCACAacatcgaggacggcagCGTGCAGCTCGCCGA	117	13.5	13.5
26	23	TGTTCACCGGGGTGGTgcccatcctggtcgagCTGGACGGCGACGTAA	118	14.5	14.5
27	38	TGCCCATCCTGGTCGAgctggacggcgacgtaAACGGCCACAAGTTCA	119	14.5	14.5
28	89	TGTCCGGCGAGGGCGAgggcgatgccacctacGGCAAGCTGACCCTGA	120	14.5	14.5
29	140	TCATCTGCACCACCGGcaagctgcccgtgcccTGGCCCACCCTCGTGA	121	14.5	14.5
30	452	TCTATATCATGGCCGAcaagcagaagaacggcATCAAGGTGAACTTCA	122	14.5	14.5
31	199	TACGGCGTGCAGTGCTTcagccgctaccccgacCACATGAAGCAGCACGA	123	15.5	15.5
32	223	TACCCCGACCACATGAAgcagcacgacttcttcAAGTCCGCCATGCCCGA	124	15.5	15.5
33	259	TCCGCCATGCCCGAAGGctacgtccaggagcgcACCATCTTCTTCAAGGA	125	15.5	15.5
34	391	TTCAAGGAGGACGGCAAcatcctggggcacaagCTGGAGTACAACTACAA	126	15.5	15.5
35	430	TACAACTACAACAGCCAcaacgtctatatcatgGCCGACAAGCAGAAGAA	127	15.5	15.5
36	26	TCACCGGGGTGGTGCCCAtcctggtcgagctggaCGGCGACGTAAACGGCCA	128	16.5	16.5
37	68	TAAACGGCCACAAGTTCAgcgtgtccggcgagggCGAGGGCGATGCCACCTA	129	16.5	16.5
38	206	TGCAGTGCTTCAGCCGCTaccccgaccacatgaaGCAGCACGACTTCTTCAA	130	16.5	16.5

TABLE 6-continued

EGFP reporter gene sequences targeted by 48 pairs of TALENs

TALEN pair #	Position within EGFP of the first nucleotide in the binding site	Target site (half-sites in CAPS, spacer in lowercase)	SEQ ID NO:	# of repeat domains in Left TALEN	# of repeat domains in Right TALEN
39	83	TCAGCGTGTCCGGCGAGGGcgagggcgatgccaccTACGGCAAGCTGACCCTGA	131	17.5	17.5
40	134	TGAAGTTCATCTGCACCACcggcaagctgcccgtgCCCTGGCCCACCCTCGTGA	132	17.5	17.5
41	182	TCGTGACCACCCTGACCTAcggcgtgcagtgcttcAGCCGCTACCCCGACCACA	133	17.5	17.5
42	458	TCATGGCCGACAAGCAGAAgaacggcatcaaggtgAACTTCAAGATCCGCCACA	134	17.5	17.5
43	25	TTCACCGGGGTGGTGCCCATcctggtcgagctggacGGCGACGTAAACGGCCACAA	135	18.5	18.5
44	145	TGCACCACCGGCAAGCTGCCcgtgccctggcccaccCTCGTGACCACCCTGACCTA	136	18.5	18.5
45	253	TTCAAGTCCGCCATGCCCGAaggctacgtccaggagCGCACCATCTTCTTCAAGGA	137	18.5	18.5
46	454	TATATCATGGCCGACAAGCAgaagaacggcatcaagGTGAACTTCAAGATCCGCCA	138	18.5	18.5
47	139	TTCATCTGCACCACCGGCAAGctgcccgtgccctggcCCACCCTCGTGACCACCCTGA	139	19.5	19.5
48	338	TGAAGTTCGAGGGCGACACCCtggtgaaccgcatcgaGCTGAAGGGCATCGACTTCAA	140	19.5	19.5

[0222] Each of the 48 TALEN pairs was tested in human cells for its ability to disrupt the coding sequence of a chromosomally integrated EGFP reporter gene. In this assay, NHEJ-mediated repair of TALEN-induced breaks within the EGFP coding sequence led to loss of EGFP expression, which was quantitatively assessed using flow cytometry 2 and 5 days following transfection. (To ensure that activities of each active TALEN pair could be detected, we only targeted sites located at or upstream of nucleotide position 503 in the gene, a position we had previously shown would disrupt EGFP function when mutated with a zinc finger nuclease (ZFN) (Maeder et al., 2008, Mol. Cell. 31:294-301).) Strikingly, all 48 TALEN pairs showed significant EGFP gene-disruption activities in this assay (FIG. **19**A). The net percentage of EGFP-disrupted cells induced by TALENs on day 2 post-transfection ranged from 9.4% to 68.0%, levels comparable to the percentage disruption observed with four EGFP-targeted ZFN pairs originally made by the Oligomerized Pool Engineering (OPEN) method (FIG. **19**A). These results demonstrate that TALENs containing as few as 8.5 TALE repeats possess significant nuclease activities and provide a large-scale demonstration of the robustness of TALENs in human cells.

[0223] Interestingly, re-quantification of the percentage of EGFP-negative cells at day 5 post-transfection revealed that cells expressing shorter-length TALENs (such as those composed of 8.5 to 10.5 repeats) showed significant reductions in the percentage of EGFP-disrupted cells whereas those expressing longer TALENs did not (FIGS. **19**A-B and **20**A). One potential explanation for this effect is cellular toxicity associated with expression of shorter-length TALENs. Consistent with this hypothesis, in cells transfected with plasmids encoding shorter-length TALENs, greater reductions in the percentage of tdTomato-positive cells were observed from day 2 to day 5 post-transfection (FIG. **20**D) (a tdTomato-encoding plasmid was co-transfected together with the TALEN expression plasmids on day 0). Taken together, our results suggest that although shorter-length TALENs are as active as longer-length TALENs, the former can cause greater cytotoxicity in human cells.

[0224] Our EGFP experiments also provided an opportunity to assess four of five computationally-derived design guidelines (Cermak et al., 2011, Nucleic Acids Res., 39:e82). The guidelines proposed by Cermak are as follows:

[0225] 1. The nucleotide just 5' to the first nucleotide of the half-site should be a thymine.

[0226] 2. The first nucleotide of the half-site should not be a thymine.

[0227] 3. The second nucleotide of the half-site should not be an adenosine.

[0228] 4. The 3' most nucleotide in the target half-site should be a thymine.

[0229] 5. The composition of each nucleotide within the target half-site should not vary from the observed percentage composition of naturally occurring binding sites by more than 2 standard deviations. The percentage composition of all naturally occurring TALE binding sites is: A=31±16%, C=37±13%, G=9±8%, T=22±10%. Hence, the nucleotide composition of potential TALE binding sites should be: A=0% to 63%, C=11% to 63%, G=0% to 25% and T=2% to 42%.

[0230] These guidelines have been implemented in the TALE-NT webserver (boglabx.plp.iastate.edu/TALENT/TALENT/) to assist users in identifying potential TALEN target sites. All 48 of the sequences we targeted in EGFP did not meet one or more of these guidelines (however, note that all of our sites did meet the requirement for a 5' T). The ~100% success rate observed for these 48 sites demonstrates that TALENs can be readily obtained for target sequences that do not follow these guidelines. In addition, for each of the four design guidelines, we did not find any statistically significant correlation between guideline violation and the level of TALEN-induced mutagenesis on either day 2 or day 5 post-transfection. We also failed to find a significant correlation between the total number of guideline violations and the level of mutagenic TALEN activity. Thus, our results show that failure to meet four of the five previously described design guidelines when identifying potential TALEN target sites does not appear to adversely affect success rates or nuclease efficiencies.

Example 7

High-Throughput Alteration of Endogenous Human Genes Using Assembled TALENs

[0231] Having established the robustness of the TALEN platform with a chromosomally integrated reporter gene, it was next determined whether this high success rate would also be observed with endogenous genes in human cells. To test this, the assembly method described in Example 5 was used to engineer TALEN pairs targeted to 96 different human genes: 78 genes implicated in human cancer (Vogelstein and Kinzler, 2004, Nat. Med., 10:789-799) and 18 genes involved in epigenetic regulation of gene expression (Table 7). For each gene, a TALEN pair was designed to cleave near the amino-terminal end of the protein coding sequence, although in a small number of cases the presence of repetitive sequences led us to target alternate sites in neighboring downstream exons or introns (Table 7). Guided by the results with the EGFP TALENs, TALENs composed of 14.5, 15.5, or 16.5 repeats were constructed that cleaved sites with 16, 17, 18, 19 or 21 bp spacer sequences. All of the target sites had a T at the 5' end of each half-site.

TABLE 7

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
ABL1	22.5 ± 7.1	TACCTATTATTACTTTATggggcagcagcctggaaAAGTACTTGGGGACCAA	141.	16.5	17	15.5	Cancer
AKT2	14.1 ± 7.3	TGTGTCTTGGGATGAGTGggtcagtgttctggtgCTCACAGGATGGCTGGCA	142.	16.5	16	16.5	Cancer
ALK	12.7 ± 2.9	TCCTGTGGCTCCTGCCGCtgctgctttccacggcAGCTGTGGGCTCCGGGA	143.	16.5	16	15.5	Cancer
APC	48.8 ± 9.8	TATGTACGCCTCCCTGGGctcgggtccggtcgccCCTTTGCCCGCTTCTGTA	144.	16.5	16	16.5	Cancer
ATM	35.5 ± 15.6	TGAATTGGGATGCTGTTTttaggtattctattcaaaTTTATTTTACTGTCTTTA	145.	16.5	18	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
AXIN2	2.5 ± 0.6	TCCCTCACCATGAGTAGCgctatgttggtgacttGCCTCCCGGACCCCAGCA	146.	16.5	16	16.5	Cancer
BAX	14.7 ± 11.6	TGTGCGATCTCCAAGCACtgaggggcagaaactcCCGGATCGGGCGCTGCCA	147.	16.5	16	16.5	Cancer
BCL6	14.9 ± 5.9	TTTTCAAGTGAAGACAAAatggcctcgccggctgACAGCTGTATCCAGTTCA	148.	16.5	16	16.5	Cancer
BMPR1A	50.4 ± 16.4	TACAATTGAACAATGCCTcagctatacatttacatCAGATTATTGGGAGCCTA	149.	16.5	17	16.5	Cancer
BRCA1	44.5 ± 15.5	TCCGAAGCTGACAGATGGgtattctttgacggggGGTAGGGGCGGAACCTGA	150.	16.5	16	16.5	Cancer
BRCA2	41.6 ± 10.5	TTAGACTTAGGTAAGTAAtgcaatatggtagactGGGGAGAACTACAAACTA	151.	16.5	16	16.5	Cancer
CBX3	35.2 ± 22.6	TCTGCAATAAAAAATGGCctccaacaaaactacaTTGGTAAGTTAATGAAAA	152.	16.5	16	16.5	Epigenetic
CBX8	13.5 ± 3.4	TGGAGCTTTCAGCGGTGGgggagcgggtgttcgcgGCCGAAGCCCTCCTGAA	153.	16.5	17	15.5	Epigenetic
CCND1	40.5 ± 2.2	TGGAACACCAGCTCCTGTgctgcgaagtggaaaccatCCGCCGCGCGTACCCCGA	154.	16.5	19	16.5	Cancer
CDC73	36.3 ± 7.7	TGCTTAGCGTCCTGCGACagtacaacatccagaaGAAGGAGATTGTGGTGAA	155.	16.5	16	16.5	Cancer
CDH1	none	TGCTGCAGGTACCCCGGAtcccctgacttgcgagGGACGCATTCGGGCCGCA	156.	16.5	16	16.5	Cancer
CDK4	21.5 ± 17.4	TCCCTTGATCTGAGAAtggctacctctcgataTGAGCCAGTGGCTGAAA	157.	14.5	16	15.5	Cancer
CHD4	9.6 ± 0.1	TGGCGTCGGGCCTGGGCtccccgtccccctgctcGGCGGGCAGTGAGGAGGA	158.	15.5	17	16.5	Epigenetic
CHD7	11.4 ± 2.7	TGTGTTGGAAGAAGATGGcagatccaggaatgat	159.	16.5	16	16.5	Epigenetic

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
		GAGTCTTTTTGGCGAGGA					
CTNNB1	26.0 ± 8.1	TCCAGCGTGGACAATGGctactcaaggtttgtgTCATTAAATCTTTAGTTA	160.	15.5	16	16.5	Cancer
CYLD	24.7 ± 2.3	TAATATCACAATGAGTTCaggcttatggagccaagaAAAAGTCACTTCACCCTA	161.	16.5	18	16.5	Cancer
DDB2	15.8 ± 7.2	TCACACGGAGGACGCGatggctcccaagaaacGCCCAGAAACCCAGAAGA	162.	14.5	16	16.5	Cancer
ERCC2	55.8 ± 12.7	TCCGGCCGGCGCCATGAagtgagaagggggctgGGGGTCGCGCTCGCTA	163.	15.5	16	14.5	Cancer
ERCC5	none	TCCGGGATCGCCATGGGAactcaatagaaaatcctcaTCTTCTCACTTTGTTTCA	164.	16.5	19	16.5	Cancer
EWSR1	14.3 ± 8.2	TGGCGTCCACGGGTGAGTatggtggaactgcggtcGCGCCGGCGGTAGCCGGA	165.	16.5	17	16.5	Cancer
EXT1	9.5 ± 3.0	TGACCCAGGCAGGACACAtgcaggccaaaaaacgcTATTTCATCCTGCTCTCA	166.	16.5	17	16.5	Cancer
EXT2	none	TTCCTCCCAGGGGGATGTcctgcgcctcagggtcCGGTGGTGGCCTGCGGCA	167.	16.5	16	16.5	Cancer
EZH2	41.3 ± 2.6	TGCTTTTAGAATAATCATgggccagactgggaagAAATCTGAGAAGGGACCA	168.	16.5	16	16.5	Epigenetic
FANCA	9.7 ± 5.0	TAGGCGCCAAGGCCATGTccgactcgtgggtcccGAACTCCGCCTCGGGCCA	169.	16.5	16	16.5	Cancer
FANCC	23.7 ± 17.8	TGAAGGGACATCACCTTTtcgctttttccaagatgGCTCAAGATTCAGTAGA	170.	16.5	17	15.5	Cancer
FANCE	none	TGCCCCGGCATGGCGACAccggacgcggggctcccTGGGGCTGAGGGCGTGGA	171.	16.5	17	16.5	Cancer
FANCF	46.0 ± 7.7	TTCGCGCACCTCATGGaatcccttctgcagcaCCTGGATCGCTTTTCCGA	172.	14.5	16	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
FANCG	26.9 ± 16.2	TCGGCCACCATGTCCCgccagaccacctctgtGGGCTCCAGCTGCCTGGA	173.	14.5	16	16.5	Cancer
FES	12.6 ± 10.6	TCCCCAGAACAGCACTATgggcttctcttccgagctGTGCAGCCCCCAGGGCCA	174.	16.5	18	16.5	Cancer
FGFR1	17.4 ± 6.2	TCTGCTCCCCACCGAGGAcctctgcatgcaggcaTGAATCCCAGGAGCCTA	175.	16.5	16	15.5	Cancer
FH	20.9 ± 11.8	TGTACCGAGCACTTCGGCtcctcgcgcgctcgcgtCCCCTCGTGCGGGCTCCA	176.	16.5	17	16.5	Cancer
FLCN	11.1 ± 4.4	TCTCCAAGGCACCATGAAtgccatcgtggctctctgCCACTTCTGCGAGCTCCA	177.	16.5	18	16.5	Cancer
FLT3	none	TCCGGAGGCCATGCCGGCgttggcgcgcgacggcggccaGCTGCCGCTGCTCGGTA	178.	16.5	21	15.5	Cancer
FLT4	9.9 ± 5.0	TGCAGCGGGGCGCCGCGCtgtgcctgcgactgtggctCTGCCTGGGACTCCTGGA	179.	16.5	19	16.5	Cancer
FOXO1	8.5 ± 1.1	TCACCATGGCCGAGGCGcctcaggtggtggagaTCGACCCGGACTTCGA	180.	15.5	16	14.5	Cancer
FOXO3	7.3 ± 2.3	TCTCCGCTCGAAGTGGAGctggacccggagttcgagCCCCAGAGCCGTCCGCGA	181.	16.5	18	16.5	Cancer
GLI1	21.5 ± 12.4	TCCTCTGAGACGCCATGTtcaactcgatgaccccACCACCAATCAGTAGCTA	182.	16.5	16	16.5	Cancer
HDAC1	10.8 ± 3.0	TGGCGCAGACGCAGGGCacccggaggaaagtctgTTACTACTACGACGGTGA	183.	15.5	17	16.5	Epigenetic
HDAC2	4.2 ± 0.9	TGCGCTCACCTCCCTGCGgcctcctgaggtggtttgGTGGCCCCCTCCTCGCGA	184.	16.5	18	16.5	Epigenetic
HDAC6	21.4 ± 2.1	TCCTCAACTATGACCTCAaccggccaggattccaCCACAACCAGGCAGCGAA	185.	16.5	16	16.5	Epigenetic
HMGA2	3.0 ± 1.5	TGAGCGCACGCGGTGAGGgcgcggggcagccgtcCACTTCAGCCCAGGGACA	186.	16.5	16	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
HOXA13	7.6 ± 3.1	TCCGTGCTCCTCCACCCCcgctggatcgagcccacCGTCATGTTTCTCTACGA	187.	16.5	17	16.5	Cancer
HOXA9	6.4 ± 2.7	TGGGCACGGTGATGGCcaccactggggccctgGGCAACTACTACGTGGA	188.	14.5	16	15.5	Cancer
HOXC13	10.5 ± 0.3	TCCAGCAGATCATGTCATgacgacttcgctgctcctGCATCCACGCTGGCCGGA	189.	16.5	18	16.5	Cancer
HOXD11	none	TTGACGAGTGCGGCCAGagcgcagccagcatgtaCCTGCCGGGCTGCGCCTA	190.	15.5	17	16.5	Cancer
HOXD13	none	TGCGGGCAGACGGCGGGGgcgccggtggcgccccgGCCTCTTCCTCCTCCTCA	191.	16.5	17	16.5	Cancer
JAK2	44.9 ± 16.9	TCTGAAAAAGACTCTGCAtgggaatggcctgcctTACGATGACAGAAATGGA	192.	16.5	16	16.5	Cancer
KIT	none	TACCGCGATGAGAGGCGCtcgcggcgcctgggattttCTCTGCGTTCTGCTCCTA	193.	16.5	19	16.5	Cancer
KRAS	9.4 ± 0.9	TGAAAATGACTGAATATAaacttgtggtagttggaGCTGGTGGCGTAGGCAA	194.	16.5	17	15.5	Cancer
MAP2K4	11.9 ± 7.1	TAGGGTCCCCGGCGCCAGgccacccggccgtcagCAGCATGCAGGGTAAGGA	195.	16.5	16	16.5	Cancer
MDM2	33.0 ± 20.2	TCCAAGCGCGAAAACCCCggatggtgaggagcaggTACTGGCCCGGCAGCGA	196.	16.5	17	15.5	Cancer
MET	40.4 ± 10.7	TTATTATTACATGGCTTTgccttactgaggcttcATCTTGTCCTCTGGTCCA	197.	16.5	16	16.5	Cancer
MLH1	44.9 ± 6.3	TCTGGCGCCAAAATGTCGttcgtggcaggggttaTTCGGCGGCTGGACGAGA	198.	16.5	16	16.5	Cancer
MSH2	27.5 ± 10.4	TGAGGAGGTTTCGACATGgcggtgcagccgaaggAGACGCTGCAGTTGGAGA	199.	16.5	16	16.5	Cancer
MUTYH	24.9 ± 8.4	TCACTGTCGGCGGCCATGacaccgctcgtctccc	200.	16.5	18	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
		gcCTGAGTCGTCTGTGGGTA					
MYC	13.4 ± 4.0	TGCTTAGACGCTGGATTTttttcgggtagtggaaAACCAGGTAAGCACCGAA	201.	16.5	16	16.5	Cancer
MYCL1	17.3 ± 0.6	TCCCGCAGGGAGCGGACAtggactacgactcgtaCCAGCACTATTTCTACGA	202.	16.5	16	16.5	Cancer
MYCN	16.3 ± 11.6	TGCCGAGCTGCTCCACgtccaccatgccgggcATGATCTGCAAGAACCCA	203.	14.5	16	16.5	Cancer
NBN	46.3 ± 15.5	TGAGGAGCCGGACCGAtgtggaaactgctgccCGCCGCGGGCCCGGCA	204.	14.5	16	14.5	Cancer
NCOR1	29.6 ± 13.1	TCTTTACTGATAATGTCAagttcatgttaccctcCCAACCAAGGAGCATTCA	205.	16.5	16	16.5	Epigenetic
NCOR2	3.3 ± 0.6	TGGAGGGCCACTGAGCcccgctacccgcccccaCAGCCTTTCCTACCCA	206.	14.5	16	14.5	Epigenetic
NTRK1	none	TCGGCGCATGAAGGAGGTactcctcattttcgttCTCTCTCTCTGTGCCCCA	207.	16.5	16	16.5	Cancer
PDGFRA	16.0 ± 4.3	TTGCGCTCGGGGCGGCCAtgtcggccggcgaggtCGAGCGCCTAGTGTCGGA	208.	16.5	16	16.5	Cancer
PDGFRB	16.0 ± 3.2	TCTGCAGGACACCATGCGgcttccgggtgcgatgCCAGCTCTGGCCCTCAAA	209.	16.5	16	16.5	Cancer
PHF8	22.2 ± 6.1	TGAGTACTCCGCCTCTACcccggctgaagcccgcCCCCGCCGCCACCTATTA	210.	16.5	16	16.5	Epigenetic
PMS2	26.9 ± 9.5	TCGGGTGTTGCATCCATGgagcgagctgagagctcgAGGTGAGCGGGGCTCGCA	211.	16.5	18	16.5	Cancer
PTCH1	27.5 ± 15.9	TGGAACTGCTTAATAGaaacaggcttgtaattGTGAGTCCGCGCTGCA	212.	14.5	16	14.5	Cancer
PTEN	31.5 ± 11.7	TCCCAGACATGACAGCCatcatcaaagagatcgTTAGCAGAAACAAAAGGA	213.	15.5	16	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
RARA	13.4 ± 6.1	TGGCATGGCCAGCAACAGcagctcctgcccgacacCTGGGGGCGGGCACCTCA	214.	16.5	17	16.5	Cancer
RBBP5	15.7 ± 9.5	TGCTGGGTGAGAAGGGCtgtggctgcgttttagaGAAGCGTTGGGTACTGGA	215.	15.5	17	16.5	Epigenetic
RECQL4	22.1 ± 16.2	TGCGGGACGTGCGGGAGCggctgcaggcgtgggaGCGCGCGTTCCGACGGCA	216.	16.5	16	16.5	Cancer
REST	none	TCAGAATACAGTTATGGCcacccaggtaatggggCAGTCTTCTGGAGGAGGA	217.	16.5	16	16.5	Epigenetic
RET	5.4 ± 1.8	TGAGTTCTGCCGGCCGCCggctcccgcaggggccaGGGCGAAGTTGGCGCCGA	218.	16.5	17	16.5	Cancer
RNF2	none	TTCTTTATTTCCAGCAATgtctcaggctgtgcagACAAACGGAACTCAACCA	219.	16.5	16	16.5	Epigenetic
RUNX1	25.1 ± 6.9	TTCAGGAGGAAGCGATGGcttcagacagcatattTGAGTCATTTCCTTCGTA	220.	16.5	16	16.5	Epigenetic
SDHB	36.4 ± 19.2	TCTCCTTGAGGCGCCGGTtgccggccacaaccctTGGCGGAGCCTGCCTGCA	221.	16.5	16	16.5	Cancer
SDHC	13.7 ± 3.4	TGTTGCTGAGGTGACTTCagtgggactgggagttggtGCCTGCGGCCCTCCGGA	222.	16.5	19	15.5	Cancer
SDHD	42.0 ± 7.8	TCAGGAACGAGATGGCGGttctctggaggctgagtGCCGTTTGCGGTGCCCTA	223.	16.5	17	16.5	Cancer
SETDB1	33.5 ± 6.1	TGCAGAGGACAAAAGCATgtcttcccttcctgggTGCATTGGTTTGGATGCA	224.	16.5	16	16.5	Epigenetic
SIRT6	43.3 ± 3.1	TTACGCGGCGGGGCTGTCgccgtacgcggacaagggCAAGTGCGGCCTCCCGGA	225.	16.5	18	16.5	Epigenetic
SMAD2	3.9 ± 1.6	TTTGGTAAGAACATGTCGtccatcttgccattcacGCCGCCAGTTGTGAAGA	226.	16.5	17	15.5	Cancer
SS18	31.4 ± 7.9	TGGTGACGGCGGCAACATgtctgtggctttcgc	227.	16.5	17	16.5	Cancer

TABLE 7-continued

Endogenous human gene sequences targeted by 96 pairs of TALENs

Target gene name	% NHEJ	Target site (half-sites in CAPS, spacer in lowercase, ATG underlined)	SEQ ID NO:	Length of LEFT half site (include 5' 1)	Length of spacer	Length of RIGHT half site (include 5' T)	Gene Type
		ggCCCCGAGGCAGCGAGGCA					
SUZ12	13.1 ± 0.4	TGGCGCCTCAGAAGCAcggcggtgggggagggGGCGGCTCGGGGCCCA	228.	14.5	16	14.5	Epigenetic
TFE3	17.3 ± 2.4	TCATGTCTCATGCGGCCGaaccagctcgggatggCGTAGAGGCCAGCGCGGA	229.	16.5	16	16.5	Cancer
TGFBR2	none	TCGGGGGCTGCTCAGGGGcctgtggccgctgcacaTCGTCCTGTGGACGCGTA	230.	16.5	17	16.5	Cancer
TLX3	none	TTCCGCCCGCCCAGGATGgaggcgcccgccagcgcGCAGACCCCGCACCCGCA	231.	16.5	17	16.5	Cancer
TP53	19.9 ± 3.6	TTGCCGTCCCAAGCAATGgatgatttgatgctgtcCCCGGACGATATTGAACA	232.	16.5	17	16.5	Cancer
TSC2	30.7 ± 22.7	TCCTGGTCCACCATGGCcaaaccaacaagcaaagATTCAGGCTTGAAGGAGA	233.	15.5	17	16.5	Cancer
VHL	19.4 ± 1.1	TCTGGATCGCGGAGGGAAtgccccggagggcggaGAACTGGGACGAGGCCGA	234.	16.5	16	16.5	Cancer
XPA	12.9 ± 2.2	TGGGCCAGAGATGGCGGCggccgacggggctttgCCGGAGGCGGCGGCTTTA	235.	16.5	16	16.5	Cancer
XPC	31.4 ± 4.2	TGCCCAGACAAGCAACATggctcggaaacgcgcggccGGCGGGGAGCCGCGGGGA	236.	16.5	19	16.5	Cancer

[0232] The abilities of the 96 TALEN pairs to introduce NHEJ-mediated insertion or deletion (indel) mutations at their intended endogenous gene targets were tested in cultured human cells using a slightly modified version of a previously described T7 Endonuclease I (T7EI) assay (Mussolino et al., 2011, Nucleic Acids Res., 39:9283-93; Kim et al., 2009, Genome Res., 19:1279-88). With this T7EI assay, 83 of the 96 TALEN pairs showed evidence of NHEJ-mediated mutagenesis at their intended endogenous gene target sites, an overall success rate of ~86% (Table 7). The efficiencies of TALEN-induced mutagenesis we observed ranged from 2.5% to 55.8% with a mean of 22.5%. To provide molecular confirmation of the mutations we identified by T7EI assay, we sequenced target loci for 11 different TALEN pairs that induced varying efficiencies of mutagenesis (FIGS. **21**A-D). As expected, this sequencing revealed indels at the expected target gene sites with frequencies similar to those determined by the T7EI assays.

[0233] The nucleotide and amino acid sequences for 14 of the 96 pairs of TALENs targeted to the endogenous human genes in Table 7 are presented below. Each TALEN monomer is presented as follows:

[0234] (1) A header with information presented in the format: Gene target_Left or Right monomer Target DNA site shown 5' to 3' TALE repeat monomers and 0.5 repeat plasmid used with code as shown in Table 4.

[0235] (2) DNA sequence encoding the N-terminal part of the TALE required for activity, the TALE repeat array, the C-terminal 0.5 TALE repeat domain, and the C-terminal 63 amino acids required for activity from a NheI site to a BamHI site. This sequence is present in the "Vector Sequence" plasmid shown below, taking the place of the underlined X's flanked by NheI and BamHI sites

[0236] (3) Amino acid sequences the N-terminal part of the TALE required for activity, the TALE repeat array, the C-terminal 0.5 TALE repeat domain, and the C-terminal 63 amino acids required for activity shown from the start of translation (located just 3' to the NheI site and including an N-terminal FLAG epitope tag) to a Gly-Ser sequence (encoded by the BamHI site) that serves as a linker from the TALE repeat array to the FokI cleavage domain.

VECTOR SEQUENCE

SEQ ID NO: 244

GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTA

AGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAAC

AAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATG

TACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTA

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CGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGAC

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CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTT

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TAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGC

TTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTG**GCTAGCXXXXXXXXXXGGATCC**CAACTAG

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
>APC_Left_TATGTACGCCTCCCTGGG_TAL/006/015/019/025/026/012/019/022/027/015/017/022/027/015/019/024/JDS74/ (‘TATGTACGCCTCCCTGGG’ disclosed as SEQ ID NO: 412)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA	245.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	246.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTAATAATAACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>APC_Right_TACAGAAGCGGGCAAAGG_TAL/006/012/016/024/026/011/019/022/029/014/019/022/026/011/016/024/JDS74/(‘TACAGAAGCGGGCAAAGG’ disclosed as SEQ ID NO: 413)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAA	247.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGETHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	248.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
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>BRCA1_Left_TCCGAAGC TGACAGATGG_TAL/ 007/012/ 019/021/ 026/014/017/ 025/029/ 011/017/021 029/011/ 020/024/JDS74/ ('TCCGAAGC TGACAGATGG' disclosed as SEQ ID NO: 414)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCACATGAC GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCATCC CACGACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGAATAACAATGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCTCCAATATTGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCGAACATTGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAATAATAACGG	249.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANN NGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALET VQRLLPVLCQAHGLTPDQVVAIASEDGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLP VLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH GLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLT PAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQ VVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNG GKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	250.

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TALE REPEAT SEQUENCES				
Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGCA TGACGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GRTTGACGCCTGCACAAGTGGTCGCCATCGC CTCGAATGGCGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGAACAATAATGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAACATCGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGCATGACGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCTCCAATA TTGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGA ACAATAATGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCAAGCAACATCGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCCAACGGTGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCAACAACAACGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTAATAATAAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>BRCA1_Right_TCAGGTT CCGCCCCTAC C_TAL/007/ 011/019/024/ 030/015/ 017/022/029/ 012/017/ 022/027/015/ 016/022/ JDS71/ ('TCAGGTTC CGCCCCTACC' disclosed as SEQ ID N: 415)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCACATGAC GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAGC AACATCGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGAATAACAATGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC	251.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANN NGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALET VQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQR LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLP VLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLC QDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH GLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLT PAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDG GKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	252.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>BRCA2_Left_TTAGACTTAGGTAAGTAA_TAL/010/011/019/021/027/015/020/021/029/014/020/021/026/014/020/021/JDS70/ ('TTAGACTTAGGTAAGTAA' disclosed as SEQ ID NO: 416)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCC	253.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGRP	254.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TTACACCGGAGCAAGTCGTGGCCATTGCAAGC		ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD	
	AACATCGGTGGCAAACAGGCTCTTGAGACGGT		AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	
	TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC			
	ACGGGCTGACTCCCGATCAAGTTGTAGCGATT			
	GCGAATAACAATGGAGGGAAACAAGCATTGGA			
	GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC			
	AAGCCCACGGTTTGACGCCTGCACAAGTGGTC			
	GCCATCGCCTCCAATATTGGCGCTAAGCAGGC			
	GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC			
	TGTGCCAGGATCATGGACTGACCCCAGACCAG			
	GTAGTCGCAATCGCGTCACATGACGGGGGAAA			
	GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC			
	CGGTCCTTTGTCAAGACCACGGCCTTACACCG			
	GAGCAAGTCGTGGCCATTGCAAGCAATGGGGG			
	TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC			
	TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG			
	ACTCCCGATCAAGTTGTAGCGATTGCGTCCAA			
	CGGTGGAGGGAAACAAGCATTGGAGACTGTCC			
	AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC			
	GGTTTGACGCCTGCACAAGTGGTCGCCATCGC			
	CTCCAATATTGGCGGTAAGCAGGCGCTGGAAA			
	CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG			
	GATCATGGACTGACCCCAGACCAGGTAGTCGC			
	AATCGCGAACAATAATGGGGGAAAGCAAGCCC			
	TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT			
	TGTCAAGACCACGGCCTTACACCGGAGCAAGT			
	CGTGGCCATTGCAAATAATAACGGTGGCAAAC			
	AGGCTCTTGAGACGCTTCAGAGACTTCTCCCA			
	GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA			
	TCAAGTTGTAGCGATTGCGTCCAACGGTGGAG			
	GGAAACAAGCATTGGAGACTGTCCAACGGCTC			
	CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC			
	GCCTGCACAAGTGGTCGCCATCGCCTCCAATA			
	TTGGCGGTAAGCAGGCGCTGGAAACAGTACAG			
	CGCCTGCTGCCTGTACTGTGCCAGGATCATGG			
	ACTGACCCCAGACCAGGTAGTCGCAATCGCGT			
	CGAACATTGGGGGAAAGCAAGCCCTGGAAACC			
	GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA			
	CCACGGCCTTACACCGGAGCAAGTCGTGGCCA			
	TTGCAAATAATAACGGTGGCAAACAGGCTCTT			
	GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG			
	TCAAGCCCACGGGCTGACTCCCGATCAAGTTG			
	TAGCGATTGCGTCCAACGGTGGAGGGAAACAA			
	GCATTGGAGACTGTCCAACGGCTCCTTCCCGT			
	GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC			
	AAGTGGTCGCCATCGCCTCCAATATTGGCGGT			
	AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT			
	GCCTGTACTGTGCCAGGATCATGGACTGACAC			
	CCGAACAGGTGGTCGCCATTGCTTCTAACATC			
	GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC			
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	CGTTAACGAATGACCATCTGGTGGCGTTGGCA			
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TAGTTCTCCC	TGATTATAAAGATCATGACATCGATTACAAGG		HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL	
C_TAL/006/	ATGACGATGACAAGATGGCCCCCAAGAAGAAG		VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA	
014/020/025/	AGGAAGGTGGGCATTCACCGCGGGGTACCTAT		THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT	
030/014/	GGTGGACTTGAGGACACTCGGTTATTCGCAAC		GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNTPDQV	
020/021/029/	AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG		VAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAI	
015/020/	AGCACCGTCGCGCAACACCACGAGGCGCTTGT		ANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN	
022/030/012/	GGGGCATGGCTTCACTCATGCGCATATTGTCG		GGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGG	
017/022/	CGCTTTCACAGCACCCTGCGGCGCTTGGGACG		KQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQA	
JDS71/	GTGGCTGTCAAATACCAAGATATGATTGCGGC		LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALET	
(‘TAGTTTGT	CCTGCCCGAAGCCACGCACGAGGCAATTGTAG		VQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQR	
AGTTCTCCCC’	GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA		LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP	
disclosed	CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT		VLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLC	

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TALE REPEAT SEQUENCES				
Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
as SEQ ID NO: 417)	TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCGAACATT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAAT AATAACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCCAACGGTGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCTCGAATGGCGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCAAACGGAGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAATAATAACGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCCAA CGGTGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCCAATATTGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGAACAATAATGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAATGGGGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCCAACGGTGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAG GCCTGCACAAGTGGTCGCCATCGCCAGCCATG ATGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CAAACGGAGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCATCCCACGACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCGCATGACGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCAGCCATGATGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCCCACGAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC		QDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH GLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLT PAQVVAIASHDGGKQALETVQRLLPVLCQDRUTPDQ VVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS HDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDG GKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	
>ERCC2_Left_TCCGGCCG GCGCCATGA_TAL/ 007/012/ 019/024/ 027/012/019/ 024/027/	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG	257.	ASTMDYKDHDGDYKDRDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAI	258.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
014/017/022/026/015/034/JDS70/ (‘TCCGGCCGGCGCCATGA’ disclosed as SEQ ID NO: 418)	AGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCATTGCTTCTAACATCGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC		ASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDRGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVRGLPHAPALIKRTNRRIPERTSHRVAGS	
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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
006/014/ 017/024/ 026/014/017/ 024/027/ 014/016/022/ 027/012/ JDS71/ ('TAGCGAGC GCGACCCC' disclosed as SEQ ID NO: 419)	ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCGAACATT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAAT AATAACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCGCATGACGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAACAACAACGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCGAACATTGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAATAATAACGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGCA TGACGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CAACAACAACGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCACATGACGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAATAATAACGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGAACATTGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCAGCCATG ATGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CACATGACGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCATCCCACGACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACACCCGAACAGGTGG TCGCCATTGCTTCCCACGACGGAGGACGGCCA GCCTTGGAGTCCATCGTAGCCCAATTGTCCAG GCCCGATCCCGCGTTGGCTGCGTTAACGAATG ACCATCTGGTGGCGTTGGCATGTCTTGGTGGA CGACCCGCGCTCGATGCAGTCAAAAAGGGTCT GCCTCATGCTCCCGCATTGATCAAAAGAACCA ACCGGCGGATTCCCGAGAGAACTTCCCATCGA GTCGCGGATCC		VGHGETHARIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASNIGGKQALETVQRLLPVLCQDHGLTPEQWAI ANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASH DGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALET VQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQR LLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLP VLCQDHGITPDQVVAIASHDGGKQALETVQRLLPVLC QDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAH GLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLT PAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS HDGGRPALESIVAQLSRPDPALAALTNDHLVALACLG GRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
>FANCA_Left_TAGGGCC AAGGCCATGT_TAL/ 006/014/ 019/022/ 029/012/017/ 021/026/ 014/019/022/ 027/011/ 020/024/JDS78/ ('TAGGCGCC AAGGCCATGT' disclosed as SEQ ID NO: 420)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCGAACATT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAAT AATAACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGAATAACAATGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAGCCATGATGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGAACAATAATGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCATCCCACGACGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGCA TGACGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCCAATATTGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCGAACATTGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAATAATAACGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGAATAACAATGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCAGCCATG ATGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CACATGACGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCAAGCAACATCGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCCAACGGTGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCAACAACAACGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCTAATGGG	261.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAI ANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANN NGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG KQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALET VQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP VLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLC QDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAH GLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLT PAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NGGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	262.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>FANCA_Right_TGGCCCGAGGCGGAGTTC_TAL/009/014/017/022/027/014/016/024/029/012/019/024/026/014/020/025/JDS71/ (‘TGGCCCGAGGCGGAGTTC’ disclosed as SEQ ID NO: 421)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTSTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTG	263.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	264.

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TALE REPEAT SEQUENCES				
Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TAGCGATTGCGTCCAACGGTGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCTCGAATGGCGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCCCACGAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>FANCC_Left_TGAAGGGA CATCACCTTT_TAL/ 009/011/ 016/024/ 029/014/016/ 022/026/ 015/017/021/ 027/012/ 020/025/JDS78/ ('TGAAGGGA CATCACCTTT' disclosed as SEQ ID NO: 422)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAGC AACATCGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCGAACATTGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAACAACAACGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGAACAATAATGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAATAATAACGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGAA CATTGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CAGCCATGATGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCGAACATTGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAATGGGGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGCATGACGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCTCCAATA TTGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG	265.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN IGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGG KQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQA LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALET VQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLP VLCQDHGLTPDQVVAIASNIGGKALETVQRLLPVLC QDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH GLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLT PAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	266.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	ACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCTAATGGGGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>FANCC_Right_TCTACTGAATCTTGAGC_TAL/007/015/016/022/030/014/016/021/030/012/020/025/029/011/034/JDS71/('TCTACTGAATCTTGAGC' disclosed as SEQ ID NO: 423)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCA	267.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	268.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>FANCG_Left_TCGGCCACCATGTCCC_TAL/007/014/019/022/027/011/017/022/026/015/019/025/027/012/JDS71/('TCGGCCACCATGTCCC' disclosed as SEQ ID NO: 424	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACAATGGGGGAAAGCAAGCCC	269.	ASTMDYKDHDGDYKDHDIDYKDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	270.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGAGGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACACCCGAACAGGTTGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>FANCG_Right_TCCAGGCAGCTGGAGCCC_TAL/007/012/016/024/029/012/016/024/027/015/019/024/026/014/017/022/JDS71/ (‘TCCAGGCAGCTGGAGCCC’ disclosed as SEQ ID NO: 425)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGC	271.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDRGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	272.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	AATCGCGTCACATGACGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAATGGGGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGAATAACAATGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCAACAACA ACGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CGAACATTGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCAAATAATAACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCGCATGACGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCAGCCATGATGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCCCACGAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>JAK2_Left_TCTGAAAAAGA CTCTGCA_TAL/007/015/ 019/021/ 026/011/016/ 021/029/ 011/017/025/ 027/015/ 019/022/JDS70/ ('TCTGAAAA AGACTCTGCA' disclosed as SEQ ID NO: 426)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCACATGAC GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAGC AATGGGGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGAATAACAATGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCTCCAATATTGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCGAACATTGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAACATCGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG	273.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPEKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEANGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHARNALTGAPLNLTPDQV VAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASNGGGKQALETVQRLLPVLCQAEGLTPDQVVAIANN NGGKQALETVQRLLPVLCQAHGLTPAQWAIASNIGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALET VQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP VLCQDRGLTPDQVVAIANNNGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH GLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLT PAQWAIASNGGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKALETVQRLLPVLCQDHGLTPEQVVA IASNGGGKQUETVQRLLPVLCQAHGLTPDQVVAIAN NNGGKQALETVQRLLPVLCQAHUTPAQVVAIASEDG GKQALETVQRLLPVLCQDHGLTPENVAIASNIGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	274.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	ACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCTAACATCGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>JAK2_Right_TCCATTTCTGTCATCGTA_TAL/007/012/016/025/030/015/017/025/029/015/017/021/030/012/019/025/JDS70/ ('TCCATTTCTGTCATCGTA' disclosed as SEQ ID NO: 427)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTAC	275.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLIPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVORLLPVLCQDHGLTPEQVVAIASNIGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	276.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCAAACGGAGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAATGGGGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGCA TGACGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCGAATGGCGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGAACAATAATGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAATGGGGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGCATGACGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCTCCAATA TTGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CAAACGGAGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCATCCCACGACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGAATAACAATGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCTCGAATGGCGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCTAACATC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>KRAS_Left_TGAAAATGA CTGAATATA_TAL/ 009/011/ 016/021/ 026/015/019/ 021/027/ 015/019/021/ 026/015/ 016/025/JDS70/ ('TGAAAATG ACTGAATATA' disclosed as SEQ ID NO: 428)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAGC AACATCGGTGGCAAACAGGCTCTTGAGACGGT	277.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN IGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALET VQRLLPVLCQAHLTPDQVVAIANNNGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP VLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH GLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLT PAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQ VVATASNIGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	278.

-continued

TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAATGGGGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCTAACATCGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>KRAS_Right_TTGCCTAC GCCACCAGC_TAL/ 010/014/ 017/022/ 030/011/017/ 024/027/ 012/016/022/ 027/011/ 034/JDS71/ ('TTGCCTAC GCCACCAGC' disclosed as SEQ ID NO: 429)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA	279.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQQMIAALPEATHEATVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNGGGNALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLT	280.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC		PAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	
>MYC_Left_TGCTTAGACGCTGGATTT_TAL/009/012/020/025/026/014/016/022/029/012/020/024/029/011/020/025/JDS78/('TGCTTAGACGCTGGATTT'	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAG	281.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR	282.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
disclosed as SEQ ID NO: 430)	GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCATCC CACGACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCCAACGGTGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCTCGAATGGCGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCGAACATTGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAATAATAACGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGAA CATTGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CAGCCATGATGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGAACAATAATGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCATCCCACGACGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCCAACGGTGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCAACAACA ACGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGA ACAATAATGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCAAGCAACATCGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCCAACGGTGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCTCGAATGGCGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCTAATGGG GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC		LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLP VLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLC QDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH GLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLT PAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQ VVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	
>MYC_Right_TTCGGTGCT TACCTGGTT_TAL/ 010/012/ 019/024/	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT	283.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT	284.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
030/014/017/025/030/011/017/022/030/014/019/025/JDS78/ ('TTCGGTGC TTACCTGGTT' disclosed as SEQ ID NO: 431)	GGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCGAATGGCGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCTAATGGGGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGA		GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>PTEN_Left_TCCCAGACATGAGAGCC_TAL/007/012/017/021/029/011/017/021/030/014/016/022/026/014/032/JDS71/(‘TCCCAGACATGACAGCC’ disclosed as SEQ ID NO: 432)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCTCCAATATTGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCAAACGGAGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAGCCATGATGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAATAATAACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGCATGACGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTCTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATT	285.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVAGS	286.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GTCCAGGCCCGATCCCGCGTTGGCTGCGTTAA CGAATGACCATCTGGTGGCGTTGGCATGTCTT GGTGGACGACCCGCGCTCGATGCAGTCAAAAA GGGTCTGCCTCATGCTCCCGCATTGATCAAAA GAACCAACCGGCGGATTCCCGAGAGAACTTCC CATCGAGTCGCGGGATCC			
>PTEN_Right_TCCTTTG TTTCTGCTAA_TAL/ 007/012/ 020/025/ 030/015/019/ 025/030/ 015/017/025/ 029/012/ 020/021/JDS70/ ('TCCTTTG TTTCTGCTAA' disclosed as SEQ ID NO: 433)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCACATGAC GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCATCC CACGACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCCAACGGTGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCTCGAATGGCGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCAAACGGAGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAATGGGGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGAATAA CAATGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCGAATGGCGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCAAACGGAGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAATGGGGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGCATGACGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCTCGAATG GCGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGA ACAATAATGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCATCCCACGACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCCAACGGTGGAGGGAAACAA	287.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN GGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALET VQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNGGGKQALETVQRLLP VLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH GLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLT PAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQ VVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNIGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	288.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCTCCAATATTGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTTCTAACATC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>TP53_Left_TTGCCGTCC CAAGCAATG_TAL/ 010/014/ 017/022/ 029/015/017/ 022/027/ 011/016/024/ 027/011/ 016/025/JDS74/ ('TTGCCGTC CCAAGCAATG' disclosed as SEQ ID NO: 434)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGTCAAACGGA GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAAT AATAACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCGCATGACGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAGCCATGATGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGAACAATAATGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAATGGGGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCGCA TGACGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CAGCCATGATGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCACATGACGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCAAGCAACATCGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA TCAAGTTGTAGCGATTGCGTCGAACATTGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCAACAACA ACGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT	289.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAI ANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASH DGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG KQALETVQRLLPVLCQDHGLTPDQVVAIANNNGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNGGGKQALET VQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQR LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLP VLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH GLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLT PAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS NIGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNGG GKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	290.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	CACATGACGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCAAGCAACATCGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGTCGAACATTGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCTCGAATGGCGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTAATAATAAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>TP53_Right_TGTTCAAT ATCGTCCGGG_TAL/ 009/015/ 020/022/ 026/011/020/ 021/030/ 012/019/025/ 027/012/ 019/024/JDS74/ ('TGTTCAAT ATCGTCCGGG' disclosed as SEQ ID NO: 435)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAGC AATGGGGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCCAACGGTGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAGCCATGATGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCGAACATTGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAACATCGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGTCCAA CGGTGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCCAATATTGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG GATCATGGACTGACCCCAGACCAGGTAGTCGC AATCGCGTCAAACGGAGGGGGAAAGCAAGCCC TGGAAACCGTGCAAAGGTTGTTGCCGGTCCTT TGTCAAGACCACGGCCTTACACCGGAGCAAGT CGTGGCCATTGCATCCCACGACGGTGGCAAAC AGGCTCTTGAGACGGTTCAGAGACTTCTCCCA GTTCTCTGTCAAGCCCACGGGCTGACTCCCGA	291.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASNGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASN GGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALET VQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP VLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLC QDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH GLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLT PAQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAN NNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNG GKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	292.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	TCAAGTTGTAGCGATTGCGAATAACAATGGAG GGAAACAAGCATTGGAGACTGTCCAACGGCTC CTTCCCGTGTTGTGTCAAGCCCACGGTTTGAC GCCTGCACAAGTGGTCGCCATCGCCTCGAATG GCGGCGGTAAGCAGGCGCTGGAAACAGTACAG CGCCTGCTGCCTGTACTGTGCCAGGATCATGG ACTGACCCCAGACCAGGTAGTCGCAATCGCGT CACATGACGGGGGAAAGCAAGCCCTGGAAACC GTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGA CCACGGCCTTACACCGGAGCAAGTCGTGGCCA TTGCATCCCACGACGGTGGCAAACAGGCTCTT GAGACGGTTCAGAGACTTCTCCCAGTTCTCTG TCAAGCCCACGGGCTGACTCCCGATCAAGTTG TAGCGATTGCGAATAACAATGGAGGGAAACAA GCATTGGAGACTGTCCAACGGCTCCTTCCCGT GTTGTGTCAAGCCCACGGTTTGACGCCTGCAC AAGTGGTCGCCATCGCCAACAACAACGGCGGT AAGCAGGCGCTGGAAACAGTACAGCGCCTGCT GCCTGTACTGTGCCAGGATCATGGACTGACAC CCGAACAGGTGGTCGCCATTGCTAATAATAAC GGAGGACGGCCAGCCTTGGAGTCCATCGTAGC CCAATTGTCCAGGCCCGATCCCGCGTTGGCTG CGTTAACGAATGACCATCTGGTGGCGTTGGCA TGTCTTGGTGGACGACCCGCGCTCGATGCAGT CAAAAAGGGTCTGCCTCATGCTCCCGCATTGA TCAAAAGAACCAACCGGCGGATTCCCGAGAGA ACTTCCCATCGAGTCGCGGGATCC			
>XPA_Left_TGGGCCAGAG ATGGCGGC_TAL/ 009/014/ 019/022/027/ 011/019/ 021/029/011/ 020/024/ 029/012/019/ 024/JDS71/ (‘TGGGCCAG AGATGGCGGC disclosed as SEQ ID NO: 436)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCAAAT AATAACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGAATAACAATGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAGCCATGATGGCGGTAAGCAGGC GCTGGAAACAGTACAGCGCCTGCTGCCTGTAC TGTGCCAGGATCATGGACTGACCCCAGACCAG GTAGTCGCAATCGCGTCACATGACGGGGGAAA GCAAGCCCTGGAAACCGTGCAAAGGTTGTTGC CGGTCCTTTGTCAAGACCACGGCCTTACACCG GAGCAAGTCGTGGCCATTGCAAGCAACATCGG TGGCAAACAGGCTCTTGAGACGGTTCAGAGAC TTCTCCCAGTTCTCTGTCAAGCCCACGGGCTG ACTCCCGATCAAGTTGTAGCGATTGCGAATAA CAATGGAGGGAAACAAGCATTGGAGACTGTCC AACGGCTCCTTCCCGTGTTGTGTCAAGCCCAC GGTTTGACGCCTGCACAAGTGGTCGCCATCGC CTCCAATATTGGCGGTAAGCAGGCGCTGGAAA CAGTACAGCGCCTGCTGCCTGTACTGTGCCAG	293.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAI ANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIANN NGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG KQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQA LETVQRLLPVLCQDHGLTPEQVVAIASNIGGKQALET VQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQR LLPVLCQAHGLTPAQVVAIASNIGGKQALETVQRLLP VLCQDHGLTPDQVVAIANNNGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH GLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLT PAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQ VVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVA IASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIAN NNGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNG GKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	294.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
	GATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCCAACGGTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGAACAATAATGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGAATAACAATGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACACCCGAACAGGTGGTCGCCATTGCTTCCCACGACGGAGGACGGCCAGCCTTGGAGTCCATCGTAGCCCAATTGTCCAGGCCCGATCCCGCGTTGGCTGCGTTAACGAATGACCATCTGGTGGCGTTGGCATGTCTTGGTGGACGACCCGCGCTCGATGCAGTCAAAAAGGGTCTGCCTCATGCTCCCGCATTGATCAAAAGAACCAACCGGCGGATTCCCGAGAGAACTTCCCATCGAGTCGCGGGATCC			
>XPA_Right_TAAAGCCGCCGCCTCCGG_TAL/006/011/016/024/027/012/019/022/027/014/017/022/030/012/017/024/JDS74/('TAAAGCCGCCGCCTCCGG' disclosed as SEQ ID NO: 437)	GCTAGCaccATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGCCCCCAAGAAGAAGAGGAAGGTGGGCATTCACCGCGGGGTACCTATGGTGGACTTGAGGACACTCGGTTATTCGCAACAGCAACAGGAGAAAATCAAGCCTAAGGTCAGGAGCACCGTCGCGCAACACCACGAGGCGCTTGTGGGGCATGGCTTCACTCATGCGCATATTGTCGCGCTTTCACAGCACCCTGCGGCGCTTGGGACGGTGGCTGTCAAATACCAAGATATGATTGCGGCCCTGCCCGAAGCCACGCACGAGGCAATTGTAGGGGTCGGTAAACAGTGGTCGGGAGCGCGAGCACTTGAGGCGCTGCTGACTGTGGCGGGTGAGCTTAGGGGGCCTCCGCTCCAGCTCGACACCGGGCAGCTGCTGAAGATCGCGAAGAGAGGGGGAGTAACAGCGGTAGAGGCAGTGCACGCCTGGCGCAATGCGCTCACCGGGGCCCCCTTGAACCTGACCCCAGACCAGGTAGTCGCAATCGCGTCGAACATTGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCAAGCAACATCGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGACTTCTCCCAGTTCTCTGTCAAGCCCACGGGCTGACTCCCGATCAAGTTGTAGCGATTGCGTCGAACATTGGAGGGAAACAAGCATTGGAGACTGTCCAACGGCTCCTTCCCGTGTTGTGTCAAGCCCACGGTTTGACGCCTGCACAAGTGGTCGCCATCGCCAACAACAACGGCGGTAAGCAGGCGCTGGAAACAGTACAGCGCCTGCTGCCTGTACTGTGCCAGGATCATGGACTGACCCCAGACCAGGTAGTCGCAATCGCGTCACATGACGGGGGAAAGCAAGCCCTGGAAACCGTGCAAAGGTTGTTGCCGGTCCTTTGTCAAGACCACGGCCTTACACCGGAGCAAGTCGTGGCCATTGCATCCCACGACGGTGGCAAACAGGCTCTTGAGACGGTTCAGAGAC	295.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRVGIHRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQVVAIASNIGGKQALETVQPLLPVLCQDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQLLPVLCQDHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQDHGLPEVVAIANNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQDHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPAQVVAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAIANNNGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTNPRIPERTSHRVAGS	296.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
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>XPC_Left_TGCCCAGACA AGCAACAT_TAL/ 009/012/ 017/022/026/ 014/016/ 022/026/011/ 019/022/ 026/011/017/ 021/JDS78/ ('TGCCCAGA CAAGCAACAT' disclosed as SEQ ID NO: 438)	GCTAGCaccATGGACTACAAAGACCATGACGG TGATTATAAAGATCATGACATCGATTACAAGG ATGACGATGACAAGATGGCCCCCAAGAAGAAG AGGAAGGTGGGCATTCACCGCGGGGTACCTAT GGTGGACTTGAGGACACTCGGTTATTCGCAAC AGCAACAGGAGAAAATCAAGCCTAAGGTCAGG AGCACCGTCGCGCAACACCACGAGGCGCTTGT GGGGCATGGCTTCACTCATGCGCATATTGTCG CGCTTTCACAGCACCCTGCGGCGCTTGGGACG GTGGCTGTCAAATACCAAGATATGATTGCGGC CCTGCCCGAAGCCACGCACGAGGCAATTGTAG GGGTCGGTAAACAGTGGTCGGGAGCGCGAGCA CTTGAGGCGCTGCTGACTGTGGCGGGTGAGCT TAGGGGGCCTCCGCTCCAGCTCGACACCGGGC AGCTGCTGAAGATCGCGAAGAGAGGGGGAGTA ACAGCGGTAGAGGCAGTGCACGCCTGGCGCAA TGCGCTCACCGGGGCCCCCTTGAACCTGACCC CAGACCAGGTAGTCGCAATCGCGAACAATAAT GGGGGAAAGCAAGCCCTGGAAACCGTGCAAAG GTTGTTGCCGGTCCTTTGTCAAGACCACGGCC TTACACCGGAGCAAGTCGTGGCCATTGCATCC CACGACGGTGGCAAACAGGCTCTTGAGACGGT TCAGAGACTTCTCCCAGTTCTCTGTCAAGCCC ACGGGCTGACTCCCGATCAAGTTGTAGCGATT GCGTCGCATGACGGAGGGAAACAAGCATTGGA GACTGTCCAACGGCTCCTTCCCGTGTTGTGTC AAGCCCACGGTTTGACGCCTGCACAAGTGGTC GCCATCGCCAGCCATGATGGCGGTAAGCAGGC	297.	ASTMDYKDHDGDYKDHDIDYKDDDDKMAPKKKRKVGI HRGVPMVDLRTLGYSQQQQEKIKPKVRSTVAQHHEAL VGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEA THEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDT GQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPDQV VAIANNNGGKQALETVQRLLPVLCQDHGLTPEQVVAI ASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASH DGGKQALETVQRLLPVLCQAHGLTPAQVVAIASHDGG KQALETVQRLLPVLCQDHGLTPDQVVAIASNIGGKQA LETVQRLLPVLCQDHGLTPEQVVAIANNNGGKQALET VQRLLPVLCQAHGLTPDQVVAIASNIGGKQALETVQR LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLP VLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLC QDHGLTPEQVVAIASNIGGKQALETVQRLLPVLCQAH GLTPDQVVAIANNNGGKQALETVQRLLPVLCQAHGLT PAQVVAIASHDGGKQALETVQRLLPVLCQDHGLTPDQ VVAIASNIGGKQALETVQRLLPVLCQDHGLTPEQVVA IASNIGGKQALETVQRLLPVLCQAHGLTPDQVVAIAS HDGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIG GKQALETVQRLLPVLCQDHGLTPEQVVAIASNGGGRP ALESIVAQLSRPDPALAALTNDHLVALACLGGRPALD AVKKGLPHAPALIKRTNRRIPERTSHRVAGS	298.

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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
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TALE REPEAT SEQUENCES

Target	SEQEUNCE	SEQ ID NO:	SEQUENCE	SEQ ID NO:
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Other Embodiments

[0237] A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

SEQUENCE LISTING

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<210> SEQ ID NO 1
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<220> FEATURE:
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ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc    180

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ttaattgcgt tgcgctcact gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat    660

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aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa catgtgagca    840

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His Gly
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<220> FEATURE:
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
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His Gly
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Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
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<223> OTHER INFORMATION: a, c, t, g, unknown or other

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tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

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aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780

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gtagaggcag tgcacgcctg gcgcaatgcg ctcaccgggg ccccttgaa cagagacgat 1440

taatgcgtct cgctgacacc cgaacaggtg gtcgccattg ctnnnnnnnn nggaggacgg 1500

ccagccttgg agtccatcgt agcccaattg tccaggcccg atcccgcgtt ggctgcgtta 1560

acgaatgacc atctggtggc gttggcatgt cttggtggac gacccgcgct cgatgcagtc 1620

aaaaagggtc tgcctcatgc tcccgcattg atcaaaagaa ccaaccggcg gattcccgag 1680

agaacttccc atcgagtcgc gggatcccaa ctagtcaaaa gtgaactgga ggagaagaaa 1740

tctgaacttc gtcataaatt gaaatatgtg cctcatgaat atattgaatt aattgaaatt 1800

gccagaaatt ccactcagga tagaattctt gaaatgaagg taatggaatt ttttatgaaa 1860

gtttatggat atagaggtaa acatttgggt ggatcaagga aaccggacgg agcaatttat 1920

actgtcggat ctcctattga ttacggtgtg atcgtggata ctaaagctta tagcggaggt 1980

tataatctgc caattggcca agcagatgaa atgcaacgat atgtcgaaga aaatcaaaca 2040

cgaaacaaac atatcaaccc taatgaatgg tggaaagtct atccatcttc tgtaacggaa 2100

tttaagtttt tatttgtgag tggtcacttt aaaggaaact acaaagctca gcttacacga 2160

ttaaatcata tcactaattg taatggagct gttcttagtg tagaagagct tttaattggt 2220

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ggcgagataa acttttaagg gcccttcgaa ggtaagccta tccctaaccc tctcctcggt 2340

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gcctcgactg tgccttctag ttgccagcca tctgttgttt gcccctcccc cgtgccttcc 2460

ttgaccctgg aaggtgccac tcccactgtc ctttcctaat aaaatgagga aattgcatcg 2520

cattgtctga gtaggtgtca ttctattctg gggggtgggg tggggcagga cagcaagggg 2580

gaggattggg aagacaatag caggcatgct ggggatgcgg tgggctctat ggcttctgag 2640

gcggaaagaa ccagctgggg ctctaggggg tatccccacg cgccctgtag cggcgcatta 2700

agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta cacttgccag cgccctagcg 2760

cccgctcctt tcgctttctt cccttccttt ctcgccacgt tcgccggctt tccccgtcaa 2820

gctctaaatc ggggcatccc tttagggttc cgatttagtg ctttacggca cctcgacccc 2880

aaaaaacttg attagggtga tggttcacgt agtgggccat cgccctgata gacggttttt 2940

cgccctttga cgttggagtc cacgttcttt aatagtggac tcttgttcca aactggaaca 3000

acactcaacc ctatctcggt ctattctttt gatttataag ggattttggg gatttcggcc 3060

tattggttaa aaaatgagct gatttaacaa aaatttaacg cgaattaatt ctgtggaatg 3120

tgtgtcagtt agggtgtgga aagtccccag gctccccagg caggcagaag tatgcaaagc 3180

atgcatctca attagtcagc aaccaggtgt ggaaagtccc caggctcccc agcaggcaga 3240

agtatgcaaa gcatgcatct caattagtc 3269

<210> SEQ ID NO 11
<211> LENGTH: 3178
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 11

agcaaccata gtcccgcccc taactccgcc catcccgccc ctaactccgc ccagttccgc 60

ccattctccg ccccatggct gactaatttt ttttatttat gcagaggccg aggccgcctc 120

tgcctctgag ctattccaga agtagtgagg aggctttttt ggaggcctag gcttttgcaa 180

aaagctcccg ggagcttgta tatccatttt cggatctgat cagcacgtgt tgacaattaa 240

tcatcggcat agtatatcgg catagtataa tacgacaagg tgaggaacta aaccatggcc 300

aagcctttgt ctcaagaaga atccaccctc attgaaagag caacggctac aatcaacagc 360

atccccatct ctgaagacta cagcgtcgcc agcgcagctc tctctagcga cggccgcatc 420

ttcactggtg tcaatgtata tcattttact gggggacctt gtgcagaact cgtggtgctg 480

ggcactgctg ctgctgcggc agctggcaac ctgacttgta tcgtcgcgat cggaaatgag 540

aacaggggca tcttgagccc ctgcggacgg tgtcgacagg tgcttctcga tctgcatcct 600

gggatcaaag cgatagtgaa ggacagtgat ggacagccga cggcagttgg gattcgtgaa 660

ttgctgccct ctggttatgt gtgggagggc taagcacttc gtggccgagg agcaggactg 720

acacgtgcta cgagatttcg attccaccgc cgccttctat gaaaggttgg gcttcggaat 780

cgttttccgg gacgccggct ggatgatcct ccagcgcggg gatctcatgc tggagttctt 840

cgcccacccc aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac 900

aaatttcaca aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat 960

caatgtatct tatcatgtct gtataccgtc gacctctagc tagagcttgg cgtaatcatg 1020

gtcatagctg tttcctgtgt gaaattgtta tccgctcaca attccacaca acatacgagc 1080

cggaagcata aagtgtaaag cctggggtgc ctaatgagtg agctaactca cattaattgc 1140

gttgcgctca ctgcccgctt tccagtcggg aaacctgtcg tgccagctgc attaatgaat 1200

cggccaacgc gcggggagag gcggtttgcg tattgggcgc tcttccgctt cctcgctcac 1260

tgactcgctg cgctcggtcg ttcggctgcg gcgagcggta tcagctcact caaaggcggt 1320

aatacggtta tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca 1380

gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc 1440

ccctgacgag catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact 1500

ataaagatac caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct 1560

gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc tttctcaatg 1620

ctcacgctgt aggtatctca gttcggtgta ggtcgttcgc tccaagctgg gctgtgtgca 1680

cgaacccccc gttcagcccg accgctgcgc cttatccggt aactatcgtc ttgagtccaa 1740

cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc 1800

gaggtatgta ggcggtgcta cagagttctt gaagtggtgg cctaactacg gctacactag 1860

aaggacagta tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg 1920

tagctcttga tccggcaaac aaaccaccgc tggtagcggt ggtttttttg tttgcaagca 1980

gcagattacg cgcagaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc 2040

tgacgctcag tggaacgaaa actcacgtta agggattttg gtcatgagat tatcaaaaag 2100

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tgagtaaact tggtctgaca gttaccaatg cttaatcagt gaggcaccta tctcagcgat 2220

ctgtctattt cgttcatcca tagttgcctg actccccgtc gtgtagataa ctacgatacg 2280

ggagggctta ccatctggcc ccagtgctgc aatgataccg cgagacccac gctcaccggc 2340

tccagattta tcagcaataa accagccagc cggaagggcc gagcgcagaa gtggtcctgc 2400

aactttatcc gcctccatcc agtctattaa ttgttgccgg gaagctagag taagtagttc 2460

gccagttaat agtttgcgca acgttgttgc cattgctaca ggcatcgtgg tgtcacgctc 2520

gtcgtttggt atggcttcat tcagctccgg ttcccaacga tcaaggcgag ttacatgatc 2580

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gttggccgca gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat 2700

gccatccgta agatgctttt ctgtgactgg tgagtactca accaagtcat tctgagaata 2760

gtgtatgcgg cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca 2820

tagcagaact ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag 2880

gatcttaccg ctgttgagat ccagttcgat gtaacccact cgtgcaccca actgatcttc 2940

agcatctttt actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc 3000

aaaaaaggga ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata 3060

ttattgaagc atttatcagg gttattgtct catgagcgga tacatatttg aatgtattta 3120

gaaaaataaa caaatagggg ttccgcgcac atttccccga aaagtgccac ctgacgtc 3178

<210> SEQ ID NO 12
<211> LENGTH: 111
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

ctacggcgtg cagtgcttca gccgctaccc cgaccacatg aagcagcacg acttcttcaa 60

gtccgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg a 111

<210> SEQ ID NO 13
<211> LENGTH: 108
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

ctacggcgtg cagtgcttca gccgctaccc cgacatgaag cagcacgact tcttcaagtc 60

cgccatgccc gaaggctacg tccaggagcg caccatcttc ttcaagga 108

<210> SEQ ID NO 14
<211> LENGTH: 95
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

ctacggcgtg cagtgcttca gccgaagcag cacgacttct tcaagtccgc catgcccgaa 60

ggctacgtcc aggagcgcac catcttcttc aagga 95

<210> SEQ ID NO 15
<211> LENGTH: 90
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

ctacggcgtg cagtgcttca gccgctacga cttcttcaag tccgccatgc ccgaaggcta 60

cgtccaggag cgcaccatct tcttcaagga 90

<210> SEQ ID NO 16
<211> LENGTH: 89
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: a, c, t, g, unknown or other

<400> SEQUENCE: 16

ctacggcgtg cagtgcttca gccgcacgac ttcttccagt ccgccatgcc cgaaggctac 60

ntccaggagc gcaccatctt cttcaagga 89

<210> SEQ ID NO 17
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

ctacggcgtg cagtgcttca gcacttcaag tccgccatgc ccgaaggcta cgtccaggag 60

cgcaccatct tcttcaagga 80

<210> SEQ ID NO 18
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

ctacggcgtg cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg 60

caccatcttc ttcaagga 78

<210> SEQ ID NO 19
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

ctacggcgtg cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg 60

caccatcttc ttcaagga 78

<210> SEQ ID NO 20
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

ctacggcgtg cagtgcttgc ccgaaggcta cgtccaggag cgcaccatct tcttcaagga 60

<210> SEQ ID NO 21
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 21

ctacggcgtg cagtgcttca gccgctacgt ccaggagcgc accatcttct tcaagga        57


<210> SEQ ID NO 22
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

ctacgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg a              51


<210> SEQ ID NO 23
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

ctacggcgtg cagtgcttct tcaagga                                         27


<210> SEQ ID NO 24
<211> LENGTH: 113
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

ctacggcgtg cagtgcttca gccgctaccc cgacaccaca tgaagcagca cgacttcttc     60

aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa gga           113


<210> SEQ ID NO 25
<211> LENGTH: 2328
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 25

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc     60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac    120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa    180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc    240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct    300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg    360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag    420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg    480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg    540

aacctgaccc cagaccaggt agtcgcaatc gcgaacaata atgggggaaa gcaagccctg    600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa    660

gtcgtggcca ttgcatccca cgacggtggc aaacaggctc ttgagacggt tcagagactt    720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg    780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa    840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag    900
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gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca 960

gaccaggtag tcgcaatcgc gtcaaacgga gggggaaagc aagccctgga aaccgtgcaa 1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt 1080

gcaaataata acggtggcaa acaggctctt gagacggttc agagacttct cccagttctc 1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgtcgca tgacggaggg 1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg 1260

acgcctgcac aagtggtcgc catcgcctcg aatggcggcg gtaagcaggc gctggaaaca 1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc 1380

gcaatcgcgt caaacggagg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg 1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc atcccacgac 1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac 1560

gggctgactc ccgatcaagt tgtagcgatt gcgtcgaaca ttggagggaa acaagcattg 1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa 1680

gtggtcgcca tcgccaacaa caacggcggt aagcaggcgc tggaaacagt acagcgcctg 1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca 1800

catgacgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa 1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcat cccacgacgg tggcaaacag 1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc 1980

gatcaagttg tagcgattgc gaataacaat ggagggaaac aagcattgga gactgtccaa 2040

cggctccttc ccgtgttgtg tcaagcccac ggtctgacac ccgaacaggt ggtcgccatt 2100

gcttcccacg acggaggacg gccagccttg gagtccatcg tagcccaatt gtccaggccc 2160

gatcccgcgt tggctgcgtt aacgaatgac catctggtgg cgttggcatg tcttggtgga 2220

cgacccgcgc tcgatgcagt caaaaagggt ctgcctcatg ctcccgcatt gatcaaaaga 2280

accaaccggc ggattcccga gagaacttcc catcgagtcg cgggatcc 2328

<210> SEQ ID NO 26
<211> LENGTH: 771
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 26

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
20 25 30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val

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                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

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

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
                485                 490                 495
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro Ala
    690                 695                 700

Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala
705                 710                 715                 720

Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg
                725                 730                 735

Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala Leu
            740                 745                 750

Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val
        755                 760                 765

Ala Gly Ser
    770


<210> SEQ ID NO 27
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 27

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc      60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac     120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa     180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc     240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct     300
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gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg    360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag    420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg    480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg    540

aacctgaccc cagaccaggt agtcgcaatc gcgaacaata atgggggaaa gcaagccctg    600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa    660

gtcgtggcca ttgcatccca cgacggtggc aaacaggctc ttgagacggt tcagagactt    720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg    780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa    840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag    900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca    960

gaccaggtag tcgcaatcgc gtcaaacgga gggggaaagc aagccctgga aaccgtgcaa   1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt   1080

gcaaataata acggtggcaa acaggctctt gagacggttc agagacttct cccagttctc   1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgtcgca tgacggaggg   1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg   1260

acgcctgcac aagtggtcgc catcgcctcg aatggcggcg gtaagcaggc gctggaaaca   1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc   1380

gcaatcgcgt caaacggagg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg   1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc atcccacgac   1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac   1560

gggctgactc ccgatcaagt tgtagcgatt gcgtcgaaca ttggagggaa acaagcattg   1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa   1680

gtggtcgcca tcgccaacaa caacggcggt aagcaggcgc tggaaacagt acagcgcctg   1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca   1800

catgacgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa   1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcat cccacgacgg tggcaaacag   1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc   1980

gatcaagttg tagcgattgc gaataacaat ggagggaaac aagcattgga gactgtccaa   2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc   2100

gccagccatg atggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg   2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgcttctaa tgggggagga   2220

cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg   2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca   2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc   2400

gagagaactt cccatcgagt cgcgggatcc                                    2430
```

<210> SEQ ID NO 28
<211> LENGTH: 805
<212> TYPE: PRT

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```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 28

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

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

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365
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-continued

```
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
    690                 695                 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
705                 710                 715                 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg
                725                 730                 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
            740                 745                 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
        755                 760                 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
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    770                 775                 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785                 790                 795                 800

Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 29
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 29

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc     60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac    120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa    180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc    240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct    300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg    360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag    420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg    480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg    540

aacctgaccc cagaccaggt agtcgcaatc gcgtcaaacg gagggggaaa gcaagccctg    600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa    660

gtcgtggcca ttgcaaataa taacggtggc aaacaggctc ttgagacggt tcagagactt    720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg    780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa    840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcct ccaatattgg cggtaagcag    900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca    960

gaccaggtag tcgcaatcgc gaacaataat gggggaaagc aagccctgga aaccgtgcaa   1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt   1080

gcaagcaaca tcggtggcaa acaggctctt gagacggttc agagacttct cccagttctc   1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgtcgaa cattggaggg   1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg   1260

acgcctgcac aagtggtcgc catcgccaac aacaacggcg gtaagcaggc gctggaaaca   1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc   1380

gcaatcgcgt caaacggagg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg   1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc atcccacgac   1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac   1560

gggctgactc ccgatcaagt tgtagcgatt gcgaataaca atggagggaa acaagcattg   1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa   1680

gtggtcgcca tcgcctcgaa tggcggcggt aagcaggcgc tggaaacagt acagcgcctg   1740
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ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgaac 1800

aataatgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa 1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcat cccacgacgg tggcaaacag 1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc 1980

gatcaagttg tagcgattgc gtccaacggt ggagggaaac aagcattgga gactgtccaa 2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc 2100

gccaacaaca acggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg 2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgcttccca cgacggagga 2220

cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg 2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca 2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc 2400

gagagaactt cccatcgagt cgcgggatcc 2430

<210> SEQ ID NO 30
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 30

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1 5 10 15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
20 25 30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
130 135 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
165 170 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
180 185 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
195 200 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly

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    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

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

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn
        515                 520                 525

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620
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-continued

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
625 630 635 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
645 650 655

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
660 665 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
675 680 685

Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala
690 695 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
705 710 715 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg
725 730 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
740 745 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
755 760 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
770 775 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785 790 795 800

Arg Val Ala Gly Ser
805

<210> SEQ ID NO 31
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 31

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc 60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac 120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa 180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc 240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct 300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg 360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag 420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg 480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg 540

aacctgaccc cagaccaggt agtcgcaatc gcgaacaata atgggggaaa gcaagccctg 600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa 660

gtcgtggcca ttgcaagcaa catcggtggc aaacaggctc ttgagacggt tcagagactt 720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg 780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa 840

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gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag    900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca    960

gaccaggtag tcgcaatcgc gtcgaacatt gggggaaagc aagccctgga aaccgtgcaa   1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt   1080

gcaagcaaca tcggtggcaa acaggctctt gagacggttc agagacttct cccagttctc   1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgaataa caatggaggg   1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg   1260

acgcctgcac aagtggtcgc catcgcctcg aatggcggcg gtaagcaggc gctggaaaca   1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc   1380

gcaatcgcgt cacatgacgg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg   1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc aaataataac   1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac   1560

gggctgactc ccgatcaagt tgtagcgatt gcgtccaacg gtggagggaa acaagcattg   1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa   1680

gtggtcgcca tcgccaacaa caacggcggt aagcaggcgc tggaaacagt acagcgcctg   1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca   1800

catgacgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa   1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcaa gcaatggggg tggcaaacag   1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc   1980

gatcaagttg tagcgattgc gaataacaat ggagggaaac aagcattgga gactgtccaa   2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc   2100

gccagccatg atggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg   2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgcttctaa tgggggagga   2220

cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg   2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca   2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc   2400

gagagaactt cccatcgagt cgcgggatcc                                    2430
```

<210> SEQ ID NO 32
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 32

```
Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60
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Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

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

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
    450                 455                 460
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
    690                 695                 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
705                 710                 715                 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg
                725                 730                 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
            740                 745                 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
        755                 760                 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
    770                 775                 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785                 790                 795                 800

Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 33
<211> LENGTH: 2328
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 33

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tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc     60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac    120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa    180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc    240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct    300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg    360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag    420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg    480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg    540

aacctgaccc cagaccaggt agtcgcaatc gcgtcacatg acgggggaaa gcaagccctg    600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa    660

gtcgtggcca ttgcaaataa taacggtggc aaacaggctc ttgagacggt tcagagactt    720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg    780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa    840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag    900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca    960

gaccaggtag tcgcaatcgc gtcacatgac gggggaaagc aagccctgga aaccgtgcaa   1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt   1080

gcaagcaatg gggtggcaa acaggctctt gagacggttc agagacttct cccagttctc   1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgaataa caatggaggg   1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg   1260

acgcctgcac aagtggtcgc catcgcctcc aatattggcg gtaagcaggc gctggaaaca   1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc   1380

gcaatcgcgt cgaacattgg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg   1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc aaataataac   1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac   1560

gggctgactc ccgatcaagt tgtagcgatt gcgaataaca atggagggaa acaagcattg   1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa   1680

gtggtcgcca tcgccaacaa caacggcggt aagcaggcgc tggaaacagt acagcgcctg   1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca   1800

catgacgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa   1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcaa gcaacatcgg tggcaaacag   1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc   1980

gatcaagttg tagcgattgc gtccaacggt ggagggaaac aagcattgga gactgtccaa   2040

cggctccttc ccgtgttgtg tcaagcccac ggtctgacac ccgaacaggt ggtcgccatt   2100

gcttcccacg acggaggacg gccagccttg gagtccatcg tagcccaatt gtccaggccc   2160

gatcccgcgt tggctgcgtt aacgaatgac catctggtgg cgttggcatg tcttggtgga   2220

cgacccgcgc tcgatgcagt caaaaagggt ctgcctcatg ctcccgcatt gatcaaaaga   2280
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accaaccggc ggattcccga gagaacttcc catcgagtcg cgggatcc                2328


<210> SEQ ID NO 34
<211> LENGTH: 771
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 34

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
            180                 185                 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335
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Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn
        515                 520                 525

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro Ala
    690                 695                 700

Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala
705                 710                 715                 720

Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg
                725                 730                 735
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Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala Leu
            740                 745                 750

Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg Val
        755                 760                 765

Ala Gly Ser
    770


<210> SEQ ID NO 35
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 35

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc     60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac    120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa    180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc    240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct    300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg    360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag    420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg    480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg    540

aacctgaccc cagaccaggt agtcgcaatc gcgtcacatg acgggggaaa gcaagccctg    600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa    660

gtcgtggcca ttgcaaataa taacggtggc aaacaggctc ttgagacggt tcagagactt    720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcg    780

aacattggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa    840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag    900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca    960

gaccaggtag tcgcaatcgc gtcacatgac gggggaaagc aagccctgga aaccgtgcaa   1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt   1080

gcaagcaatg gggtggcaa acaggctctt gagacggttc agagacttct cccagttctc    1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgaataa caatggaggg   1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg   1260

acgcctgcac aagtggtcgc catcgcctcc aatattggcg gtaagcaggc gctggaaaca   1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc   1380

gcaatcgcgt cgaacattgg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg   1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc aaataataac   1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac   1560

gggctgactc ccgatcaagt tgtagcgatt gcgaataaca atggagggaa acaagcattg   1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa   1680
```

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```
gtggtcgcca tcgccaacaa caacggcggt aagcaggcgc tggaaacagt acagcgcctg   1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca   1800

catgacgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa   1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcaa gcaacatcgg tggcaaacag   1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc   1980

gatcaagttg tagcgattgc gtccaacggt ggagggaaac aagcattgga gactgtccaa   2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc   2100

gccagccatg atggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg   2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgctaataa taacggagga   2220

cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg   2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca   2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc   2400

gagagaactt cccatcgagt cgcgggatcc                                    2430


<210> SEQ ID NO 36
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 36

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
            180                 185                 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205
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His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn
        515                 520                 525

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
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    610                 615                 620

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
    690                 695                 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
705                 710                 715                 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Arg
                725                 730                 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
            740                 745                 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
        755                 760                 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
    770                 775                 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785                 790                 795                 800

Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 37
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 37

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc      60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac     120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa     180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc     240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct     300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg     360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag     420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg     480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg     540

aacctgaccc cagaccaggt agtcgcaatc gcgtcaaacg gagggggaaa gcaagccctg     600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa     660

gtcgtggcca ttgcaaataa taacggtggc aaacaggctc ttgagacggt tcagagactt     720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgtcc     780

aacggtggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa     840
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gcccacggtt tgacgcctgc acaagtggtc gccatcgcca acaacaacgg cggtaagcag 900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca 960

gaccaggtag tcgcaatcgc gtcacatgac gggggaaagc aagccctgga aaccgtgcaa 1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt 1080

gcatcccacg acggtggcaa acaggctctt gagacggttc agagacttct cccagttctc 1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgtcgca tgacggaggg 1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg 1260

acgcctgcac aagtggtcgc catcgccagc catgatggcg gtaagcaggc gctggaaaca 1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc 1380

gcaatcgcgt cgaacattgg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg 1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc aaataataac 1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac 1560

gggctgactc ccgatcaagt tgtagcgatt gcgaataaca atggagggaa acaagcattg 1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa 1680

gtggtcgcca tcgcctccaa tattggcggt aagcaggcgc tggaaacagt acagcgcctg 1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgtca 1800

aacggagggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa 1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcaa ataataacgg tggcaaacag 1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc 1980

gatcaagttg tagcgattgc gtccaacggt ggagggaaac aagcattgga gactgtccaa 2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc 2100

gcctcgaatg gcggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg 2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgctaataa taacggagga 2220

cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg 2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca 2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc 2400

gagagaactt cccatcgagt cgcgggatcc 2430

<210> SEQ ID NO 38
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 38

```
Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
```

-continued

```
    50                  55                  60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
            180                 185                 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
    450                 455                 460
```

-continued

```
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn
        515                 520                 525

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
    690                 695                 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
705                 710                 715                 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Arg
                725                 730                 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
            740                 745                 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
        755                 760                 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
    770                 775                 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785                 790                 795                 800

Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 39
<211> LENGTH: 2430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

-continued

<400> SEQUENCE: 39

tctagagcta gcaccatgga ctacaaagac catgacggtg attataaaga tcatgacatc 60

gattacaagg atgacgatga caagatggcc cccaagaaga agaggaaggt gggcattcac 120

cgcggggtac ctatggtgga cttgaggaca ctcggttatt cgcaacagca acaggagaaa 180

atcaagccta aggtcaggag caccgtcgcg caacaccacg aggcgcttgt ggggcatggc 240

ttcactcatg cgcatattgt cgcgctttca cagcaccctg cggcgcttgg gacggtggct 300

gtcaaatacc aagatatgat tgcggccctg cccgaagcca cgcacgaggc aattgtaggg 360

gtcggtaaac agtggtcggg agcgcgagca cttgaggcgc tgctgactgt ggcgggtgag 420

cttagggggc ctccgctcca gctcgacacc gggcagctgc tgaagatcgc gaagagaggg 480

ggagtaacag cggtagaggc agtgcacgcc tggcgcaatg cgctcaccgg ggcccccttg 540

aacctgaccc cagaccaggt agtcgcaatc gcgaacaata atgggggaaa gcaagccctg 600

gaaaccgtgc aaaggttgtt gccggtcctt tgtcaagacc acggccttac accggagcaa 660

gtcgtggcca ttgcaagcaa tgggggtggc aaacaggctc ttgagacggt tcagagactt 720

ctcccagttc tctgtcaagc ccacgggctg actcccgatc aagttgtagc gattgcgaat 780

aacaatggag ggaaacaagc attggagact gtccaacggc tccttcccgt gttgtgtcaa 840

gcccacggtt tgacgcctgc acaagtggtc gccatcgcca gccatgatgg cggtaagcag 900

gcgctggaaa cagtacagcg cctgctgcct gtactgtgcc aggatcatgg actgacccca 960

gaccaggtag tcgcaatcgc gtcacatgac gggggaaagc aagccctgga aaccgtgcaa 1020

aggttgttgc cggtcctttg tcaagaccac ggccttacac cggagcaagt cgtggccatt 1080

gcatcccacg acggtggcaa acaggctctt gagacggttc agagacttct cccagttctc 1140

tgtcaagccc acgggctgac tcccgatcaa gttgtagcga ttgcgtcgca tgacggaggg 1200

aaacaagcat tggagactgt ccaacggctc cttcccgtgt tgtgtcaagc ccacggtttg 1260

acgcctgcac aagtggtcgc catcgcctcc aatattggcg gtaagcaggc gctggaaaca 1320

gtacagcgcc tgctgcctgt actgtgccag gatcatggac tgaccccaga ccaggtagtc 1380

gcaatcgcga acaataatgg gggaaagcaa gccctggaaa ccgtgcaaag gttgttgccg 1440

gtcctttgtc aagaccacgg ccttacaccg gagcaagtcg tggccattgc aaataataac 1500

ggtggcaaac aggctcttga gacggttcag agacttctcc cagttctctg tcaagcccac 1560

gggctgactc ccgatcaagt tgtagcgatt gcgtcgaaca ttggagggaa acaagcattg 1620

gagactgtcc aacggctcct tcccgtgttg tgtcaagccc acggtttgac gcctgcacaa 1680

gtggtcgcca tcgcctcgaa tggcggcggt aagcaggcgc tggaaacagt acagcgcctg 1740

ctgcctgtac tgtgccagga tcatggactg accccagacc aggtagtcgc aatcgcgaac 1800

aataatgggg gaaagcaagc cctggaaacc gtgcaaaggt tgttgccggt cctttgtcaa 1860

gaccacggcc ttacaccgga gcaagtcgtg gccattgcaa gcaatggggg tggcaaacag 1920

gctcttgaga cggttcagag acttctccca gttctctgtc aagcccacgg gctgactccc 1980

gatcaagttg tagcgattgc gtccaacggt ggagggaaac aagcattgga gactgtccaa 2040

cggctccttc ccgtgttgtg tcaagcccac ggtttgacgc ctgcacaagt ggtcgccatc 2100

gccaacaaca acggcggtaa gcaggcgctg gaaacagtac agcgcctgct gcctgtactg 2160

tgccaggatc atggactgac acccgaacag gtggtcgcca ttgcttccca cgacggagga 2220

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cggccagcct tggagtccat cgtagcccaa ttgtccaggc ccgatcccgc gttggctgcg   2280

ttaacgaatg accatctggt ggcgttggca tgtcttggtg gacgacccgc gctcgatgca   2340

gtcaaaaagg gtctgcctca tgctcccgca ttgatcaaaa gaaccaaccg gcggattccc   2400

gagagaactt cccatcgagt cgcgggatcc                                    2430


<210> SEQ ID NO 40
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 40

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1               5                   10                  15

Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30

Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140

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

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175

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

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
        195                 200                 205

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
    210                 215                 220

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240

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

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
        275                 280                 285

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300
```

-continued

```
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
305                 310                 315                 320

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
    370                 375                 380

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415

Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
            420                 425                 430

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
        435                 440                 445

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys
    450                 455                 460

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
465                 470                 475                 480

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly
                485                 490                 495

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510

Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540

Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala
545                 550                 555                 560

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
            580                 585                 590

Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp
                645                 650                 655

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685

Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala
    690                 695                 700

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
```

-continued

```
705                 710                 715                 720

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg
                725                 730                 735

Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala
            740                 745                 750

Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly
        755                 760                 765

Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro
    770                 775                 780

Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His
785                 790                 795                 800

Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 41
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

gcagtgcttc agccgc                                                      16


<210> SEQ ID NO 42
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 42

tctagagaag acaagaacct gacc                                             24


<210> SEQ ID NO 43
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer
<220> FEATURE:
<223> OTHER INFORMATION: 5'-biotin

<400> SEQUENCE: 43

ggatccggtc tcttaaggcc gtgg                                             24


<210> SEQ ID NO 44
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

gcagtgcttc agccgc                                                      16


<210> SEQ ID NO 45
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
```

```
<400> SEQUENCE: 45

tctaacatc                                                              9


<210> SEQ ID NO 46
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> SEQUENCE: 46

tcccacgac                                                              9


<210> SEQ ID NO 47
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> SEQUENCE: 47

aataataac                                                              9


<210> SEQ ID NO 48
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> SEQUENCE: 48

tccaataaa                                                              9


<210> SEQ ID NO 49
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> SEQUENCE: 49

tctaatggg                                                              9


<210> SEQ ID NO 50
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

tgcagtgctt cagccgc                                                    17


<210> SEQ ID NO 51
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

tgcagtgctt cagccgct                                                   18
```

-continued

```
<210> SEQ ID NO 52
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

ttgaagaagt cgtgctgc                                                18


<210> SEQ ID NO 53
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

tgaagaagtc gtgctgct                                                18


<210> SEQ ID NO 54
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

tcgagctgaa gggcatc                                                 17


<210> SEQ ID NO 55
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

tcgagctgaa gggcatcg                                                18


<210> SEQ ID NO 56
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

ttgtgcccca ggatgttg                                                18


<210> SEQ ID NO 57
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

tgtgccccag gatgttgc                                                18


<210> SEQ ID NO 58
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 58

tctagagaag acaagaacct gaccccagac caggtagtcg caatcgcgtc gaacattggg     60

ggaaagcaag ccctggaaac cgtgcaaagg ttgttgccgg tcctttgtca agaccacggc    120
```

-continued

```
cttaagagac cggatcc                                                 137


<210> SEQ ID NO 59
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 59

tctagagaag acaagaacct gaccccagac caggtagtcg caatcgcgtc acatgacggg     60

ggaaagcaag ccctggaaac cgtgcaaagg ttgttgccgg tcctttgtca agaccacggc    120

cttaagagac cggatcc                                                 137


<210> SEQ ID NO 60
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 60

tctagagaag acaagaacct gaccccagac caggtagtcg caatcgcgtc gaacaaaggg     60

ggaaagcaag ccctggaaac cgtgcaaagg ttgttgccgg tcctttgtca agaccacggc    120

cttaagagac cggatcc                                                 137


<210> SEQ ID NO 61
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 61

tctagagaag acaagaacct gaccccagac caggtagtcg caatcgcgaa caataatggg     60

ggaaagcaag ccctggaaac cgtgcaaagg ttgttgccgg tcctttgtca agaccacggc    120

cttaagagac cggatcc                                                 137


<210> SEQ ID NO 62
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 62

tctagagaag acaagaacct gaccccagac caggtagtcg caatcgcgtc aaacggaggg     60

ggaaagcaag ccctggaaac cgtgcaaagg ttgttgccgg tcctttgtca agaccacggc    120

cttaagagac cggatcc                                                 137


<210> SEQ ID NO 63
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

```
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 63

tctagagaag acaacttaca ccggagcaag tcgtggccat tgcaagcaac atcggtggca     60

aacaggctct tgagacggtt cagagacttc tcccagttct ctgtcaagcc cacgggctga    120

agagaccgga tcc                                                       133


<210> SEQ ID NO 64
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 64

tctagagaag acaacttaca ccggagcaag tcgtggccat tgcatcccac gacggtggca     60

aacaggctct tgagacggtt cagagacttc tcccagttct ctgtcaagcc cacgggctga    120

agagaccgga tcc                                                       133


<210> SEQ ID NO 65
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 65

tctagagaag acaacttaca ccggagcaag tcgtggccat tgcatcaaat aaaggtggca     60

aacaggctct tgagacggtt cagagacttc tcccagttct ctgtcaagcc cacgggctga    120

agagaccgga tcc                                                       133


<210> SEQ ID NO 66
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 66

tctagagaag acaacttaca ccggagcaag tcgtggccat tgcaaataat aacggtggca     60

aacaggctct tgagacggtt cagagacttc tcccagttct ctgtcaagcc cacgggctga    120

agagaccgga tcc                                                       133


<210> SEQ ID NO 67
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 67

tctagagaag acaacttaca ccggagcaag tcgtggccat tgcaagcaat gggggtggca     60

aacaggctct tgagacggtt cagagacttc tcccagttct ctgtcaagcc cacgggctga    120
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agagaccgga tcc 133

<210> SEQ ID NO 68
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 68

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtcgaac attggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtttga 120

agagaccgga tcc 133

<210> SEQ ID NO 69
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 69

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtcgcat gacggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtttga 120

agagaccgga tcc 133

<210> SEQ ID NO 70
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 70

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtccaac aagggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtttga 120

agagaccgga tcc 133

<210> SEQ ID NO 71
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 71

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgaataac aatggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtttga 120

agagaccgga tcc 133

<210> SEQ ID NO 72
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 72

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtccaac ggtggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtttga 120

agagaccgga tcc 133

<210> SEQ ID NO 73
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 73

tctagagaag acaattgacg cctgcacaag tggtcgccat cgcctccaat attggcggta 60

agcaggcgct ggaaacagta cagcgcctgc tgcctgtact gtgccaggat catggactga 120

agagaccgga tcc 133

<210> SEQ ID NO 74
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 74

tctagagaag acaattgacg cctgcacaag tggtcgccat cgccagccat gatggcggta 60

agcaggcgct ggaaacagta cagcgcctgc tgcctgtact gtgccaggat catggactga 120

agagaccgga tcc 133

<210> SEQ ID NO 75
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 75

tctagagaag acaattgacg cctgcacaag tggtcgccat cgccagcaat aagggcggta 60

agcaggcgct ggaaacagta cagcgcctgc tgcctgtact gtgccaggat catggactga 120

agagaccgga tcc 133

<210> SEQ ID NO 76
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 76

tctagagaag acaattgacg cctgcacaag tggtcgccat cgccaacaac aacggcggta 60 agcaggcgct ggaaacagta cagcgcctgc tgcctgtact gtgccaggat catggactga 120

agagaccgga tcc 133

<210> SEQ ID NO 77
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 77

tctagagaag acaattgacg cctgcacaag tggtcgccat cgcctcgaat ggcggcggta 60

agcaggcgct ggaaacagta cagcgcctgc tgcctgtact gtgccaggat catggactga 120

agagaccgga tcc 133

<210> SEQ ID NO 78
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 78

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcgaac attgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctta 120

agagaccgga tcc 133

<210> SEQ ID NO 79
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 79

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcacat gacgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctta 120

agagaccgga tcc 133

<210> SEQ ID NO 80
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 80

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcgaac aaagggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctta 120

agagaccgga tcc 133

<210> SEQ ID NO 81
<211> LENGTH: 133
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 81

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgaacaat aatgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctta 120

agagaccgga tcc 133

<210> SEQ ID NO 82
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 82

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcaaac ggagggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctta 120

agagaccgga tcc 133

<210> SEQ ID NO 83
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 83

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtcgaac attggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtctga 120

agagaccgga tcc 133

<210> SEQ ID NO 84
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 84

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtcgcat gacggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtctga 120

agagaccgga tcc 133

<210> SEQ ID NO 85
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 85

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtccaac aagggaggga 60

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aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtctga 120

agagaccgga tcc 133

<210> SEQ ID NO 86
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 86

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgaataac aatggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtctga 120

agagaccgga tcc 133

<210> SEQ ID NO 87
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 87

tctagagaag acaactgact cccgatcaag ttgtagcgat tgcgtccaac ggtggaggga 60

aacaagcatt ggagactgtc caacggctcc ttcccgtgtt gtgtcaagcc cacggtctga 120

agagaccgga tcc 133

<210> SEQ ID NO 88
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 88

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcgaac attgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctga 120

agagaccgga tcc 133

<210> SEQ ID NO 89
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 89

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcacat gacgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctga 120

agagaccgga tcc 133

<210> SEQ ID NO 90
<211> LENGTH: 133

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 90

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcgaac aaagggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctga 120

agagaccgga tcc 133

<210> SEQ ID NO 91
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 91

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgaacaat aatgggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctga 120

agagaccgga tcc 133

<210> SEQ ID NO 92
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 92

tctagagaag acaactgacc ccagaccagg tagtcgcaat cgcgtcaaac ggagggggaa 60

agcaagccct ggaaaccgtg caaaggttgt tgccggtcct ttgtcaagac cacggcctga 120

agagaccgga tcc 133

<210> SEQ ID NO 93
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

tcgccaccat ggtgagcaag ggcgaggagc tgttca 36

<210> SEQ ID NO 94
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 94

tggtgcccat cctggtcgag ctggacggcg acgtaa 36

<210> SEQ ID NO 95
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

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tctgcaccac cggcaagctg cccgtgccct ggccca 36

<210> SEQ ID NO 96
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 96

tggagtacaa ctacaacagc cacaacgtct atatca 36

<210> SEQ ID NO 97
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 97

ttcagcgtgt ccggcgaggg cgagggcgat gccaccta 38

<210> SEQ ID NO 98
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 98

tgccacctac ggcaagctga ccctgaagtt catctgca 38

<210> SEQ ID NO 99
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 99

tggcccaccc tcgtgaccac cctgacctac ggcgtgca 38

<210> SEQ ID NO 100
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 100

ttcaagatcc gccacaacat cgaggacggc agcgtgca 38

<210> SEQ ID NO 101
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 101

tagaggatcc accggtcgcc accatggtga gcaagggcga 40

<210> SEQ ID NO 102
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 102

tccggcgagg gcgagggcga tgccacctac ggcaagctga 40

<210> SEQ ID NO 103
<211> LENGTH: 40
<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 103

tgacctacgg cgtgcagtgc ttcagccgct accccgacca 40

<210> SEQ ID NO 104
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

tccgccacaa catcgaggac ggcagcgtgc agctcgccga 40

<210> SEQ ID NO 105
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 105

tcctggtcga gctggacggc gacgtaaacg gccacaagtt ca 42

<210> SEQ ID NO 106
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

tcagccgcta ccccgaccac atgaagcagc acgacttctt ca 42

<210> SEQ ID NO 107
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

tcttcaagtc cgccatgccc gaaggctacg tccaggagcg ca 42

<210> SEQ ID NO 108
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 108

tcaaggagga cggcaacatc ctggggcaca agctggagta ca 42

<210> SEQ ID NO 109
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 109

tcaaggtgaa cttcaagatc cgccacaaca tcgaggacgg ca 42

<210> SEQ ID NO 110
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 110

tccaccggtc gccaccatgg tgagcaaggg cgaggagctg ttca 44

<210> SEQ ID NO 111
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 111

ttcagcgtgt ccggcgaggg cgagggcgat gccacctacg gcaa 44

<210> SEQ ID NO 112
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 112

ttcagccgct accccgacca catgaagcag cacgacttct tcaa 44

<210> SEQ ID NO 113
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaa 44

<210> SEQ ID NO 114
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

tggtgcccat cctggtcgag ctggacggcg acgtaaacgg ccacaa 46

<210> SEQ ID NO 115
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacga 46

<210> SEQ ID NO 116
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 116

tgaaccgcat cgagctgaag ggcatcgact tcaaggagga cggcaa 46

<210> SEQ ID NO 117
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

tcaagatccg ccacaacatc gaggacggca gcgtgcagct cgccga 46

<210> SEQ ID NO 118
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 118

tgttcaccgg ggtggtgccc atcctggtcg agctggacgg cgacgtaa 48

<210> SEQ ID NO 119
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

tgcccatcct ggtcgagctg gacggcgacg taaacggcca caagttca 48

<210> SEQ ID NO 120
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctga 48

<210> SEQ ID NO 121
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

tcatctgcac caccggcaag ctgcccgtgc cctggcccac cctcgtga 48

<210> SEQ ID NO 122
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 122

tctatatcat ggccgacaag cagaagaacg gcatcaaggt gaacttca 48

<210> SEQ ID NO 123
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

tacggcgtgc agtgcttcag ccgctacccc gaccacatga agcagcacga 50

<210> SEQ ID NO 124
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

taccccgacc acatgaagca gcacgacttc ttcaagtccg ccatgcccga 50

<210> SEQ ID NO 125
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125

tccgccatgc ccgaaggcta cgtccaggag cgcaccatct tcttcaagga 50

<210> SEQ ID NO 126

<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

ttcaaggagg acggcaacat cctggggcac aagctggagt acaactacaa 50

<210> SEQ ID NO 127
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

tacaactaca acagccacaa cgtctatatc atggccgaca agcagaagaa 50

<210> SEQ ID NO 128
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

tcaccggggt ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc ca 52

<210> SEQ ID NO 129
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc ta 52

<210> SEQ ID NO 130
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

tgcagtgctt cagccgctac cccgaccaca tgaagcagca cgacttcttc aa 52

<210> SEQ ID NO 131
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 131

tcagcgtgtc cggcgagggc gagggcgatg ccacctacgg caagctgacc ctga 54

<210> SEQ ID NO 132
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc gtga 54

<210> SEQ ID NO 133
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 133

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tcgtgaccac cctgacctac ggcgtgcagt gcttcagccg ctaccccgac caca          54


<210> SEQ ID NO 134
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc caca          54


<210> SEQ ID NO 135
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

ttcaccgggg tggtgcccat cctggtcgag ctggacggcg acgtaaacgg ccacaa        56


<210> SEQ ID NO 136
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

tgcaccaccg gcaagctgcc cgtgccctgg cccaccctcg tgaccaccct gaccta        56


<210> SEQ ID NO 137
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

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<210> SEQ ID NO 138
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

tatatcatgg ccgacaagca gaagaacggc atcaaggtga acttcaagat ccgcca        56


<210> SEQ ID NO 139
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccctga      58


<210> SEQ ID NO 140
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<400> SEQUENCE: 140

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<210> SEQ ID NO 141
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

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<210> SEQ ID NO 142
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<400> SEQUENCE: 142

tgtgtcttgg gatgagtggg tcagtgttct ggtgctcaca ggatggctgg ca 52

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 144

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<210> SEQ ID NO 145
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<212> TYPE: DNA
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<400> SEQUENCE: 145

tgaattggga tgctgttttt aggtattcta ttcaaattta ttttactgtc ttta 54

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<400> SEQUENCE: 146

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<400> SEQUENCE: 147

tgtgcgatct ccaagcactg aggggcagaa actcccggat cgggcgctgc ca 52

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<400> SEQUENCE: 148

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<400> SEQUENCE: 150

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<400> SEQUENCE: 151

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<400> SEQUENCE: 152

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<400> SEQUENCE: 154

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<400> SEQUENCE: 155

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<400> SEQUENCE: 157

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<400> SEQUENCE: 158

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<212> TYPE: DNA
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<400> SEQUENCE: 160

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

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<400> SEQUENCE: 162

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<400> SEQUENCE: 163

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<211> LENGTH: 55
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<400> SEQUENCE: 164

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<400> SEQUENCE: 165

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<400> SEQUENCE: 166

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<400> SEQUENCE: 167

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<400> SEQUENCE: 168

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<400> SEQUENCE: 169

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<400> SEQUENCE: 170

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<210> SEQ ID NO 171
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<400> SEQUENCE: 172

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

tcggccacca tgtcccgcca gaccacctct gtgggctcca gctgcctgga 50

<210> SEQ ID NO 174
<211> LENGTH: 54
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<400> SEQUENCE: 174

tccccagaac agcactatgg gcttctcttc cgagctgtgc agcccccagg gcca 54

<210> SEQ ID NO 175
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

tctgctcccc accgaggacc tctgcatgca ggcatgaatc ccaggagcct a 51

<210> SEQ ID NO 176
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<212> TYPE: DNA
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<400> SEQUENCE: 176

tgtaccgagc acttcggctc ctcgcgcgct cgcgtcccct cgtgcgggct cca 53

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<400> SEQUENCE: 177

tctccaaggc accatgaatg ccatcgtggc tctctgccac ttctgcgagc tcca 54

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<400> SEQUENCE: 178

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

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<400> SEQUENCE: 180

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<210> SEQ ID NO 181
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<400> SEQUENCE: 181

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<400> SEQUENCE: 182

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<400> SEQUENCE: 183

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<210> SEQ ID NO 184
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<400> SEQUENCE: 184

tgcgctcacc tccctgcggc ctcctgaggt ggtttggtgg ccccctcctc gcga 54

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<400> SEQUENCE: 185

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<400> SEQUENCE: 186

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<400> SEQUENCE: 187

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<400> SEQUENCE: 188

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<400> SEQUENCE: 189

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<400> SEQUENCE: 190

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<400> SEQUENCE: 191

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<400> SEQUENCE: 192

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<210> SEQ ID NO 193
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<400> SEQUENCE: 193

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<400> SEQUENCE: 194

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<400> SEQUENCE: 195

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<400> SEQUENCE: 196

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<400> SEQUENCE: 197

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<400> SEQUENCE: 198

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<400> SEQUENCE: 199

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<400> SEQUENCE: 201

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<400> SEQUENCE: 202

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<400> SEQUENCE: 203

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<400> SEQUENCE: 204

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<400> SEQUENCE: 205

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<400> SEQUENCE: 206

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<400> SEQUENCE: 207

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<400> SEQUENCE: 214

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<400> SEQUENCE: 215

tgctgggtga gaagggctgt ggctgcgttt tagagaagcg ttgggtactg ga 52

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<400> SEQUENCE: 216

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

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<400> SEQUENCE: 218

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<400> SEQUENCE: 220

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<400> SEQUENCE: 223

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<400> SEQUENCE: 226

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<400> SEQUENCE: 230

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

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<210> SEQ ID NO 232
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<212> TYPE: DNA
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

tctggatcgc ggagggaatg ccccggaggg cggagaactg ggacgaggcc ga            52


<210> SEQ ID NO 235
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 235

tgggccagag atggcggcgg ccgacggggc tttgccggag gcggcggctt ta            52


<210> SEQ ID NO 236
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

tgcccagaca agcaacatgg ctcggaaacg cgcggccggc ggggagccgc gggga         55


<210> SEQ ID NO 237
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer
<220> FEATURE:
<223> OTHER INFORMATION: 5'-biotin

<400> SEQUENCE: 237

tctagagaag acaagaacct gacc                                           24


<210> SEQ ID NO 238
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 238

ggatccggtc tcttaaggcc gtgg                                           24


<210> SEQ ID NO 239
<211> LENGTH: 28
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 239

gacggtggct gtcaaatacc aagatatg                                        28


<210> SEQ ID NO 240
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 240

tctcctccag ttcacttttg actagttggg                                      30


<210> SEQ ID NO 241
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 241

agtaacagcg gtagaggcag                                                 20


<210> SEQ ID NO 242
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 242

attgggctac gatggactcc                                                 20


<210> SEQ ID NO 243
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 243

ttaattcaat atattcatga ggcac                                           25


<210> SEQ ID NO 244
<211> LENGTH: 5656
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (901)..(910)
<223> OTHER INFORMATION: a, c, t, g, unknown or other

<400> SEQUENCE: 244
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gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg     60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg    120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc    180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt    240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata    300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc    360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc    420

attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt    480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc    720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg    780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca    840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc    900

nnnnnnnnnn ggatcccaac tagtcaaaag tgaactggag gagaagaaat ctgaacttcg    960

tcataaattg aaatatgtgc ctcatgaata tattgaatta attgaaattg ccagaaattc   1020

cactcaggat agaattcttg aaatgaaggt aatggaattt tttatgaaag tttatggata   1080

tagaggtaaa catttgggtg gatcaaggaa accggacgga gcaatttata ctgtcggatc   1140

tcctattgat tacggtgtga tcgtggatac taaagcttat agcggaggtt ataatctgcc   1200

aattggccaa gcagatgaaa tgcaacgata tgtcgaagaa aatcaaacac gaaacaaaca   1260

tatcaaccct aatgaatggt ggaaagtcta tccatcttct gtaacggaat ttaagttttt   1320

atttgtgagt ggtcacttta aaggaaacta caaagctcag cttacacgat taaatcatat   1380

cactaattgt aatggagctg ttcttagtgt agaagagctt ttaattggtg gagaaatgat   1440

taaagccggc acattaacct tagaggaagt cagacggaaa tttaataacg gcgagataaa   1500

cttttaaggg cccttcgaag gtaagcctat ccctaaccct ctcctcggtc tcgattctac   1560

gcgtaccggt catcatcacc atcaccattg agtttaaacc cgctgatcag cctcgactgt   1620

gccttctagt tgccagccat ctgttgtttg cccctccccc gtgccttcct tgaccctgga   1680

aggtgccact cccactgtcc tttcctaata aaatgaggaa attgcatcgc attgtctgag   1740

taggtgtcat tctattctgg ggggtggggt ggggcaggac agcaaggggg aggattggga   1800

agacaatagc aggcatgctg gggatgcggt gggctctatg gcttctgagg cggaaagaac   1860

cagctggggc tctagggggt atccccacgc gccctgtagc ggcgcattaa gcgcggcggg   1920

tgtggtggtt acgcgcagcg tgaccgctac acttgccagc gccctagcgc ccgctccttt   1980

cgctttcttc ccttcctttc tcgccacgtt cgccggcttt ccccgtcaag ctctaaatcg   2040

ggggctccct ttagggttcc gatttagtgc tttacggcac ctcgacccca aaaaacttga   2100

ttagggtgat ggttcacgta gtgggccatc gccctgatag acggtttttc gccctttgac   2160

gttggagtcc acgttcttta atagtggact cttgttccaa actggaacaa cactcaaccc   2220

tatctcggtc tattcttttg atttataagg gattttgggg atttcggcct attggttaaa   2280
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aaatgagctg atttaacaaa aatttaacgc gaattaattc tgtggaatgt gtgtcagtta   2340

gggtgtggaa agtccccagg ctccccaggc aggcagaagt atgcaaagca tgcatctcaa   2400

ttagtcagca accaggtgtg gaaagtcccc aggctcccca gcaggcagaa gtatgcaaag   2460

catgcatctc aattagtcag caaccatagt cccgccccta actccgccca tcccgcccct   2520

aactccgccc agttccgccc attctccgcc ccatggctga ctaatttttt ttatttatgc   2580

agaggccgag gccgcctctg cctctgagct attccagaag tagtgaggag gcttttttgg   2640

aggcctaggc ttttgcaaaa agctcccggg agcttgtata tccattttcg gatctgatca   2700

gcacgtgttg acaattaatc atcggcatag tatatcggca tagtataata cgacaaggtg   2760

aggaactaaa ccatggccaa gcctttgtct caagaagaat ccaccctcat tgaaagagca   2820

acggctacaa tcaacagcat ccccatctct gaagactaca gcgtcgccag cgcagctctc   2880

tctagcgacg gccgcatctt cactggtgtc aatgtatatc attttactgg gggaccttgt   2940

gcagaactcg tggtgctggg cactgctgct gctgcggcag ctggcaacct gacttgtatc   3000

gtcgcgatcg gaaatgagaa caggggcatc ttgagcccct gcggacggtg tcgacaggtg   3060

cttctcgatc tgcatcctgg gatcaaagcg atagtgaagg acagtgatgg acagccgacg   3120

gcagttggga ttcgtgaatt gctgccctct ggttatgtgt gggagggcta agcacttcgt   3180

ggccgaggag caggactgac acgtgctacg agatttcgat tccaccgccg ccttctatga   3240

aaggttgggc ttcggaatcg ttttccggga cgccggctgg atgatcctcc agcgcgggga   3300

tctcatgctg gagttcttcg cccaccccaa cttgtttatt gcagcttata atggttacaa   3360

ataaagcaat agcatcacaa atttcacaaa taaagcattt ttttcactgc attctagttg   3420

tggtttgtcc aaactcatca atgtatctta tcatgtctgt ataccgtcga cctctagcta   3480

gagcttggcg taatcatggt catagctgtt tcctgtgtga aattgttatc cgctcacaat   3540

tccacacaac atacgagccg gaagcataaa gtgtaaagcc tggggtgcct aatgagtgag   3600

ctaactcaca ttaattgcgt tgcgctcact gcccgctttc cagtcgggaa acctgtcgtg   3660

ccagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc   3720

ttccgcttcc tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc   3780

agctcactca aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa   3840

catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt   3900

tttccatagg ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg   3960

gcgaaacccg acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgtgcg   4020

ctctcctgtt ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag   4080

cgtggcgctt tctcaatgct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc   4140

caagctgggc tgtgtgcacg aaccccccgt tcagcccgac cgctgcgcct tatccggtaa   4200

ctatcgtctt gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg   4260

taacaggatt agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc   4320

taactacggc tacactagaa ggacagtatt tggtatctgc gctctgctga agccagttac   4380

cttcggaaaa agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggtgg   4440

tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag aagatccttt   4500

gatcttttct acggggtctg acgctcagtg gaacgaaaac tcacgttaag ggattttggt   4560
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catgagatta tcaaaaagga tcttcaccta gatcctttta aattaaaaat gaagttttaa 4620

atcaatctaa agtatatatg agtaaacttg gtctgacagt taccaatgct taatcagtga 4680

ggcacctatc tcagcgatct gtctatttcg ttcatccata gttgcctgac tccccgtcgt 4740

gtagataact acgatacggg agggcttacc atctggcccc agtgctgcaa tgataccgcg 4800

agacccacgc tcaccggctc cagatttatc agcaataaac cagccagccg gaagggccga 4860

gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag tctattaatt gttgccggga 4920

agctagagta agtagttcgc cagttaatag tttgcgcaac gttgttgcca ttgctacagg 4980

catcgtggtg tcacgctcgt cgtttggtat ggcttcattc agctccggtt cccaacgatc 5040

aaggcgagtt acatgatccc ccatgttgtg caaaaaagcg gttagctcct tcggtcctcc 5100

gatcgttgtc agaagtaagt tggccgcagt gttatcactc atggttatgg cagcactgca 5160

taattctctt actgtcatgc catccgtaag atgcttttct gtgactggtg agtactcaac 5220

caagtcattc tgagaatagt gtatgcggcg accgagttgc tcttgcccgg cgtcaatacg 5280

ggataatacc gcgccacata gcagaacttt aaaagtgctc atcattggaa aacgttcttc 5340

ggggcgaaaa ctctcaagga tcttaccgct gttgagatcc agttcgatgt aacccactcg 5400

tgcacccaac tgatcttcag catcttttac tttcaccagc gtttctgggt gagcaaaaac 5460

aggaaggcaa aatgccgcaa aaaagggaat aagggcgaca cggaaatgtt gaatactcat 5520

actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata 5580

catatttgaa tgtatttaga aaaataaaca aataggggtt ccgcgcacat ttccccgaaa 5640

agtgccacct gacgtc 5656

<210> SEQ ID NO 245
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 245

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaatggggg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

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```
ggtttgacgc ctgcacaagt ggtcgccatc gcctcgaatg gcggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc   1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaatg gggggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac   2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424
```

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<210> SEQ ID NO 246
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 246

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
```

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    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
            180                 185                 190

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460
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Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
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<210> SEQ ID NO 247
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

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<400> SEQUENCE: 247

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgaa cattggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac 2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca 2220

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gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 248
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 248

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
            180                 185                 190

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300
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Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
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705 710 715 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
725 730 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
740 745 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
755 760 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
770 775 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785 790 795 800

Thr Ser His Arg Val Ala Gly Ser
805

<210> SEQ ID NO 249
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 249

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gcctccaata ttggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat 1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctcgaatggc ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

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gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct ccaatattgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gaacaataat   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac   2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 250
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 250

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560
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Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 251
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 251

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa     300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt     360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg     420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta     480
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acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaacatcgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

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gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaatg ggggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgaa cattggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccagc 2100

catgatggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 252
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 252

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Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
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805

<210> SEQ ID NO 253
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 253

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca aacggagggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaacatcgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gcctccaata ttggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt ccaacggtgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcc aacggtggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcct ccaatattgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaaataata acggtggcaa acaggctctt 1920

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gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcc   2100

aatattggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaacatcgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 254
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 254

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
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                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655
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Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 255
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 255

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa     300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt     360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg     420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta     480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg     540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc     600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg     660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca     720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtccaacggt     780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac     840

ggtttgacgc ctgcacaagt ggtcgccatc gcctcgaatg gcggcggtaa gcaggcgctg     900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag     960

gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg    1020
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ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat 1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt ccaacggtgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcc aacggtggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcaaacgga 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgca tgacggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccagc 2100

catgatggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 256
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 256

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1 5 10 15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
20 25 30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
35 40 45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
50 55 60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65 70 75 80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
85 90 95

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Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
            180                 185                 190

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495
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Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 257
<211> LENGTH: 2322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 257

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180
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cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc 1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaatg gggggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtctg acacccgaac aggtggtcgc cattgcttct 2100

aacatcggag gacggccagc cttggagtcc atcgtagccc aattgtccag gcccgatccc 2160

gcgttggctg cgttaacgaa tgaccatctg gtggcgttgg catgtcttgg tggacgaccc 2220

gcgctcgatg cagtcaaaaa gggtctgcct catgctcccg cattgatcaa aagaaccaac 2280

cggcggattc ccgagagaac ttcccatcga gtcgcgggat cc 2322

<210> SEQ ID NO 258
<211> LENGTH: 774

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 258

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
        355                 360                 365
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
    690                 695                 700

Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro
705                 710                 715                 720

Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu
                725                 730                 735

Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala
            740                 745                 750

Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser
        755                 760                 765
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His Arg Val Ala Gly Ser
770

<210> SEQ ID NO 259
<211> LENGTH: 2220
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 259

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat 1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg aacattggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

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ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac acccgaacag   1980

gtggtcgcca ttgcttccca cgacggagga cggccagcct tggagtccat cgtagcccaa   2040

ttgtccaggc ccgatcccgc gttggctgcg ttaacgaatg accatctggt ggcgttggca   2100

tgtcttggtg gacgacccgc gctcgatgca gtcaaaaagg gtctgcctca tgctcccgca   2160

ttgatcaaaa gaaccaaccg gcggattccc gagagaactt cccatcgagt cgcgggatcc   2220
```

```
<210> SEQ ID NO 260
<211> LENGTH: 740
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 260

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
            180                 185                 190

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285
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```
Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro
            660                 665                 670

Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu
        675                 680                 685
```

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```
Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly
    690                 695                 700

Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala
705                 710                 715                 720

Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg
                725                 730                 735

Val Ala Gly Ser
            740
```

<210> SEQ ID NO 261
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 261

```
gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60

aaggatgacg atgacaagat ggccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgccccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc   1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcgaaca ttgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact   1620
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gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac   2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaatggggg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc   2424

<210> SEQ ID NO 262
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 262

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1   5   10   15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20   25   30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35   40   45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50   55   60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65   70   75   80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85   90   95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100   105   110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115   120   125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130   135   140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165   170   175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
            180   185   190

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```
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
```

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595 600 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
610 615 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625 630 635 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
645 650 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
660 665 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
675 680 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
690 695 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705 710 715 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly
725 730 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
740 745 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
755 760 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
770 775 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785 790 795 800

Thr Ser His Arg Val Ala Gly Ser
805

<210> SEQ ID NO 263
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 263

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

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gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat   1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca acaacaacgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaaataata acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg   2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                           2424
```

<210> SEQ ID NO 264
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 264

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Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
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        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445
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```
Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 265
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 265

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaacatcgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat 1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcgaaca ttgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcct ccaatattgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg 2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

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gatcatggac tgacacccga acaggtggtc gccattgctt ctaatggggg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                           2424


<210> SEQ ID NO 266
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 266

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285
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```
Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
```

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690 695 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705 710 715 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly
725 730 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
740 745 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
755 760 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
770 775 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785 790 795 800

Thr Ser His Arg Val Ala Gly Ser
805

<210> SEQ ID NO 267
<211> LENGTH: 2322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 267

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaatggggg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaaa cggagggggа aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat 1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

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```
gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcaaacg gagggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcc aacggtggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct cgaatggcgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gaacaataat   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtctg acacccgaac aggtggtcgc cattgcttcc   2100

cacgacggag gacggccagc cttggagtcc atcgtagccc aattgtccag gcccgatccc   2160

gcgttggctg cgttaacgaa tgaccatctg gtggcgttgg catgtcttgg tggacgaccc   2220

gcgctcgatg cagtcaaaaa gggtctgcct catgctcccg cattgatcaa aagaaccaac   2280

cggcggattc ccgagagaac ttcccatcga gtcgcgggat cc                      2322
```

<210> SEQ ID NO 268
<211> LENGTH: 774
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 268

```
Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

Gln Leu Asp Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val
145                 150                 155                 160
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```
Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560
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Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
565 570 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
580 585 590

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
595 600 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
610 615 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625 630 635 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
645 650 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
660 665 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
675 680 685

Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
690 695 700

Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro
705 710 715 720

Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu
725 730 735

Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala
740 745 750

Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser
755 760 765

His Arg Val Ala Gly Ser
770

<210> SEQ ID NO 269
<211> LENGTH: 2220
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 269

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

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```
gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc   1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcgaaca ttgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct cgaatggcgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac acccgaacag   1980

gtggtcgcca ttgcttccca cgacggagga cggccagcct tggagtccat cgtagcccaa   2040

ttgtccaggc ccgatcccgc gttggctgcg ttaacgaatg accatctggt ggcgttggca   2100

tgtcttggtg gacgacccgc gctcgatgca gtcaaaaagg gtctgcctca tgctcccgca   2160

ttgatcaaaa gaaccaaccg gcggattccc gagagaactt cccatcgagt cgcgggatcc   2220
```

```
<210> SEQ ID NO 270
<211> LENGTH: 740
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 270

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80
```

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```
His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480
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```
Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Arg Pro
            660                 665                 670

Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu
        675                 680                 685

Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly
    690                 695                 700

Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Ala
705                 710                 715                 720

Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser His Arg
                725                 730                 735

Val Ala Gly Ser
            740
```

```
<210> SEQ ID NO 271
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 271

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa     300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt     360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg     420
```

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gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc 1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca acaacaacgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaaataata acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgca tgacggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccagc 2100

catgatggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 272
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

-continued

```
<400> SEQUENCE: 272

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
                20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
            35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
        50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
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385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800
```

```
Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 273
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 273

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcaa gcaatggggg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gcctccaata ttggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc   1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct cgaatggcgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860
```

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ggccttacac cggagcaagt cgtggccatt gcaagcaatg ggggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccagc   2100

catgatggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaacatcgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 274
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 274

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240
```

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Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
625                 630                 635                 640
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Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
    675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
    755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 275
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 275

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa     300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt     360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg     420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta     480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg     540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc     600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg     660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca     720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt     780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac     840

ggtttgacgc ctgcacaagt ggtcgccatc gcctcgaatg gcggcggtaa gcaggcgctg     900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag     960
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gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc   1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctcgaatggc ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct ccaatattgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcaaacgga   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg   2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaacatcgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 276
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 276

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80
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His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
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                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
```

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<210> SEQ ID NO 277
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 277

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120
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gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaacatcgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gcctccaata ttggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcgaa cattgggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcct ccaatattgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaatg gggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgaa cattggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg 2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaacatcgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

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acttcccatc gagtcgcggg atcc                                          2424

<210> SEQ ID NO 278
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 278

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335
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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile
                725                 730                 735
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Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
740 745 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
755 760 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
770 775 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785 790 795 800

Thr Ser His Arg Val Ala Gly Ser
805

<210> SEQ ID NO 279
<211> LENGTH: 2322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 279

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggccccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca aacggagggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc 1500

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aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg aacattggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtctg acacccgaac aggtggtcgc cattgcttcc   2100

cacgacggag gacggccagc cttggagtcc atcgtagccc aattgtccag gcccgatccc   2160

gcgttggctg cgttaacgaa tgaccatctg gtggcgttgg catgtcttgg tggacgaccc   2220

gcgctcgatg cagtcaaaaa gggtctgcct catgctcccg cattgatcaa aagaaccaac   2280

cggcggattc ccgagagaac ttcccatcga gtcgcgggat cc                      2322
```

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<210> SEQ ID NO 280
<211> LENGTH: 774
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 280

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
    35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
    115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
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        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605
```

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Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
610 615 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625 630 635 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
645 650 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
660 665 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
675 680 685

Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
690 695 700

Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro
705 710 715 720

Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu
725 730 735

Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala
740 745 750

Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser
755 760 765

His Arg Val Ala Gly Ser
770

<210> SEQ ID NO 281
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 281

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtccaacggt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gcctcgaatg gcggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

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gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat   1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcc aacggtggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca acaacaacgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gaacaataat   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg   2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaatggggg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                           2424
```

```
<210> SEQ ID NO 282
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 282

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80
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His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480
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```
Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 283
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 283

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gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60
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```
aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgtca aacggagggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat   1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctcgaatggc ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcaaacg gagggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcaaacgga   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaaataata acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg   2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaatggggg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340
```

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```
aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 284
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 284

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
```

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```
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly
                725                 730                 735
```

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```
Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 285
<211> LENGTH: 2322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 285

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gcctccaata ttggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc   1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcaaacg gagggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc   1500
```

-continued

```
aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgtcg aacattggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcaaataata acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgtcgca tgacggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtctg acacccgaac aggtggtcgc cattgcttcc   2100

cacgacggag gacggccagc cttggagtcc atcgtagccc aattgtccag gcccgatccc   2160

gcgttggctg cgttaacgaa tgaccatctg gtggcgttgg catgtcttgg tggacgaccc   2220

gcgctcgatg cagtcaaaaa gggtctgcct catgctcccg cattgatcaa aagaaccaac   2280

cggcggattc ccgagagaac ttcccatcga gtcgcgggat cc                      2322
```

```
<210> SEQ ID NO 286
<211> LENGTH: 774
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 286

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
    35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
            180                 185                 190
```

-continued

```
Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
```

-continued

```
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro
705                 710                 715                 720

Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu
                725                 730                 735

Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His Ala
            740                 745                 750

Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr Ser
        755                 760                 765

His Arg Val Ala Gly Ser
    770


<210> SEQ ID NO 287
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 287

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtccaacggt    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gcctcgaatg gcggcggtaa gcaggcgctg    900
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gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaaa cggaggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctcgaatggc ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcaaacg gagggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcct cgaatggcgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gaacaataat 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtccaa cggtggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcc 2100

aatattggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaacatcgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 288
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 288

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1 5 10 15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
20 25 30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
35 40 45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
50 55 60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr

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65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480
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Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 289
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 289

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

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aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca aacggagggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aatgggggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgcatgacgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg aacattggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca acaacaacgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgaa cattggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcg 2100

aatggcggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

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aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424


<210> SEQ ID NO 290
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 290

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320
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Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
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                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 291
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 291

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac     60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg    120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag    180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact    240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa    300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt    360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg    420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta    480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg    540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc    600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg    660

gccattgcaa gcaatggggg tggcaaacag gctcttgaga cggttcagag acttctccca    720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtccaacggt    780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac    840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg    900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag    960

gtagtcgcaa tcgcgtcgaa cattggggga aagcaagccc tggaaaccgt gcaaaggttg   1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc   1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa   1140

gcccacgggc tgactcccga tcaagttgta gcgattgcgt ccaacggtgg agggaaacaa   1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct   1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag   1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc   1380

gcgtcaaacg gagggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt   1440
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tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcatccca cgacggtggc   1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg   1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact   1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc   1680

gccatcgcct cgaatggcgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct   1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac   1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac   1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt   1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa   1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc   2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac   2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag   2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca   2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg   2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa   2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga   2400

acttcccatc gagtcgcggg atcc                                          2424
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<210> SEQ ID NO 292
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 292

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
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                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
    195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
    275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
    355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
    435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
    515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575
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Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
580 585 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
595 600 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
610 615 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625 630 635 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
645 650 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
660 665 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
675 680 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
690 695 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705 710 715 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
725 730 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
740 745 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
755 760 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
770 775 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785 790 795 800

Thr Ser His Arg Val Ala Gly Ser
805

<210> SEQ ID NO 293
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 293

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc 600

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gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa ataataacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gaataacaat 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaagc 1080

aacatcggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc ctccaatatt ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgaacaata atgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcc aacggtggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca acaacaacgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gaacaataat 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac 2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 294
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 294

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Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15
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Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
    210                 215                 220

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225                 230                 235                 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415
```

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```
Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
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<210> SEQ ID NO 295
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 295

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac 60

aaggatgacg atgacaagat ggccccccaag aagaagagga aggtgggcat tcaccgcggg 120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag 180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact 240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtcg aacattgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcaa gcaacatcgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgaacatt 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccaacaaca acggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgtcaca tgacggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc 1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaaataa taacggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcaaacgga 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

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gttgtagcga ttgcgtcgca tgacggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccaac 2100

aacaacggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgcta ataataacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 296
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 296

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1 5 10 15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
20 25 30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
35 40 45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
50 55 60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65 70 75 80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
85 90 95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
100 105 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
115 120 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
130 135 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
165 170 175

Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
180 185 190

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
195 200 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
210 215 220

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
225 230 235 240

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
245 250 255

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

```
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
    290                 295                 300

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn
                485                 490                 495

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
            660                 665                 670
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Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Asn Asn Asn
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 297
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 297

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gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240

catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa     300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt     360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg     420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta     480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg     540

accccagacc aggtagtcgc aatcgcgaac aataatgggg gaaagcaagc cctggaaacc     600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg     660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca     720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac     780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac     840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg     900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag     960

gtagtcgcaa tcgcgtcgaa cattgggggа aagcaagccc tggaaaccgt gcaaaggttg    1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcaaat    1080

aataacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa    1140
```

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gcccacgggc tgactcccga tcaagttgta gcgattgcgt cgaacattgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc cagccatgat ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcgaaca ttgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa catcggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgaat aacaatggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcgaacatt 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcaagcaaca tcggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgtcgca tgacggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgcctcc 2100

aatattggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt ctaatggggg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 298
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 298

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Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110
```

-continued

```
His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

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

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510
```

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```
Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
    530                 535                 540

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765

Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805


<210> SEQ ID NO 299
<211> LENGTH: 2424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 299

gctagcacca tggactacaa agaccatgac ggtgattata aagatcatga catcgattac      60

aaggatgacg atgacaagat ggcccccaag aagaagagga aggtgggcat tcaccgcggg     120

gtacctatgg tggacttgag gacactcggt tattcgcaac agcaacagga gaaaatcaag     180

cctaaggtca ggagcaccgt cgcgcaacac cacgaggcgc ttgtggggca tggcttcact     240
```

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catgcgcata ttgtcgcgct ttcacagcac cctgcggcgc ttgggacggt ggctgtcaaa 300

taccaagata tgattgcggc cctgcccgaa gccacgcacg aggcaattgt aggggtcggt 360

aaacagtggt cgggagcgcg agcacttgag gcgctgctga ctgtggcggg tgagcttagg 420

gggcctccgc tccagctcga caccgggcag ctgctgaaga tcgcgaagag agggggagta 480

acagcggtag aggcagtgca cgcctggcgc aatgcgctca ccggggcccc cttgaacctg 540

accccagacc aggtagtcgc aatcgcgtca catgacgggg gaaagcaagc cctggaaacc 600

gtgcaaaggt tgttgccggt cctttgtcaa gaccacggcc ttacaccgga gcaagtcgtg 660

gccattgcat cccacgacgg tggcaaacag gctcttgaga cggttcagag acttctccca 720

gttctctgtc aagcccacgg gctgactccc gatcaagttg tagcgattgc gtcgcatgac 780

ggagggaaac aagcattgga gactgtccaa cggctccttc ccgtgttgtg tcaagcccac 840

ggtttgacgc ctgcacaagt ggtcgccatc gccagccatg atggcggtaa gcaggcgctg 900

gaaacagtac agcgcctgct gcctgtactg tgccaggatc atggactgac cccagaccag 960

gtagtcgcaa tcgcgaacaa taatggggga aagcaagccc tggaaaccgt gcaaaggttg 1020

ttgccggtcc tttgtcaaga ccacggcctt acaccggagc aagtcgtggc cattgcatcc 1080

cacgacggtg gcaaacaggc tcttgagacg gttcagagac ttctcccagt tctctgtcaa 1140

gcccacgggc tgactcccga tcaagttgta gcgattgcga ataacaatgg agggaaacaa 1200

gcattggaga ctgtccaacg gctccttccc gtgttgtgtc aagcccacgg tttgacgcct 1260

gcacaagtgg tcgccatcgc caacaacaac ggcggtaagc aggcgctgga aacagtacag 1320

cgcctgctgc ctgtactgtg ccaggatcat ggactgaccc cagaccaggt agtcgcaatc 1380

gcgtcacatg acgggggaaa gcaagccctg gaaaccgtgc aaaggttgtt gccggtcctt 1440

tgtcaagacc acggccttac accggagcaa gtcgtggcca ttgcaagcaa tgggggtggc 1500

aaacaggctc ttgagacggt tcagagactt ctcccagttc tctgtcaagc ccacgggctg 1560

actcccgatc aagttgtagc gattgcgtcg catgacggag ggaaacaagc attggagact 1620

gtccaacggc tccttcccgt gttgtgtcaa gcccacggtt tgacgcctgc acaagtggtc 1680

gccatcgcca gccatgatgg cggtaagcag gcgctggaaa cagtacagcg cctgctgcct 1740

gtactgtgcc aggatcatgg actgacccca gaccaggtag tcgcaatcgc gtcacatgac 1800

gggggaaagc aagccctgga aaccgtgcaa aggttgttgc cggtcctttg tcaagaccac 1860

ggccttacac cggagcaagt cgtggccatt gcatcccacg acggtggcaa acaggctctt 1920

gagacggttc agagacttct cccagttctc tgtcaagccc acgggctgac tcccgatcaa 1980

gttgtagcga ttgcgaataa caatggaggg aaacaagcat tggagactgt ccaacggctc 2040

cttcccgtgt tgtgtcaagc ccacggtttg acgcctgcac aagtggtcgc catcgccagc 2100

catgatggcg gtaagcaggc gctggaaaca gtacagcgcc tgctgcctgt actgtgccag 2160

gatcatggac tgacacccga acaggtggtc gccattgctt cccacgacgg aggacggcca 2220

gccttggagt ccatcgtagc ccaattgtcc aggcccgatc ccgcgttggc tgcgttaacg 2280

aatgaccatc tggtggcgtt ggcatgtctt ggtggacgac ccgcgctcga tgcagtcaaa 2340

aagggtctgc ctcatgctcc cgcattgatc aaaagaacca accggcggat tcccgagaga 2400

acttcccatc gagtcgcggg atcc 2424

<210> SEQ ID NO 300

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```
<211> LENGTH: 808
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 300

Ala Ser Thr Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His
1               5                   10                  15

Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys
            20                  25                  30

Arg Lys Val Gly Ile His Arg Gly Val Pro Met Val Asp Leu Arg Thr
        35                  40                  45

Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg
    50                  55                  60

Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr
65                  70                  75                  80

His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr
                85                  90                  95

Val Ala Val Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr
            100                 105                 110

His Glu Ala Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala
        115                 120                 125

Leu Glu Ala Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu
    130                 135                 140

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

Thr Ala Val Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala
                165                 170                 175

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
        195                 200                 205

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
    210                 215                 220

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

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
                245                 250                 255

Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
            260                 265                 270

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
        275                 280                 285

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
305                 310                 315                 320

Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
                325                 330                 335

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
            340                 345                 350

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
```

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```
        355                 360                 365

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
    370                 375                 380

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
385                 390                 395                 400

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
                405                 410                 415

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly
            420                 425                 430

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
        435                 440                 445

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
    450                 455                 460

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
465                 470                 475                 480

Cys Gln Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser
                485                 490                 495

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
            500                 505                 510

Val Leu Cys Gln Ala His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
        515                 520                 525

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

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Ala Gln Val Val
545                 550                 555                 560

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
                565                 570                 575

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
            580                 585                 590

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
        595                 600                 605

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
    610                 615                 620

Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
625                 630                 635                 640

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu
                645                 650                 655

Thr Pro Asp Gln Val Val Ala Ile Ala Asn Asn Asn Gly Gly Lys Gln
            660                 665                 670

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
        675                 680                 685

Gly Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser His Asp Gly Gly
    690                 695                 700

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
705                 710                 715                 720

Asp His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp
                725                 730                 735

Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro
            740                 745                 750

Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala
        755                 760                 765
```

-continued

```
Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro
    770                 775                 780

His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg
785                 790                 795                 800

Thr Ser His Arg Val Ala Gly Ser
                805
```

<210> SEQ ID NO 301
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 301

```
ttcccagact cagtgggaag agctccctca ccatgagtag cgctatgttg gtgacttgcc     60

tcccggaccc cagcagcagc ttccgtga                                        88
```

<210> SEQ ID NO 302
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 302

```
ttcccagact cagtgggaag agctccctca ccatgagtag cgctatgttg cctcccggac     60

cccagcagca gcttccgtga                                                 80
```

<210> SEQ ID NO 303
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 303

```
ttcccagact cagtgggaag agctccctca cccggacccc agcagcagct tccgtga        57
```

<210> SEQ ID NO 304
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

```
ggcgtgggag agtggatttc cgaagctgac agatgggtat tctttgacgg ggggtagggg     60

cggaacctga gaggcgtaag gcgttgtg                                        88
```

<210> SEQ ID NO 305
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

```
ggcgtgggag agtggatttc cgaagctgac agatgggtag gggcggaacc tgagaggcgt     60

aaggcgttgt g                                                          71
```

<210> SEQ ID NO 306
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 306

```
ggcgtgggag agtggatttc cgaagctgac agaggggcgg aacctgagag gcgtaaggcg      60

ttgtg                                                                  65


<210> SEQ ID NO 307
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 307

ggcgtgggag agtggatttc cgaagctgac agatggaacc tgagaggcgt aaggcgttgt      60

g                                                                      61


<210> SEQ ID NO 308
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 308

ggcgtgggag agtggatttc cgaagctgac agatggggta aggcgttgtg                 50


<210> SEQ ID NO 309
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 309

ggcgtgggag agtggatttc cgaagctgac agatgggtaa ggcgttgtg                  49


<210> SEQ ID NO 310
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 310

agtggatttc cgaagctgac agatgtggaa gaagaggctg gtcatgaggt caggagttcc      60


<210> SEQ ID NO 311
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 311

cgctcaggag gccttcaccc tctgctctgg gtaaaggaac tggaatatgc cttgaggggg      60


<210> SEQ ID NO 312
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 312

cctgagctgt ggtttggagg agccgtgtgt tggaagaaga tggcagatcc aggaatgatg      60

agtctttttg gcgaggatgg gaatattt                                         88


<210> SEQ ID NO 313
<211> LENGTH: 79
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313
```

-continued

cctgagctgt ggtttggagg agccgtgtgt tggaagaaga tcagaatgat gagtcttttt 60

ggcgaggatg ggaatattt 79

<210> SEQ ID NO 314
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 314

cctgagctgt ggtttggagg agccgtgtgt tggaagaaga tggaatgatg agtctttttg 60

gcgaggatgg gaatattt 78

<210> SEQ ID NO 315
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 315

cctgagctgt ggtttggagg agccgtgtgt tggaagaaga tggcgaggat gggaatattt 60

<210> SEQ ID NO 316
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 316

taaagaaata tggaatgaca taaaatccag taaatcctat g 41

<210> SEQ ID NO 317
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 317

gaggggggg aagatggcgg acgtgcttag cgtcctgcga cagtacaaca tccagaagaa 60

ggagattgtg gtgaagggag acgaagtg 88

<210> SEQ ID NO 318
<211> LENGTH: 81
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 318

gaggggggg aagatggcgg acgtgcttag cgtcctgcga cagtacagaa gaaggagatt 60

gtggtgaagg gagacgaagt g 81

<210> SEQ ID NO 319
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 319

gaggggggg aagatggcgg acgtgcttag cgtcctgcga cagtacaacg aaggagattg 60

tggtgaaggg agacgaagtg 80

<210> SEQ ID NO 320
<211> LENGTH: 80
<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 320

gagggggggg aagatggcgg acgtgcttag cgtcctgcga catccagaag aaggagattg 60

tggtgaaggg agacgaagtg 80

<210> SEQ ID NO 321
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 321

gagggggggg aagatggcgg acgtgcttag cgtcctgcga cagaagaagg agattgtggt 60

gaagggagac gaagtg 76

<210> SEQ ID NO 322
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

gagggggggg aagatggcgg acgtgcttag cgtcctgcga cagtattgtg gtgaagggag 60

acgaagtg 68

<210> SEQ ID NO 323
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

gagggggggg aagatggcgg acgtgcttag cgtcctgcga cagttgtggt gaagggagac 60

gaagtg 66

<210> SEQ ID NO 324
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

gagggggggg aagatggcgg acgtgcttag cgtcctgcga cagtacaaca acatccagaa 60

gaaggagatt gtggtgaagg gagacgaa 88

<210> SEQ ID NO 325
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

agggcgaggc gacaagagaa gaaggaggca ggattgtggt gaagggagac gaagtg 56

<210> SEQ ID NO 326
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

ttagtatttt gaagttaata tcacaatgag ttcaggctta tggagccaag aaaaagtcac 60

-continued

```
ttcaccctac tgggaagagc ggattttt                                        88


<210> SEQ ID NO 327
<211> LENGTH: 79
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 327

ttagtatttt gaagttaata tcacaatgag ttcaggctta tggaaagtca cttcacccta     60

ctgggaagag cggatttt                                                   79


<210> SEQ ID NO 328
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 328

ttagtatttt gaagttaata tcacaagtca cttcacccta ctgggaagag cggatttt      59


<210> SEQ ID NO 329
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 329

ttagtatttt gaagttaata tcaccctact gggaagagcg gatttt                    47


<210> SEQ ID NO 330
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

ttagtatttt gaagttccct actgggaaga gcggatttt                            40


<210> SEQ ID NO 331
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

taagtcactt caccctactg ggaagagcgg attttt                               36


<210> SEQ ID NO 332
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

ttagtatttc cctactggga agagcggatt ttt                                  33


<210> SEQ ID NO 333
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 333

ttagtatttt gaagttgaag agcggatttt t                                    31


<210> SEQ ID NO 334
```

-continued

<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 334

ttagtatttt gaacggattt tt 22

<210> SEQ ID NO 335
<211> LENGTH: 4
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

ttag 4

<210> SEQ ID NO 336
<211> LENGTH: 116
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

taatatcaca atgagttctc aggggcacac caggccccag gggaacacca ggccctgggt 60

aagcatgcag tcccaggtgg acatcaggtg ccaggaggaa aagtcacttc acccta 116

<210> SEQ ID NO 337
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 337

tccacacagc ctgtggcaca gacgtggagg gccactgagc cccgctaccc gccccacagc 60

ctttcctacc cagtgcagat cgcccgga 88

<210> SEQ ID NO 338
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

tccacacagc ctgtggcaca gacgtggagg gccactgagc cccgctaccg ccccacagcc 60

tttcctaccc agtgcagatc gcccgga 87

<210> SEQ ID NO 339
<211> LENGTH: 81
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

tccacacagc ctgtggcaca gacgtggagg gccactgagc cccgccccac agcctttcct 60

acccagtgca gatcgcccgg a 81

<210> SEQ ID NO 340
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

tccacacagc ctgtggcaca gacgtggagg gccactgagc cccacagcct ttcctaccca 60 gtgcagatcg cccgga 76

<210> SEQ ID NO 341
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 341

tccacacaga tcgcccgga 19

<210> SEQ ID NO 342
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 342

cccccaccac ctttcctacc cagtgcagat cgcccgga 38

<210> SEQ ID NO 343
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

gcttattgcg gcctttctcc tgggagccag gct 33

<210> SEQ ID NO 344
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

tccacacagc ctgtggcaca gacgtggagg gccactgagc cccgctacca cccgccccac 60

agcctttcct acccagtgca gatcgccc 88

<210> SEQ ID NO 345
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

tttctcttac aggcaaatgt tctgaaaaag actctgcatg ggaatggcct gccttacgat 60

gacagaaatg gagggaacat ccacctct 88

<210> SEQ ID NO 346
<211> LENGTH: 84
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 346

tttctcttac aggcaaatgt tctgaaaaag actctgcatg gggcctgcct tacgatgaca 60

gaaatggagg gaacatccac ctct 84

<210> SEQ ID NO 347
<211> LENGTH: 83
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 347

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tttctcttac aggcaaatgt tctgaaaaag actctgcatg ggcctgcctt acgatgacag 60

aaatggaggg aacatccacc tct 83

<210> SEQ ID NO 348
<211> LENGTH: 82
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 348

tttctcttac aggcaaatgt tctgaaaaag actctgcatg ggaatggtta cgatgacaga 60

aatggaggga acatccacct ct 82

<210> SEQ ID NO 349
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

tttctcttac aggcaaatgt tctgaaaaag actctgcagc ctgccttacg atgacagaaa 60

tggagggaac atccacctct 80

<210> SEQ ID NO 350
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

tttctcttac aggcaaatgt tctgaaaaag actctgcctt acgatgacag aaatggaggg 60

aacatccacc tct 73

<210> SEQ ID NO 351
<211> LENGTH: 64
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

tttctcttac aggcaaatgt tctgaaaaag actctgcatg ggaatggagg gaacatccac 60

ctct 64

<210> SEQ ID NO 352
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

tttctcttac aggcaaatgt tctgaaaaag acgatgacag aaatggaggg aacatccacc 60

tct 63

<210> SEQ ID NO 353
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 353

tttctcttac aggcaaatgt tctgaaaaag actctgcaga aatggaggga acatccacct 60

ct 62

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<210> SEQ ID NO 354
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

tttctcttac aggcatggag ggaacatcca cctct 35

<210> SEQ ID NO 355
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

tacgatgaca gaaatggagg gaacatccac ctct 34

<210> SEQ ID NO 356
<211> LENGTH: 84
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 356

tttctcttac aggcaaatgt tctgaaaaag actctgcatg gagtaagtct tacgatgaca 60

gaaatggagg gaacatccac ctct 84

<210> SEQ ID NO 357
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

cggaggtttg ctgcaaacag agaaatttcg atgacagaaa tggagggaac atccacctct 60

<210> SEQ ID NO 358
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 358

cgggaggcga gccgatgccg agctgctcca cgtccaccat gccgggcatg atctgcaaga 60

acccagacct cgagtttgac tcgctaca 88

<210> SEQ ID NO 359
<211> LENGTH: 82
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

cgggaggcga gccgatgccg agctgctcca cgtcctcccc catgatctgc aggaacccag 60

acctcgagtt tgactcgcta ca 82

<210> SEQ ID NO 360
<211> LENGTH: 80
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

cgggaggcga gccgatgccg agctgctcca cgtccgggca tgatctgcaa gaacccagac 60 ctcgagtttg actcgctaca 80

<210> SEQ ID NO 361
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

cgggaggcga gccgatgccg agctgctcca cgtccaccat atctgcaaga acccagacct 60

cgagtttgac tcgctaca 78

<210> SEQ ID NO 362
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 362

cgggaggcga gccgatgccg agctgctcca cgtccaccat gctgcaagaa cccagacctc 60

gagtttgact cgctaca 77

<210> SEQ ID NO 363
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

cgggaggcga gccgatgccg agctgctcca cgtccatgat ctgcaagaac ccagacctcg 60

agtttgactc gctaca 76

<210> SEQ ID NO 364
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

cgggaggcga gccgatgccg agctgctcca cgtccaccaa gaacccagac ctcgagtttg 60

actcgctaca 70

<210> SEQ ID NO 365
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

cgggaggcga gccgatgccg agctgctcat gatctgcaag aacccagacc tcgagtttga 60

ctcgctaca 69

<210> SEQ ID NO 366
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

aaggaagcac ccccggtctt aaagacctcg agtttgactc gctaca 46

<210> SEQ ID NO 367
<211> LENGTH: 60
<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 367

agtgttggag gtcggcgccg gcccccgggc atgatctgca agaacccaga cctcgagttt      60


<210> SEQ ID NO 368
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

aaggaagcac ccccggtatt aaacgaagat gact                                  34


<210> SEQ ID NO 369
<211> LENGTH: 222
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

gaggcgagcc gatgcccgtg atctgggtca cggctgctcc agcttggagg agaggcggct      60

ctcccggcga ccctcctcgc gcgggcgccc ctgccattcc cgggaacagg ggctcagccc     120

cctttgttag tgctcgtatg tcttggcctg gggagcattt tggaggcagt gctaggggca     180

gagaggtcct gtttccccca agtcttgatc tgcaagaacc ca                        222


<210> SEQ ID NO 370
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

tgcacgtcgg ccccagccct gaggagccgg accgatgtgg aaactgctgc ccgccgcggg      60

cccggcagga ggtaagggca gaagggaa                                         88


<210> SEQ ID NO 371
<211> LENGTH: 83
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

tgcacgtcgg ccccagccct gaggagccgg accgatgtgg gctgcccgcc gcgggcccgg      60

caggaggtaa gggcagaagg gaa                                              83


<210> SEQ ID NO 372
<211> LENGTH: 81
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 372

tgcacgtcgg ccccagccct gaggagccgg accgatgtgc tgcccgccgc gggcccggca      60

ggaggtaagg gcagaaggga a                                                81


<210> SEQ ID NO 373
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 373
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tgcacgtcgg ccccagccct gaggagccgg accgatgtgg aaactggccc ggcaggaggt 60

aagggcagaa gggaa 75

<210> SEQ ID NO 374
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

tgcacgtcgg ccccagccct gaggagccgg accgatgtgg actcccggca ggaggtaagg 60

gcagaaggga a 71

<210> SEQ ID NO 375
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

tgcacgtcgg ccccagccct gaggagccgg accgatgtgg acccggcagg aggtaagggc 60

agaagggaa 69

<210> SEQ ID NO 376
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

tgcacgtcgg ccccagccct gaggagccgg accgatgcag gaggtaaggg cagaagggaa 60

<210> SEQ ID NO 377
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

tgcacgtcgg ccccagccct gaggagccgg accgatgtgg aaagtaaggg cagaagggaa 60

<210> SEQ ID NO 378
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

tgcacgtcgg ccccagccct gaggagccgg accggcagga ggtaagggca gaagggaa 58

<210> SEQ ID NO 379
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

tgcacgtcgg ccccagccct gaggagccgg aaggaggtaa gggcagaagg gaa 53

<210> SEQ ID NO 380
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 380

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tgcacgtcgg ccccgcgcgg gcccggcagg aggtaagggc agaagggaa 49

<210> SEQ ID NO 381
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

tgcacgtcgg ccccagccgg caggaggtaa gggcagaagg gaa 43

<210> SEQ ID NO 382
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

gctcccggga gcgcgcacgt cccggagccc atgcctgcgg gtgattcctg cg 52

<210> SEQ ID NO 383
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

tcgcgaagtg gaatttgccc agacaagcaa catggctcgg aaacgcgcgg ccggcgggga 60

gccgcgggga cgcgaactgc gcagccag 88

<210> SEQ ID NO 384
<211> LENGTH: 86
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

tcgcgaagtg gaatttgccc agacaagcaa catggctcgg aggaacggcc ggcggggagc 60

cgcggggacg cgaactgcgc agccag 86

<210> SEQ ID NO 385
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

tcgcgaagtg gaatttgccc agacaagcaa catggctcgg aaaggggagc cgcggggacg 60

cgaactgcgc agccag 76

<210> SEQ ID NO 386
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

tcgcgaagtg gaatttgccc agacaagcaa catggccggc ggggagccgc ggggacgcga 60

actgcgcagc cag 73

<210> SEQ ID NO 387
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 387

tcgcgaagtg gaatttgccc agacaagcaa catggctcgg ggagccgcgg ggacgcgaac     60

tgcgcagcca g                                                          71


<210> SEQ ID NO 388
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

tcgcgaagtg gaatttgccc agacaagcaa catggcgggg agccgcgggg acgcgaactg     60

cgcagccag                                                             69


<210> SEQ ID NO 389
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 389

tcgcgaagtg gaatttgccc agacaagcaa catgttgcga actgcgcagc cag            53


<210> SEQ ID NO 390
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

tcgcgaagtg gaatttgccc agacaagcaa catggctcgg cgcagccag                 49


<210> SEQ ID NO 391
<211> LENGTH: 12
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

tcgcgcagcc ag                                                         12


<210> SEQ ID NO 392
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

tcgcgaagtg gaatccaagg ccaagagcaa g                                    31


<210> SEQ ID NO 393
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 393

gtcgaccccg ctgcacagtc cggccggcgc catgaagtga gaagggggct gggggtcgcg     60

ctcgctagcg ggcgcggggg gtcttgaa                                        88


<210> SEQ ID NO 394
<211> LENGTH: 81
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 394

gtcgaccccg ctgcacagtc cggccggcgc catgaagtgg gctgggggtc gcgctcgcta 60

gcgggcgcgg ggggtcttga a 81

<210> SEQ ID NO 395
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

gtcgaccccg ctgcacagtc cggccggcgc catgaagctg ggggtcgcgc tcgctagcgg 60

gcgcgggggg tcttgaa 77

<210> SEQ ID NO 396
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 396

gtcgaccccg ctgcacagtc cggccggcgc tcgctagcgg gcgcgggggg tcttgaa 57

<210> SEQ ID NO 397
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 397

gtcgaccccg ctgcacagtc cggccggcgc catgaagtgg ggtcttgaa 49

<210> SEQ ID NO 398
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 398

ggcctctcgc tgaatattca tgatggggtc atcggtgggc gcg 43

<210> SEQ ID NO 399
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 399

gtcgaccccg ctgcacagtc cggccggcgc catgaagggt gaaggggtgg gac 53

<210> SEQ ID NO 400
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 400

gtcgaccccg ctgcacagtc cggccggcgc catgaagtgc gtccggggtg ggacgggggc 60

agccg 65

<210> SEQ ID NO 401
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 401

gtcgaccccg ctgcacagtc cggccggcgc catgaagtgg cagccgcagg gagcagcagt 60

<210> SEQ ID NO 402
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

atggtctcgt aatataggtg gagcgagccc tcgagggggg tcttgaagat g 51

<210> SEQ ID NO 403
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

gtcgaccccg ctgctgagga cctgagggtt acc 33

<210> SEQ ID NO 404
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

ggcctctcgc tgaatattca gctcctgagg acctgagggt ta 42

<210> SEQ ID NO 405
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

gtcgaccccg ctgcacagtc cggcccgtca cccttctctg ggct 44

<210> SEQ ID NO 406
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 406

gtcgaccccg ctgcacagtc cggccgctcg acgaccgggc 40

<210> SEQ ID NO 407
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

gtcgaccccg ctgcacagtc cggccggcga ccgggcactg tggagg 46

<210> SEQ ID NO 408
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

gtcgaccccg ctgcacagtc cggccgggca ctgtggagg 39

<210> SEQ ID NO 409

<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 409

gtcgacccag cagcccctg 19

<210> SEQ ID NO 410
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 410

gtcgaccccc ctgccgcca 19

<210> SEQ ID NO 411
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 411

ggcctctcgc tgaatattca tgagccgcca ggctcaacgt gga 43

<210> SEQ ID NO 412
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 412

tatgtacgcc tccctggg 18

<210> SEQ ID NO 413
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 413

tacagaagcg ggcaaagg 18

<210> SEQ ID NO 414
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 414

tccgaagctg acagatgg 18

<210> SEQ ID NO 415
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 415

tcaggttccg cccctacc 18

<210> SEQ ID NO 416
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

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ttagacttag gtaagtaa                                                    18


<210> SEQ ID NO 417
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417

tagtttgtag ttctcccc                                                    18


<210> SEQ ID NO 418
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

tccggccggc gccatga                                                     17


<210> SEQ ID NO 419
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

tagcgagcgc gacccc                                                      16


<210> SEQ ID NO 420
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

taggcgccaa ggccatgt                                                    18


<210> SEQ ID NO 421
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

tggcccgagg cggagttc                                                    18


<210> SEQ ID NO 422
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

tgaagggaca tcaccttt                                                    18


<210> SEQ ID NO 423
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

tctactgaat cttgagc                                                     17


<210> SEQ ID NO 424
<211> LENGTH: 16
<212> TYPE: DNA
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

tcggccacca tgtccc 16

<210> SEQ ID NO 425
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

tccaggcagc tggagccc 18

<210> SEQ ID NO 426
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

tctgaaaaag actctgca 18

<210> SEQ ID NO 427
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

tccatttctg tcatcgta 18

<210> SEQ ID NO 428
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

tgaaaatgac tgaatata 18

<210> SEQ ID NO 429
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429

ttgcctacgc caccagc 17

<210> SEQ ID NO 430
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430

tgcttagacg ctggattt 18

<210> SEQ ID NO 431
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 431

ttcggtgctt acctggtt 18

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<210> SEQ ID NO 432
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

tcccagacat gacagcc                                                    17


<210> SEQ ID NO 433
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 433

tccttttgtt tctgctaa                                                   18


<210> SEQ ID NO 434
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 434

ttgccgtccc aagcaatg                                                   18


<210> SEQ ID NO 435
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 435

tgttcaatat cgtccggg                                                   18


<210> SEQ ID NO 436
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 436

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<210> SEQ ID NO 437
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-continued

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<400> SEQUENCE: 439

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1. A process comprising:

(a) providing a first nucleic acid comprising a sequence encoding a first set comprising one or more transcription activator-like effector (TALE) repeat domains and/or one or more portions of one or more TALE repeat domains;

(b) contacting the first nucleic acid with a first enzyme, wherein the first enzyme creates a first ligatable end;

(c) providing a second nucleic acid comprising a sequence encoding a second set comprising one or more TALE repeat domains and/or one or more portions of one or more TALE repeat domains;

(d) contacting the second nucleic acid with a second enzyme, wherein the second enzyme creates a second ligatable end, and wherein the first and second ligatable ends are compatible; and

(e) ligating the first and second nucleic acids through the first and second ligatable ends to produce a first ligated nucleic acid,

wherein the first ligated nucleic acid is linked to a solid support, and

wherein the first ligated nucleic acid encodes a polypeptide comprising said first and second sets.

2. The process of claim **1**, wherein the first set is N-terminal to the second set in the polypeptide.

3. The process of claim **1**, wherein the second set is N-terminal to the first set in the polypeptide.

4. The process of claim **1**, wherein the first and second enzymes are a first and second restriction endonuclease, wherein the first restriction endonuclease cleaves at a site within the first nucleic acid and creates a first cut end, and the second restriction endonuclease cleaves at a site within the second nucleic acid and creates a second cut end, and wherein the first and second ligatable ends are the first and second cut ends.

5. The process of claim **4**, wherein the first ligated nucleic acid does not comprise a restriction site recognized by the first restriction endonuclease.

6. The process of claim **1**, further comprising:

(f) contacting the first ligated nucleic acid with a third enzyme, wherein the third enzyme creates a third ligatable end;

(g) providing a third nucleic acid comprising a sequence encoding a third set comprising one or more TALE repeat domains and/or one or more portions of one or more TALE repeat domains;

(h) contacting the third nucleic acid with a fourth enzyme, wherein the fourth enzyme creates a fourth ligatable end, and wherein the third and fourth ligatable ends are compatible; and

(i) ligating the first ligated and third nucleic acids through the third and fourth ligatable ends to produce a second ligated nucleic acid linked to the solid support,

wherein the second ligated nucleic acid encodes a polypeptide comprising said first, second, and third sets.

7. The process of claim **6**, wherein the third and fourth enzymes are a third and fourth restriction endonuclease, wherein the third restriction endonuclease cleaves at a site within the first ligated nucleic acid and creates a third cut end, and the fourth restriction endonuclease cleaves at a site within the third nucleic acid and creates a fourth cut end, and wherein the third and fourth ligatable ends are the third and fourth cut ends.

8. The process of claim **7**, wherein the ligated nucleic acid does not comprise a restriction site recognized by the first endonuclease, and wherein the first and third restriction endonucleases are the same.

9. The process of claim **7**, wherein the second and fourth restriction endonucleases are the same.

10. The process of claim **6**, further comprising:

(j) contacting the second ligated nucleic acid with a fifth enzyme, wherein the fifth enzyme creates a fifth ligatable end;

(k) providing a fourth nucleic acid comprising a sequence encoding a fourth set comprising one or more TALE repeat domains and/or one or more portions of one or more TALE repeat domains;

(l) contacting the fourth nucleic acid with a sixth enzyme, wherein the sixth enzyme creates a sixth ligatable end, and wherein the fifth and sixth ligatable ends are compatible; and

(m) ligating the second ligated and fourth nucleic acids through the fifth and sixth ligatable ends to produce a third ligated nucleic acid linked to the solid support, wherein the third ligated nucleic acid encodes a polypeptide comprising said first, second, third, and fourth sets.

11. The process of claim **10**, wherein the fifth and sixth enzymes are a fifth and sixth restriction endonuclease, wherein the fifth restriction endonuclease cleaves at a site within the second ligated nucleic acid and creates a fifth cut end, and the sixth restriction endonuclease cleaves at a site within the fourth nucleic acid and creates a sixth cut end, and wherein the fifth and sixth ligatable ends are the fifth and sixth cut ends.

12. The process of claim **11**, wherein the second ligated nucleic acid does not comprise a restriction site recognized by the first endonuclease, and wherein the first, third, and fifth restriction endonucleases are the same.

13. The process of claim **11**, wherein the second, fourth, and sixth restriction endonucleases are the same.

14. The process of claim **1**, wherein the second set comprises one to four TALE repeat domains.

15. The process of claim **1**, wherein the first and second ligatable ends each comprise an overhang of 1-10 nucleotides.

16. The process of claim **1**, wherein the first enzyme is a type IIS restriction endonuclease.

17. The process of claim **1**, further comprising unlinking the first ligated nucleic acid from the solid support and inserting the first ligated nucleic acid into a vector.

18. The process of claim **6**, further comprising unlinking the second ligated nucleic acid from the solid support and inserting the second ligated nucleic acid into a vector.

19. The process of claim **10**, further comprising unlinking the third ligated nucleic acid from the solid support and inserting the third ligated nucleic acid into a vector.

20. The process of claim **17**, wherein the vector is an expression vector.

21. The process of claim **20**, wherein the expression vector includes a sequence encoding an effector domain, and wherein the first, second, or third ligated nucleic acid is inserted into the vector such that the vector comprises a sequence encoding a fusion protein of the polypeptide and the effector domain.

22. The process of claim **21**, wherein the effector domain is a nuclease domain.

23. The process of claim **20**, further comprising inserting the expression vector into a cell.

24. The process of claim **23**, further comprising expressing the polypeptide or fusion protein.

25. The process of claim **24**, further comprising purifying the polypeptide or fusion protein.

26.-**33**. (canceled)

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