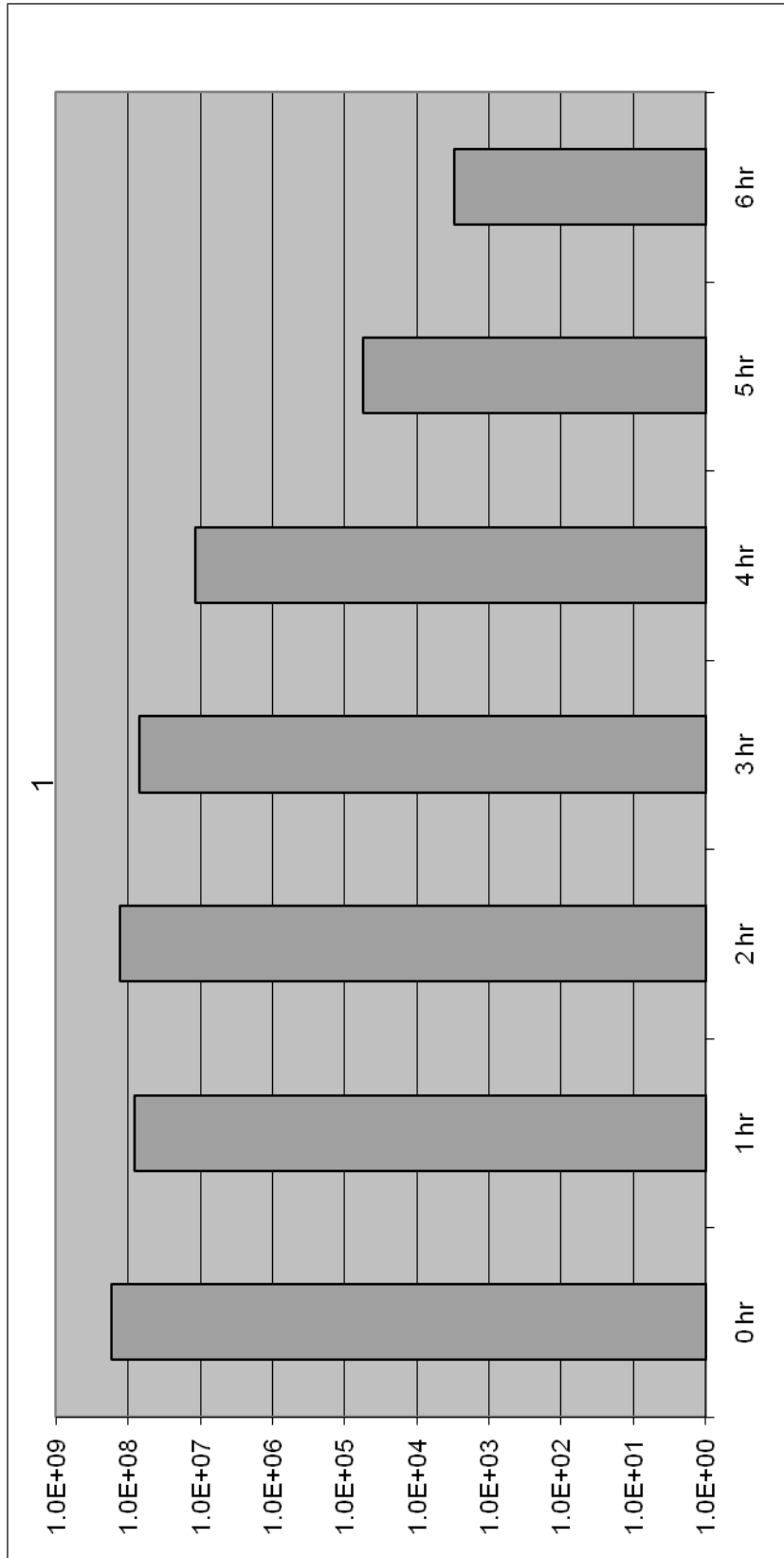


**FIGURE 1**

Oxidation of G base

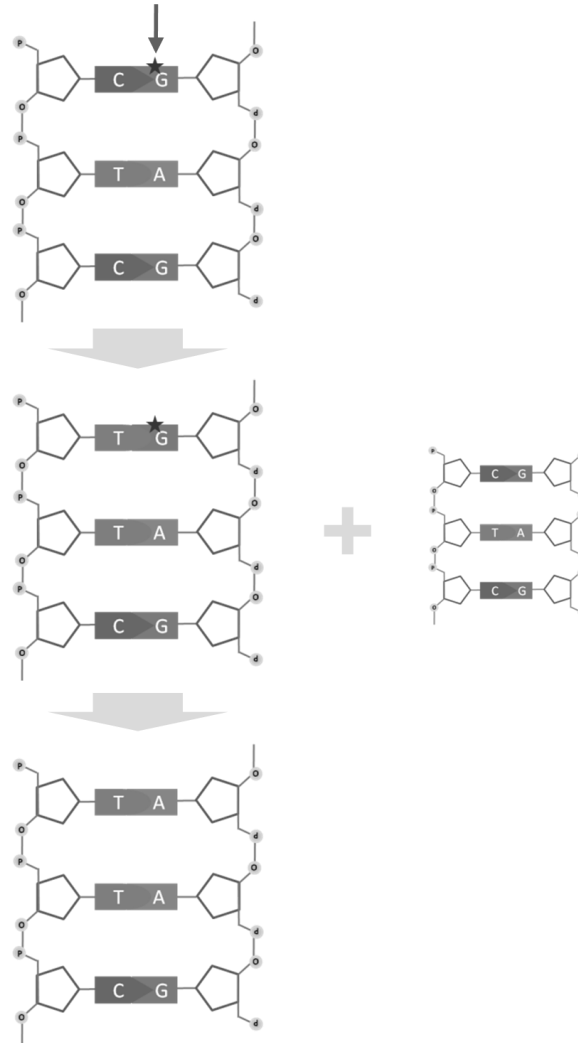


FIGURE 2

RBS

1 AAAGACGGTC ATACTATTAA TTTTGACGGA GGTTAATTT ATGACAAAGA TTTTTCCTTA CGCTATTCTG AAAGATGAAG AACCTTCTTT
M T K I F A Y A I R K D E E P F

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

181 TGACGGTGGT GTTGTTTACC AACAAATTAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC TGATGCTGGC GTAACCTAAGA TGTCAATTACG
A D G V V Y 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 TAACGTTCCCT 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

361 TGCTGAACAT GCTGCAATTC AAGCTGCTCG CGTACTACGT CAAGATAAGC GTATGGATGA AAAGATGGCT AAGCGCGACT TACGCTGGGC
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 GTTGTAGGTA CTGGTCACAT CGGTCAAGTA TTTATGAAGA TTATGGAAGG
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 AAAAGAAGGG TTACTACGTT GACTCACCTG ATGACTTATA
G F G A K V I A Y D I F K N P E L E K K G Y Y V D S L D D L

D-LDH signature 2

631 CAAGCAAGCT GATGTAATTT CACTTCACGT TCCAGATGTT CCAGCAAACG TTCACATGAT TAATGATGAA TCAATCGCTA AGATGAAAAGA
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 TCCACTTGTT 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 CGTAAGGgAC ACTTACGAAG GTGAAGTTGG TGTATTAAAC GAAGATTGGG AAGGTAAAGA ATTCCCAGAT 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

N CNCM-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 GCTTTGGACA AGAACAAAGTT CTAAAAATCA AATTATGATA ATCAAAAAGA
N L K M I N G E K P D S P V A L D K N K F *

FIGURE 3

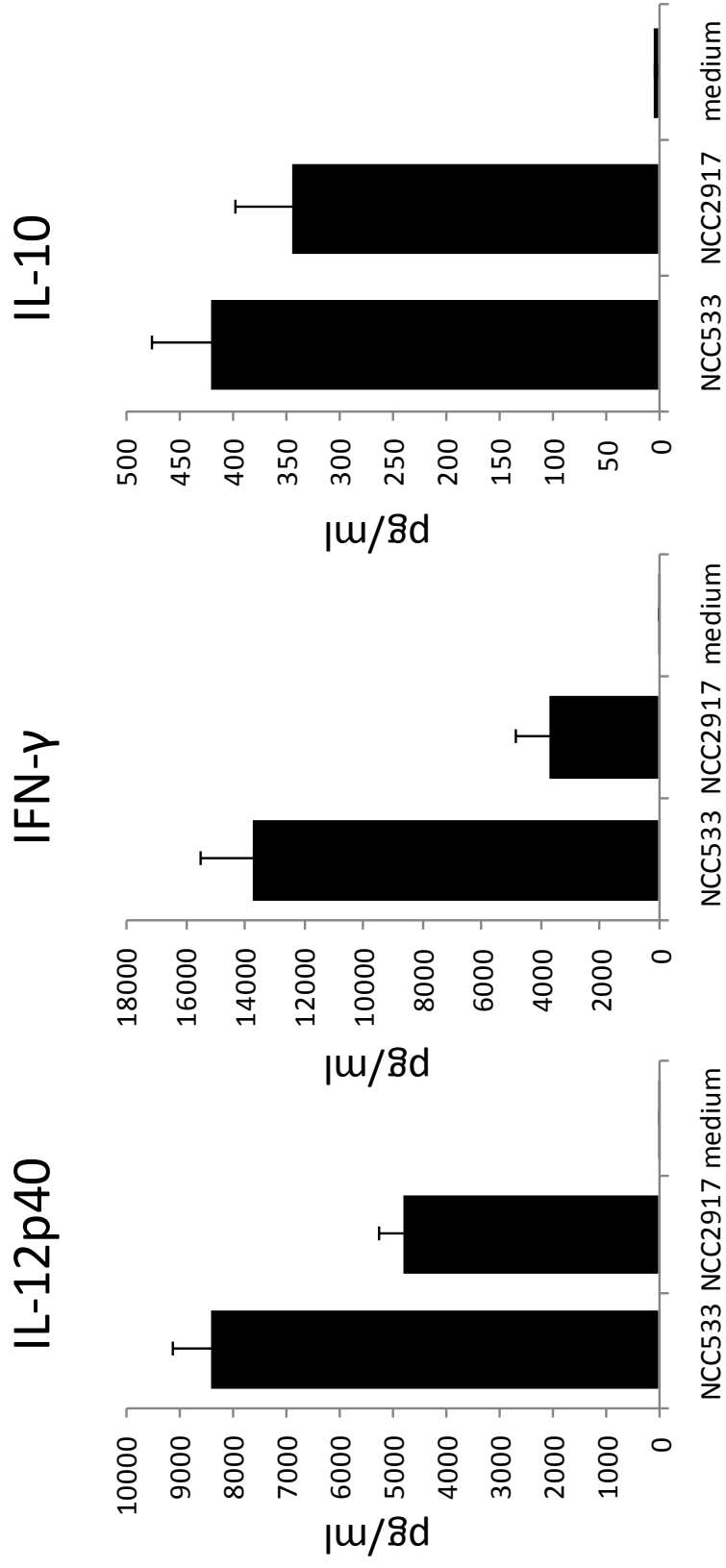


FIGURE 4

5 / 5
FIGURE 5A

SEQ ID NO: 6

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1  ATGACAAAGA TTTTGTCTTA CGCTATTCGT AAAGATGAAG AACCTTTCTT
51  AAACGAATGG AAAGATGCAC ACAAGGATAT TGAAGTTGAA TACACTGACA
101 AGCTTTTAGC CCCTGAAACT GCTAAATTAG CTAAGGGTGC TGACGGTGTG
151 GTTGTTTACC AACAATTAGA CTACACTCCT GAAACTCTTC AAGCTTTAGC
201 TGATGCTGGC GTAAC TAAGA TGTCAATTACG TAACGTTGGT GTTGACAACA
251 TCGACATGGA CAAGGCTAAA GAATTAGGCT TTGAAATCAC TAACGTTCCCT
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 CGTAATGAAC 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 KRDLRWAPT I GREVRDQVVG
151 VVGTGHIGQV FMKIMEGFGA KVIAYDIFKN PELEKKGY YV DSLDDLKQ A
201 DVISLHVPDV PANVHMINDE SIAKMKDGVV IVNCSRGPLV DTDVIRGLD
251 SGKIFGFVMN TYEGEVGVFN EDWEGKEFPD ARLADLIDRP NVLVT PHTAF
301 YTTHAVRNMV TKAFDNNLKM INGEKPDSPV ALDKNKF
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