

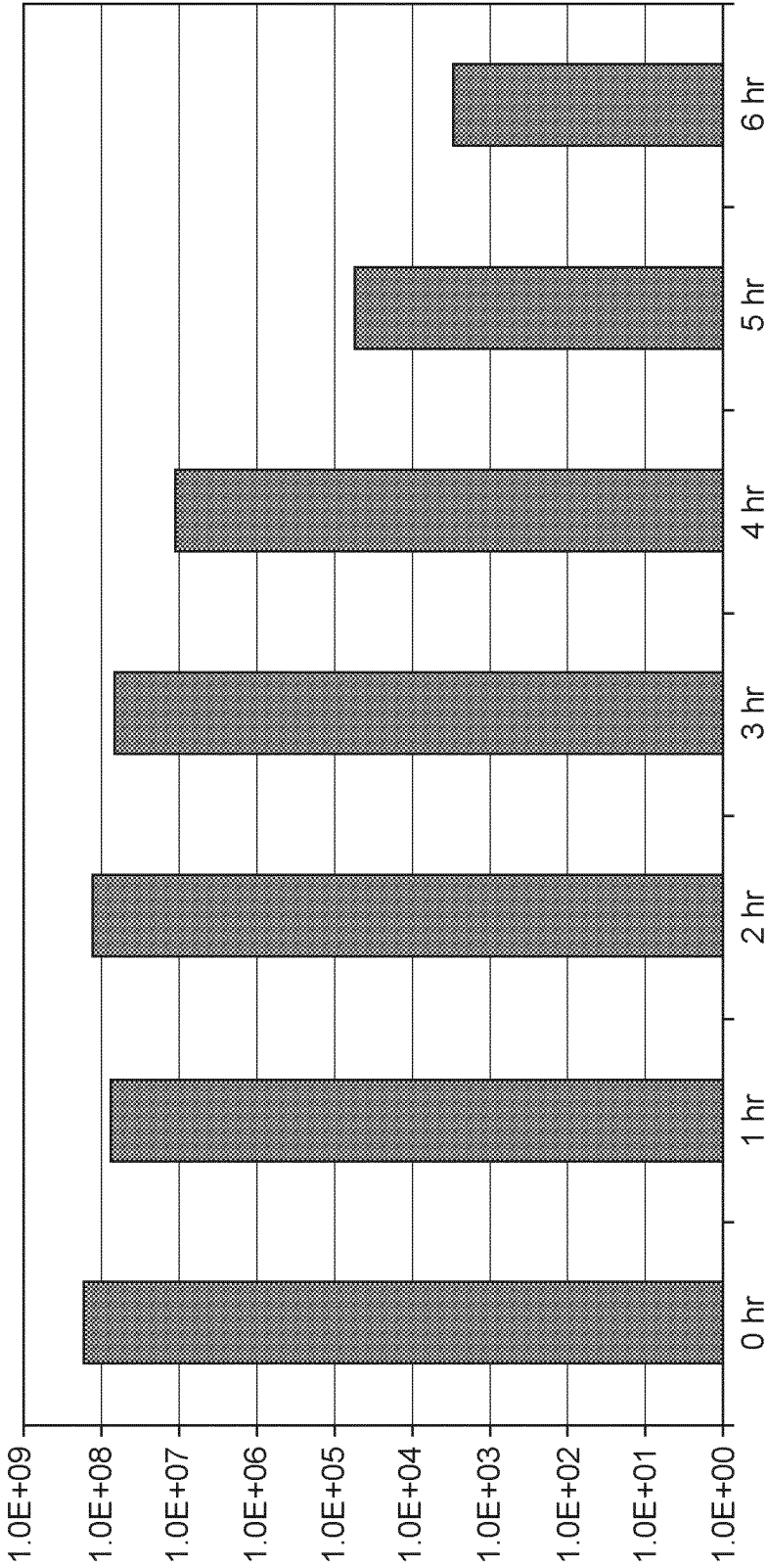


FIG. 1

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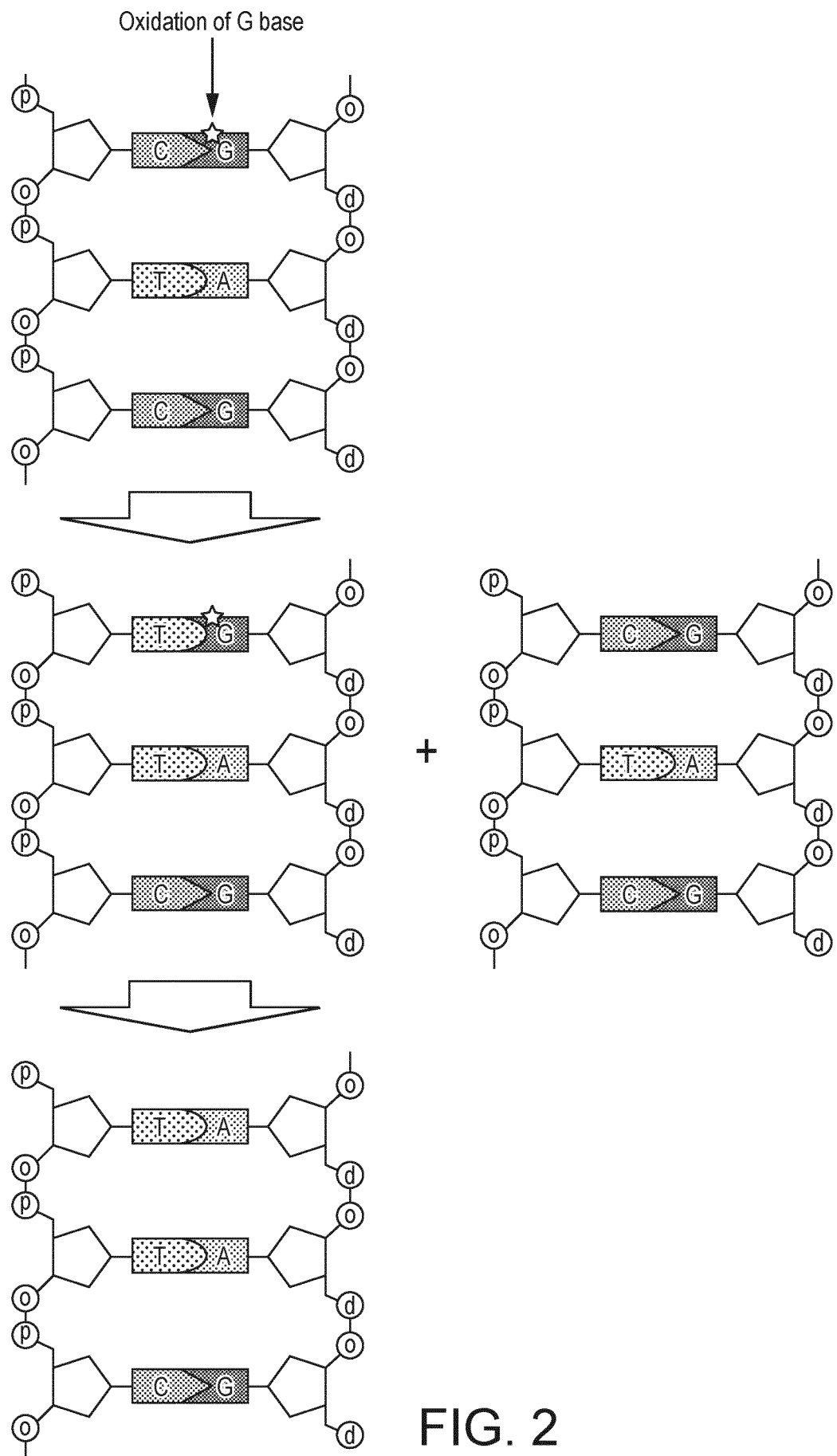


FIG. 2

1 AAAGACGGTC ATACTATTAATTTTGACGGA GGTTTAAATTT ATGACAAAGA TTTTTCGTTA CGTATTCGT AAAGATGAAG AACCTTTCTT
RBS M T K I F A Y A I R K D E E P F

91 AAACGAATGG AAAGATGCAC ACAAGGATAT TGAAGTTGAA TACACTGACA AGCTTTTAGC CCCTGAAACT GCTAAATTAG CTAAGGGTGC
L N E W K D A H K D I E V E Y T D KL L A P E T A K L A K G

181 TGACGGTGT GTTGTTTACC AACAAATAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC TGATGCTGGC GTAACATAATCATTCAG
A D G V V V Y Q Q L D Y T P E T L Q A L A D A G V T K M S L

271 TAACGTTGGT GTTGACAACA TCGACATGGA CAAGGCTAAA GAATTAGGCT TTGAAATCAC TAACGTTTCT GTATACTCTC CTGACGCAAT
R N V G V D N I D M D K A K E L G F E I T N V P V Y S P D A
H CNM I4437, CGT to CAT

361 TGCTGAACAT GCTGCAATTC AAGCTGCTCG CGTACTACGT CAAGATAAGC GTATGGATGA AAAGATGGCT AAGCGCGACT TACGCTGGC
I A E H A A I Q A A R V L R Q D K R M D E K M A K R D L R W

451 ACCTACTATT GGTGCTGAAG TTCGTGACCA AGTTGTTGGT GTTGTAGGTA CTGGTCACAT CGGTCAAGTA TTTATGAAGA TTATGGAAG
A P T I G R E V R D Q V V G V V G T G H I G Q V F M K I M E

541 CTTTGGCGCA AAAGTTATG CTTACGATAT CTTCAAGAAC CCAGAACTTG AAAAGAAGGG TTACTACGTT GACTCACCTG ATGACTTATA
G F G A K V I A Y D I F K N P E L E KK G Y Y V D S L D D L

631 CAAGCAAGCT GATGTAATTT CACTTCACGT TCCAGATGTT CCAGCAAACG TTCACATGAT TAATGATGAA TCAATCGCTA AGATGAAGA
Y K Q A D V I S L H V P D V P A N V H M I N D E S I A K M K

D-LDH signature 3

721 TGGCGTTGTA ATCGTAAACT GTCACGTGG TCCACTTGT GACACTGACG CTGTTATCCG CGGCTTAGAT TCTGGTAAGA TCCTTGGTTT
D G V V I V N C S R G P L V D T D A V I R G L D S G K I F G

811 CGTAATGGAC ACTTACGAAG GTGAAGTTGG TGTATTTAAC GAAGATTGGG AAGGTAAAGA ATTCCAGAT GCTCGTTTAG CTGACTTAAT
F V M D T Y E G E V G V F N E D W E G K E F P D A R L A D L

901 CGATCGTCCA AATGTATTGG TAACTCCACA TACTGCTTTC TACACTACTC ATGCTGTACG TAACATGGTA ACTAAAGCAT TTGACAACAA
I D R P N V L V T P H T A F Y T T H A V R N M V T K A F D N

991 CTTAAAGATG ATCAACGGTG AAAAACCAGA TTCTCCAGTT GCTTTGGACA AGAACCAAGTT CTAAAAATATTATGATA ATCAAAAAAGA
N L K M I N G E K P D S P V A L D K N K F *

FIGURE 3

FIGURE 4A

SEQ ID NO: 6

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1  ATGACAAAGA TTTTGTGCTTA CGCTATTCGT AAAGATGAAG AACCTTTCTT
51  AAACGAATGG AAAGATGCAC ACAAGGATAT TGAAGTTGAA TACACTGACA
101 AGCTTTTAGC CCCTGAAACT GCTAAATTAG CTAAGGGTGC TGACGGTGTT
151 GTTGTTTACC AACAATTAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC
201 TGATGCTGGC GTAAC TAAGA TGTCATTACA TAACGTTGGT GTTGACAACA
251 TCGACATGGA CAAGGCTAAA GAATTAGGCT TTGAAATCAC TAACGTTTCCT
301 GTATACTCTC CTGACGCAAT TGCTGAACAT GCTGCAATTC AAGCTGCTCG
351 CGTACTACGT CAAGATAAGC GTATGGATGA AAAGATGGCT AAGCGCGACT
401 TACGCTGGGC ACCTACTATT GGTCGTGAAG TTCGTGACCA AGTTGTTGGT
451 GTTGTAGGTA CTGGTCACAT CGGTCAAGTA TTTATGAAGA TTATGGAAGG
501 CTTTGGCGCA AAAGTTATTG CTTACGATAT CTTCAAGAAC CCAGAACTTG
551 AAAAGAAGGG TTACTACGTT GACTCACTTG ATGACTTATA CAAGCAAGCT
601 GATGTAATTT CACTTCACGT TCCAGATGTT CCAGCAAACG TTCACATGAT
651 TAATGATGAA TCAATCGCTA AGATGAAAGA TGGCGTTGTA ATCGTAAACT
701 GCTCACGTGG TCCACTTGTT GACACTGACG CTGTTATCCG CGGCTTAGAT
751 TCTGGTAAGA TCTTTGGTTT CGTAATGGAC ACTTACGAAG GTGAAGTTGG
801 TGTATTTAAC GAAGATTGGG AAGGTAAAGA ATTCCCAGAT GCTCGTTTAG
851 CTGACTTAAT CGATCGTCCA AATGTATTGG TAACTCCACA TACTGCTTTC
901 TACACTACTC ATGCTGTACG TAACATGGTA ACTAAAGCAT TTGACAACAA
951 CTTAAAGATG ATCAACGGTG AAAAACCAGA TTCTCCAGTT GCTTTGGACA
1001 AGAACAAGTT CTAA
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FIGURE 4B

SEQ ID NO: 7

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1  MTKIFAYAIR KDEEPFLNEW KDAHKDIEVE YTDKLLAPET AKLAKGADGV
51  VVYQQLDYTP ETLQALADAG VTKMSLHN NVG VDNIDMDKAK ELGFEITNVP
101 VYSPDAIAEH AAIQAARVLR QDKRMDEKMA KRDLRWAPTI GREVRDQVVG
151 VVGTGHIGQV FMKIMEGFGA KVIAYDIFKN PELEKKGYIV DSLDDLYKQA
201 DVISLHVPDV PANVHMINDE SIAKMKDGVV IVNCSRGPLV DTDVIRGLD
251 SGKIFGFVMD TYEGEVGVFN EDWEGKEFPD ARLADLIDRP NVLVTPHTAF
301 YTTHAVRNMV TKAFDNNLKM INGEKPDSPV ALDKNKF
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