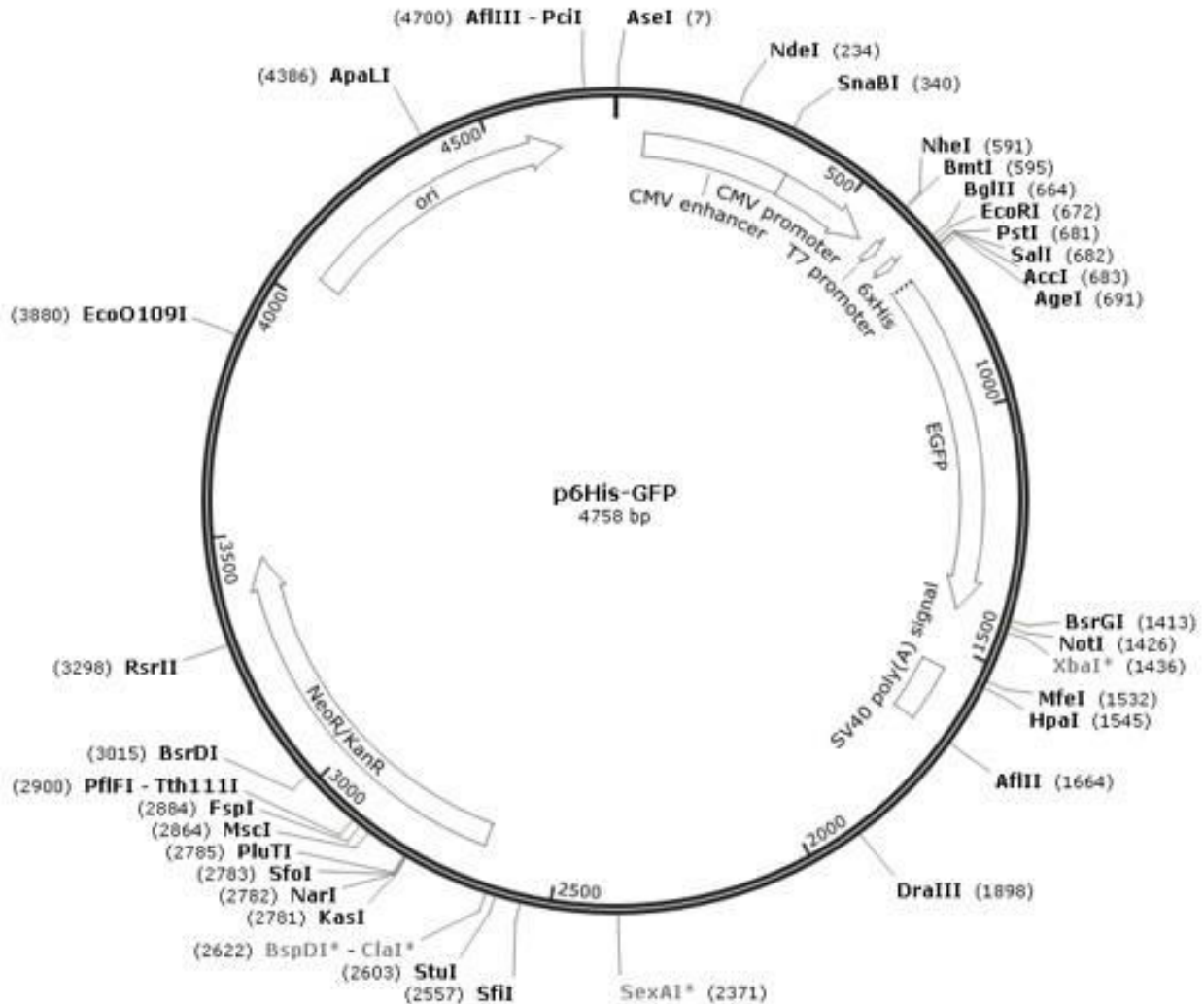


## DNA IT Control

Cat # NB-19-0033



### p6His-GFP sequence landmarks

CMVp	365..568 = 204 bp
T7p	597..615 = 19 bp
6xHis	644..661 = 18 bp
EGFP	704..1423 = 720 bp
SV40 poly(A)	1546..1667 = 122 bp
NeoR/KanR	2634..3448 = 795 bp
ori	4056..4644 = 589 bp

### p6His-GFP unique restriction enzymes

AccI, AflII, AgeI, ApaI, ApaLI, AseI, BglIII, BmtI, BspDI\*, BsrDI, BsrGI, ClaI\*, DraIII, EcoRI, FspI, HpaI, MfeI, NdeI, NheI, NotI, PciI, PflFI, PspOMI, PstI, RsrII, Sall, SexAI\*, SfiI, SnaBI, StuI, Tth111I, XbaI\*, XcmI.

(\* Blocked by Dam methylation)

## p6His-GFP cloning / expression region

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511  CCCATGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTGG TTTAGTGAAC CGTCAGATCC NheI
      GCTAGCTAAT
      CMV promoter
601  ACGACTCACT ATAGGTCTCA TAGAAGGAGT AGCCACCATG GGTTCATCACC ATCACCATCA BglIII EcoRI Sall
      CGCAGATCIT CGAATTCTGC AGTCGACGCC
      T7 promoter 6xHis
      M G H H H H H H A D L R I L Q S T
691  ACCGGTCGCC ACCATGGTGA GCAAGGGCGA GGAGCTGTTT ACCGGGGTGG TGCCCATCCT AgeI EGFP gene
      GTCGAGCTG GACGGCGACG TAAACGGCCA
      P P V A T M V S K G E E L F T G V V P I L V E L D G D V N G
781  CAAGTTCAGC GTGTCCGGCG AGGGCGAGGG CGATGCCACC TACGGCAAGC TGACCCTGAA
      GTTTCATCTGC ACCACCGGCA AGCTGCCCGT
      H K F S V S G E G E G D A T Y G K L T L K F I C T T G K L P
871  GCCCTGGCCC ACCCTCGTGA CCACCCTGAC CTACGGCGTG CAGTGCTTCA GCCGCTACCC
      CGACCACATG AAGCAGCAGC ACTTCTTCAA
      V P W P T L V T T L T Y G V Q C F S R Y P D H M K Q H D F F
961  GTCCGCCATG CCCGAAGGCT ACGTCCAGGA GCGCACCATC TTCTTCAAGG ACGACGGCAA
      CTACAAGACC CGCGCCGAGG TGAAGTTCGA
      K S A M P E G Y V Q E R T I F F K D D G N Y K T R A E V K F
1051 GGGCGACACC CTGGTGAACC GCATCGAGCT GAAGGGCATC GACTTCAAGG AGGACGGCAA
      CATCCTGGGG CACAAGCTGG AGTACAAC
      E G D T L V N R I E L K G I D F K E D G N I L G H K L E Y N
1141 CAACAGCCAC AACGTCTATA TCATGGCGGA CAAGCAGAAG AACGGCATCA AGGTGACTT
      CAAGATCCGC CACAACATCG AGGACGGCAG
      Y N S H N V Y I M A D K Q K N G I K V N F K I R H N I E D G
1231 CGTGCAGCTC GCCGACCACT ACCAGCAGAA CACCCCATC GCGCAGCGCC CCGTGCTGCT
      GCCCGACAAC CACTACCTGA GCACCCAGTC
      S V Q L A D H Y Q Q N T P I G D G P V L L P D N H Y L S T Q
1321 CGCCCTGAGC AAAGACCCCA ACGAGAAGCG CGATCACATG GTCCTGCTGG AGTTCGTGAC
      CGCCGCGGGG ATCACTCTCG GCATGGACGA
      S A L S K D P N E K R D H M V L L E F V T A A G I T L G M D
1411 GCTGTACAAG TAAAGCGGCC GCGACTCTAG ATCATAATCA GCCATACCAC BsrGI NotI XbaI+
      ATTGTAGAG
      E L Y K +
  
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