

Sequenzprotokoll_50420K_ST25
SEQUENCE LISTING

<110> Universität Duisburg-Essen
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Tennstädt, Annette

<120> Method for analysing a biological sample

<130> 50 420 K

<150> EP08006965.1
<151> 2008-04-08

<150> US61/043,204
<151> 2008-04-08

<160> 36

<170> PatentIn version 3.5

<210> 1
<211> 2100
<212> DNA
<213> Homo sapiens

<220>
<221> 3'UTR
<222> (1)..(1048)
<223> 3'UTR of the HtrA1 gene

<220>
<221> protein_bind
<222> (264)..(380)
<223> potential MBD2 binding site

<220>
<221> site
<222> (287)..(665)
<223> overall region of the HtrA1 promotor analysed for the methylation pattern/status

<220>
<221> site
<222> (461)..(1662)
<223> at least a portion of the CpG-island

<220>
<221> site
<222> (1049)..(2100)
<223> at least part of the CDS of HtrA1

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cctcagccct cctgatgact ctcggactcg catctgtccc aacggatgca ccaaagattc 120
tccagtggga aatcaaattt ttgataacaa gtgttttgaa ataatcacgc acttggtgaa 180
aaatcaaaag aggggaaaac ccctttcca tctgagaccg ctccaccctc gccagttacg 240
agctgccgag ccgcttccta ggctctctgc gaatacggac acgcatgcca cccacaacaa 300
ctttttaaaa gaatcagacg tgtgaaggat tctattcgaa ttacttctgc tctctgcttt 360
tatcacttca ctgtgggtct gggcgcgggc tttctgccag ctccgcggac gctgccttcg 420

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gctcgtcacc	gctgcgaggc	caatgggctg	ggccgcgcgg	ccgcgcgcac	tcgcaccgcg	960
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ctttgatcac	gggaccgctc	agtgaaaact	gtatgtaact	cttttgaaa	ggaacagtgt	2040
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<210> 2
 <211> 379
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 <213> Homo sapiens

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ggacgctgcc ttcgtccggc cgcagaggcc ccgcggtcag ggtcccgcgt gcgggggtacc 180
 gggggcagaa ccagcgcgtg accgggggtcc gcggtgccgc aacgccccgg gtctgcgcag 240
 agggccctgc agtcctgcc cggcccagtc cgagcttccc gggcgggccc ccagtccggc 300
 gatttgcagg aactttcccc ggcgtccca cgcgaagccg ccgcagggcc cccttgcaaa 360
 gttccattag tttgaagga 379

<210> 3
 <211> 383
 <212> DNA
 <213> Homo sapiens

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 tcaccgctgc gaggccaatg ggctgggccc cgcggccgcg cgcactcgca cccgctgccc 300
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 ccgcccgcgc cgccagagtc gcc 383

<210> 4
 <211> 614
 <212> DNA
 <213> Homo sapiens

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 tgcgagccgg cgcgctgccc gccgcagccg gagcactgcg agggcggccg ggcccgggac 180
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 aggctgcacc ggccgccggt catcgtcctg cagcgcggag cctgcggcca aggtactccg 480
 ccgcgctcct gggcagctcc cactctctc catcccagct cggacctgct tctcggggac 540
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 aggcaggtgg gccc 614

<210> 5
 <211> 117
 <212> DNA
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<400> 5
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gaaggattct attcgaatta cttctgctct ctgcttttat cacttcactg tgggtct 117

<210> 6
<211> 107
<212> DNA
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<400> 6
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agcgaatatg tggggcgcgcg agacgggggaa actgagtccc gcgagag 107

<210> 7
<211> 23
<212> DNA
<213> artificial

<220>
<223> Human HtrA1-forward primer

<400> 7
gcaactcaga catggactac atc 23

<210> 8
<211> 24
<212> DNA
<213> artificial

<220>
<223> Human-HtrA1-reverse primer

<400> 8
gtgttaattc caatcacttc accg 24

<210> 9
<211> 21
<212> DNA
<213> artificial

<220>
<223> Human-p21/CDKN1a-forward primer

<400> 9
cctcatcccg tggtctcctt t 21

<210> 10
<211> 20
<212> DNA
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<220>
<223> Human-p21/CDKN1a-reverse primer

<400> 10
gtaccaccca gcggacaagt 20

<210> 11
<211> 22
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<220>
<223> Human-GAPDH-forward primer

<400> 11
gcttgatcatc aatggaaatc cc 22

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<220>
<223> Human-GAPDH-reverse primer

<400> 12
agccttctcc atggtgg 17

<210> 13
<211> 17
<212> DNA
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<220>
<223> Human-RibProtL13a-forward primer

<400> 13
ggtggatcgtc cgctgtg 17

<210> 14
<211> 17
<212> DNA
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<220>
<223> Human-RibProtL13a-reverse primer

<400> 14
ggtccgccag aagatgc 17

<210> 15
<211> 31
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<220>
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<400> 15
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<210> 16
<211> 27
<212> DNA
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<220>
<223> HtrA1 reverse primer

<400> 16
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<210> 17

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<211> 51
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 <220>
 <223> HtrA1 forward SP6 primer

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 <210> 18
 <211> 47
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 <220>
 <223> HtrA1 reverse T7 primer

 <400> 18
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 <210> 19
 <211> 20
 <212> DNA
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 <220>
 <223> PPIA forward primer

 <400> 19
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 <210> 20
 <211> 20
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 <220>
 <223> PPIA reverse primer

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 <211> 21
 <212> DNA
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 <220>
 <223> MBD2 forward primer

 <400> 21
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 <210> 22
 <211> 23
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 <220>
 <223> MBD2 reverse primer

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23

<210> 23
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 <212> DNA
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<220>
 <223> hairpin sequence for shMBD2, sense

<220>
 <221> stem_loop
 <222> (1)..(4)
 <223> restriction site for AgeI in the hairpin sequence for shMBD2

<220>
 <221> stem_loop
 <222> (26)..(31)
 <223> loop in the hairpin sequence for shMBD2

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<210> 24
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 <212> DNA
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<220>
 <223> hairpin sequence for shMBD2, antisense

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 <221> stem_loop
 <222> (1)..(4)
 <223> restriction site for EcoRI in the hairpin sequence for shMBD2, antisense

<220>
 <221> stem_loop
 <222> (31)..(36)
 <223> loop in the hairpin sequence for shMBD2, antisense

<400> 24
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<210> 25
 <211> 58
 <212> DNA
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<220>
 <223> hairpin sequence for shHtrA1, sense

<400> 25
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<210> 26
 <211> 58
 <212> DNA
 <213> artificial

<220>

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<223> hairpin sequence for shHtrA1, antisense

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<223> ChIP_HtrA1_-4373 forward primer

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<210> 28
<211> 21
<212> DNA
<213> artificial

<220>
<223> ChIP_HtrA1_-4373 reverse primer

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<220>
<223> ChIP_HtrA1_-941 bp forward primer

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<210> 30
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<220>
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<210> 31
<211> 19
<212> DNA
<213> artificial

<220>
<223> ChIP_HtrA1_-785 bp forward primer

<400> 31
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<210> 32
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<212> DNA
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<220>
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<400> 32
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<220>
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<210> 34
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<212> DNA
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<220>
<223> ChIP_HtrA1_-413 bp reverse primer

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<210> 35
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<212> DNA
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<220>
<223> ChIP_negative control forward primer

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<210> 36
<211> 20
<212> DNA
<213> artificial

<220>
<223> ChIP_negative control reverse primer

<400> 36
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