

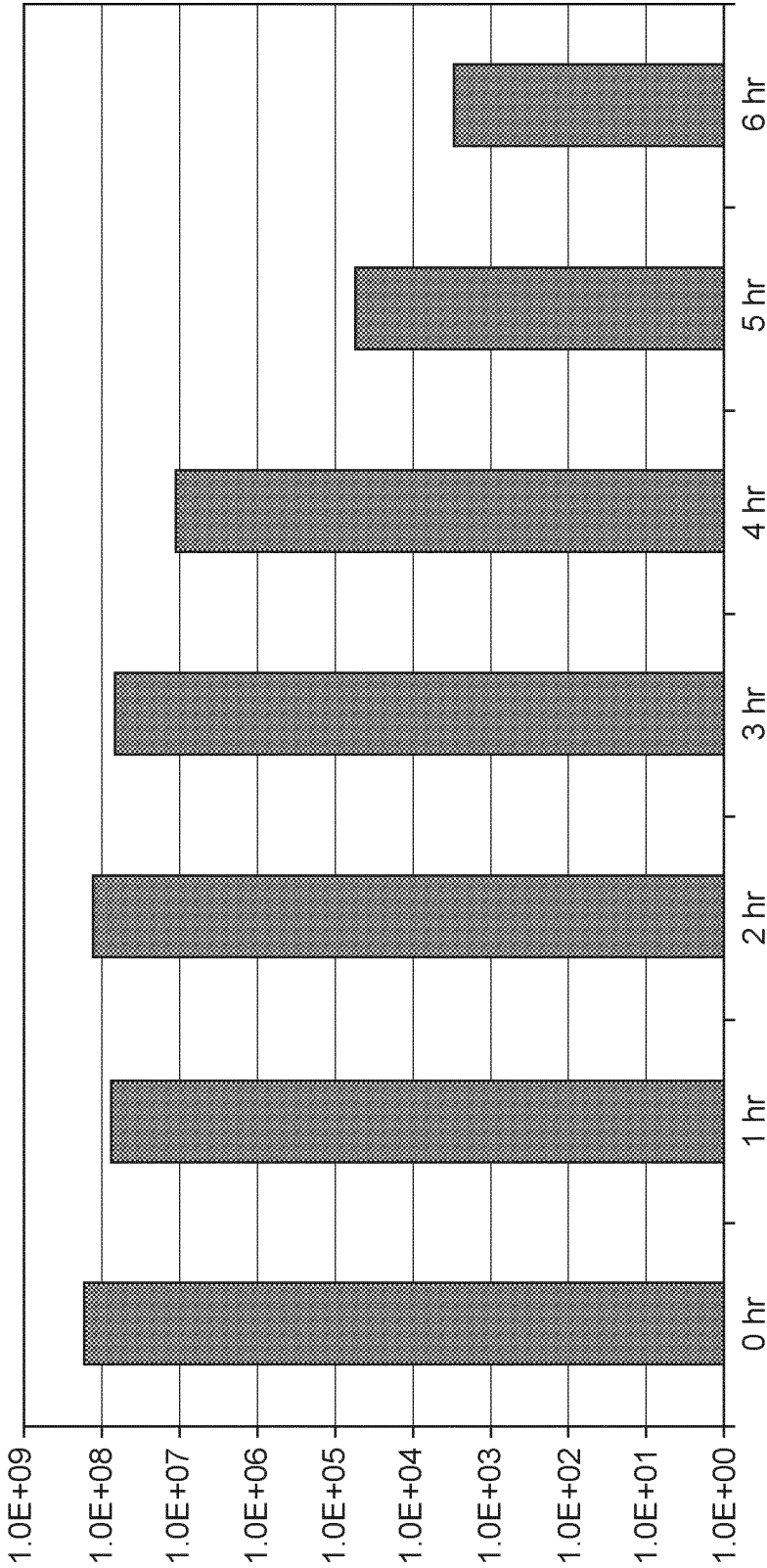


FIG. 1

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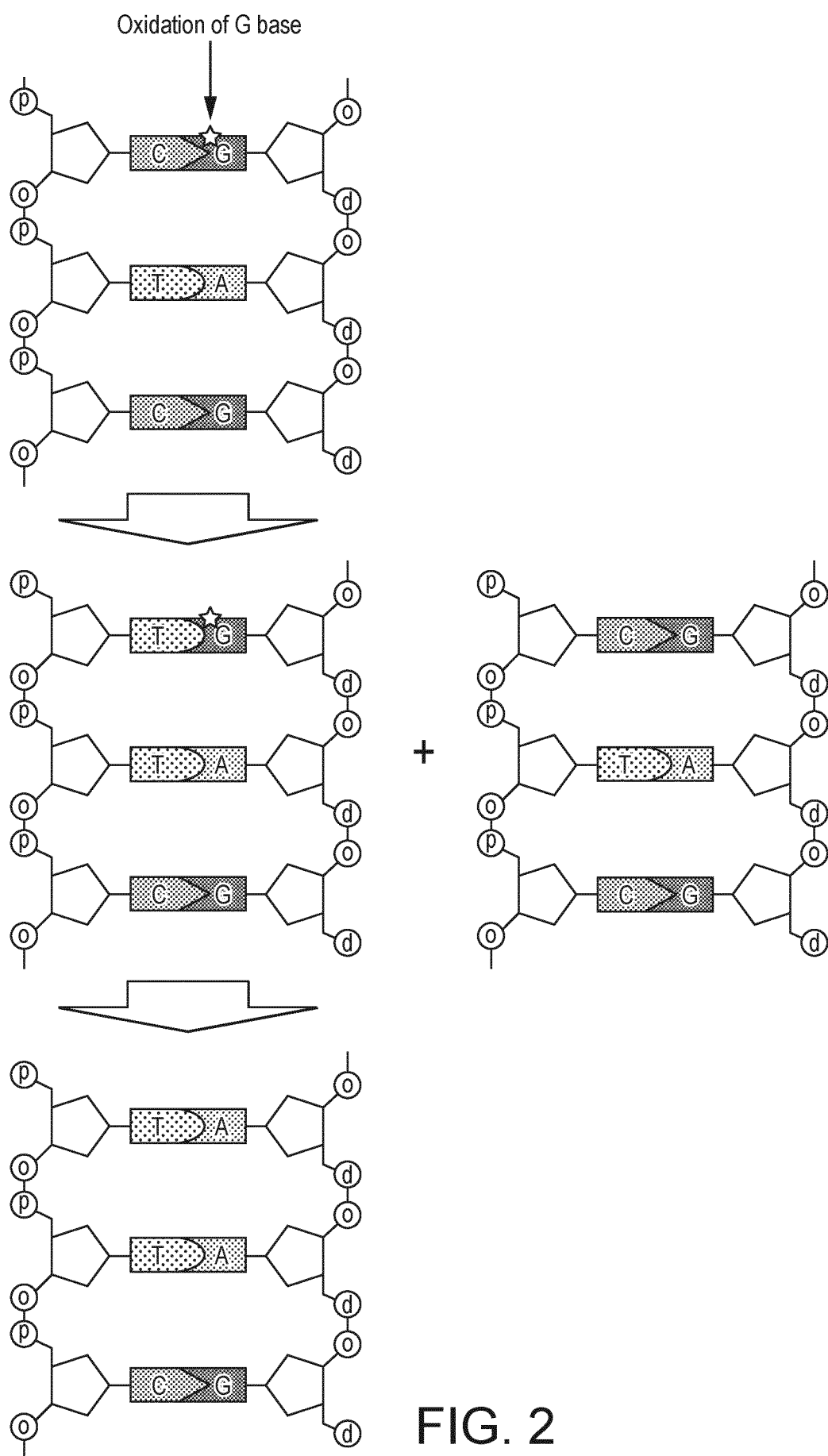


FIG. 2

RBS

1 AAAGACGGTC ATACTATTAA TTTTGGGA GGTTAATTT ATGACAAAGA TTTTGTCTTA CGCTATTCGT AAAGATGAAG AACCTTCTTT

91 AAACGAATGG AAAGATGCAC ACAAGGATAT TGAAGTTGAA TACACTGACA AGCTTTTAGC CCCTGAAACT GCTAAATTAG CTAAGGGTGC

181 L N E W K D A H K D I E V E Y T D K LL A P E T A K L A K G

181 TGACGGTGGT GTTGGTTTACC AACAAATTAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC TGATGCTGGC GTAACATAAGA TGTCAATTACG

271 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 TAACGTTTCCT GTATACTCTC CTGACGCAAT

361 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

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

D-LDH signature 1

451 ACCTACTATT GGTCGTGAAG TTCGTGACCA AGTTGTTGGT GTTGATAGGTA CTGGTCACAT CGGTCAAGTA TTTATGAAGA TTATGGAAGG

541 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 AAAGTTATTG CTTACGATAT CTTCAAGAAC CCAGAACTTG AAAAGAAAGG TTACTACTGTT GACTCACTTG 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

D-LDH signature 2

631 CAAGCAAGCT GATGTAATTT CACTTCACGT TCCAGATGTT CCAGCAAAACG TTCACATGAT TAATGATGAA TCAATCGCTA AGATGAAAGA

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 GCTCACGTGG TCCACTTGGT GACACTGACG CTGTTATCCG CGGCTTAGAT TCTGGTAAGA TCTTTGGTTT

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 CGTAAATGGC ACTTACGAAG GTGAAGTTGG TGTATTAAAC GAAGATTGGG AAGGTAAAGA ATTCCAGAT GCTCGTTTAG CTGACTTAAT

F V H D T Y E G E V G V F N F D W E G K E F P D A R L A D L

N CNM-I4435, GAC TO AAC

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 GCTTCCAGTT CTTAAATCA AATATGATA ATCAAAAAAGA

N L K M I N G E K P D S P V A L D K N K F *

FIGURE 3

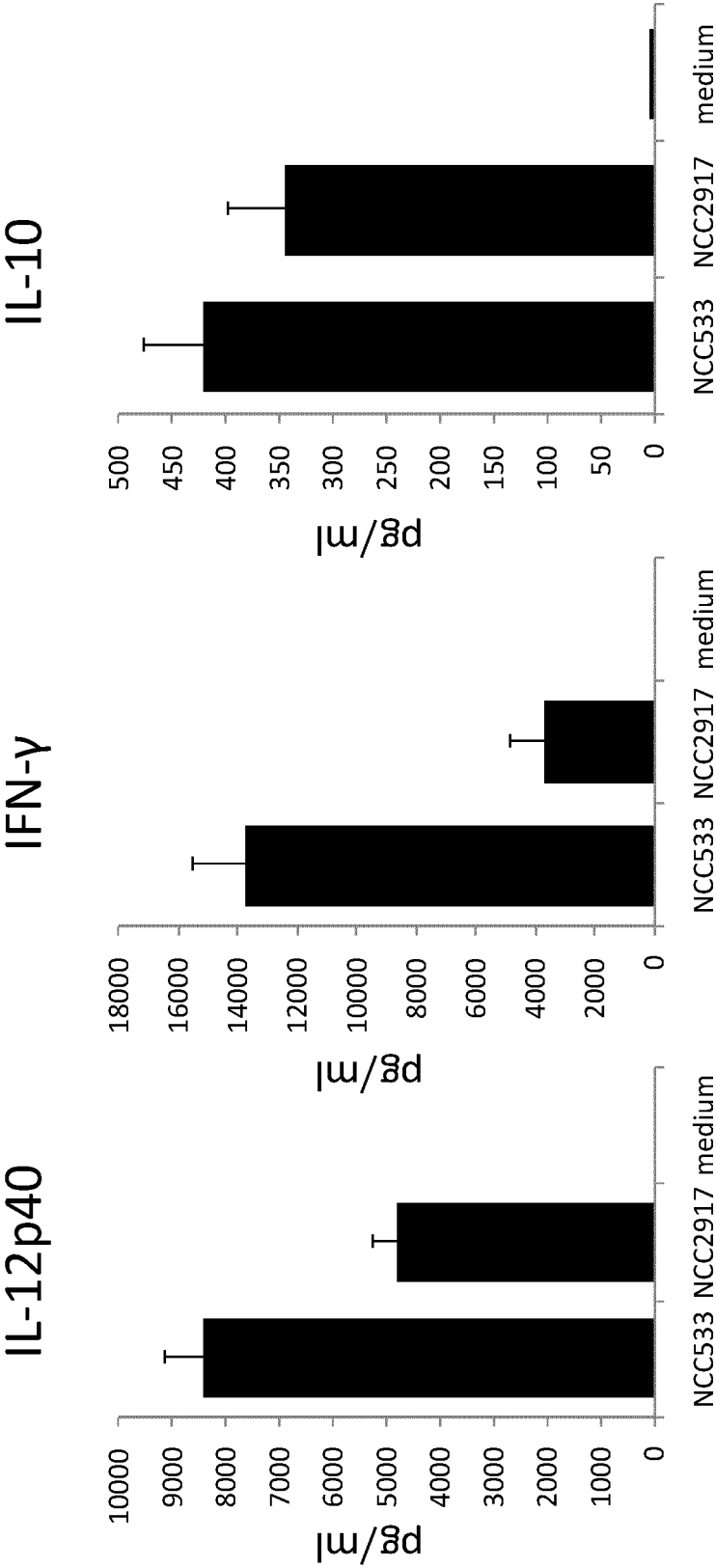


FIGURE 4

FIGURE 5A

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 TGACGGTGTG
151 GTTGTTTACC AACAATTAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC
201 TGATGCTGGC GTAACATAAGA TGTCATTACG TAACGTTGGT GTTGACAACA
251 TCGACATGGA CAAGGCTAAA GAATTAGGCT TTGAAATCAC TAACGTTCTT
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 CGTAATGAC 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 5B

SEQ ID NO: 7

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