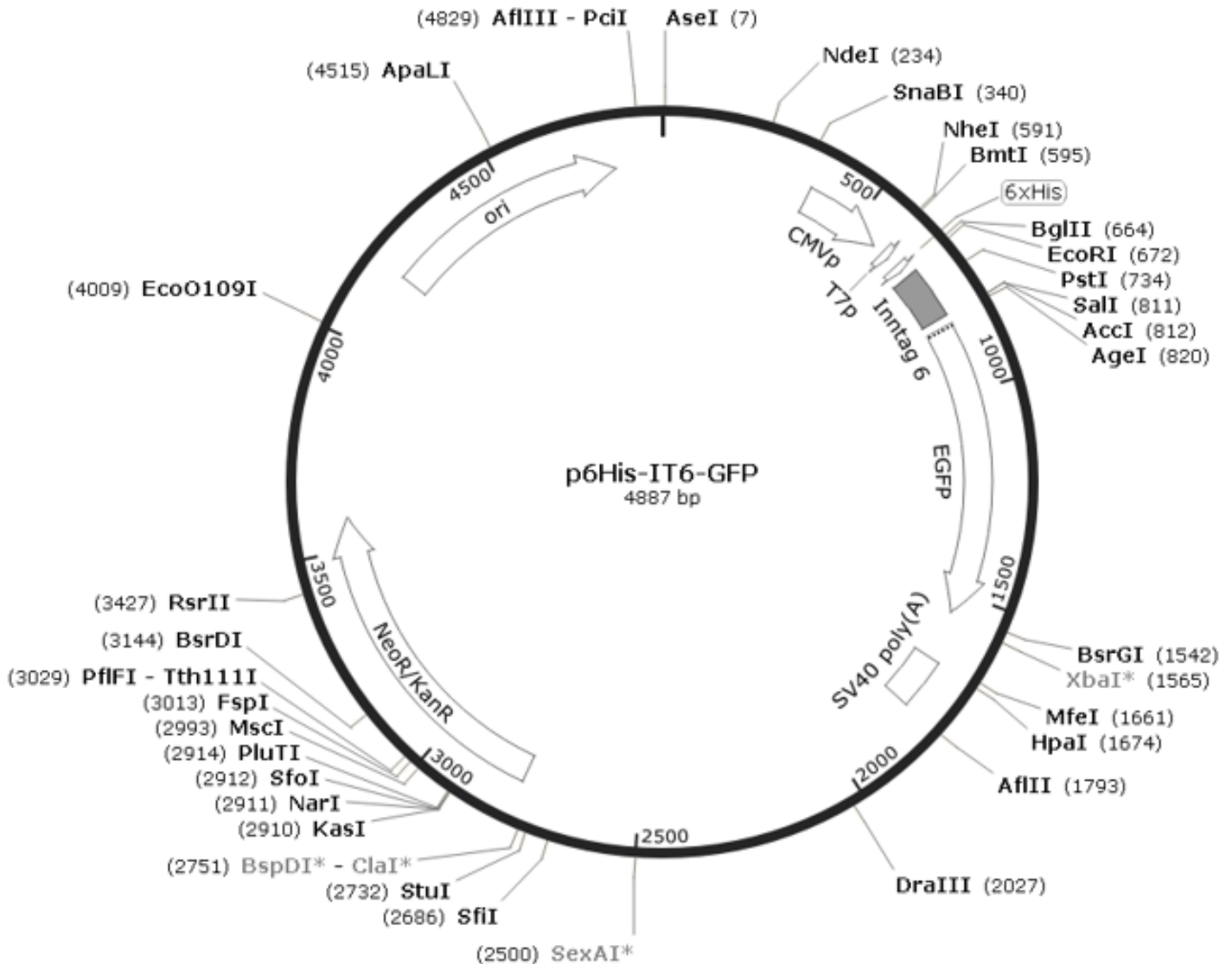


p6His-IT6-GFP

Cat # NB-19-0027

Inntag #	pdb_id	Description	prot_gi	Organism	Length (aa)
6	1WKX	Hevein isoform 2	73535415	<i>Hevea brasiliensis</i>	43



p6His-IT6-GFP sequence landmarks

CMVp	365..568 = 204 bp
T7p	597..615 = 19 bp
6xHis	644..661 = 18 bp
Inntag 6	680..808 = 129 bp
EGFP	833..1552 = 720 bp
SV40 poly(A)	1675..1796 = 122 bp
NeoR/KanR	2783..3577 = 795 bp
ori	4185..4773 = 589 bp

p6His-IT6-GFP unique restriction enzymes

AccI, AflII, AflIII, AgeI, ApaLI, AseI, BglII, BmtI, BspDI*, BsrDI, BsrGI, ClaI*, DraIII, EcoO109I, EcoRI, FspI, HpaI, KasI, MfeI, MscI, NarI, NdeI, NheI, PciI, PflFI, PluTI, PstI, RsrII, Sall, SexAI*, SfiI, SfoI, SnaBI, StuI, Tth111I, XbaI*.

(* Blocked by Dam methylation)

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p6His-IT6-GFP cloning / expression region

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532  CMV promoter
      TAGGCCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTGGT TTAGTGAACC GTCAGATCCG NheI T7 promoter
      CTAGCTAATA CGACTCACTA TAGGICTCAT

622  6xHis
      AGAAGGAGTA GCCACCATGG GTCATCACCA TCACCATCAC GCGAGATCTTC BglIII EcoRI
      M G H H H H H H A D L R I L E Q C G R Q A G G K
      ACAGTGC GGC CAGGCCG CCGGCAAAC T

712  PstI Inntag 6
      GTGCCCGGAT AACCTGTGCT GCAGCCAGTG GGGCTGGTGC GGCAGCACCG ATGAATATTG CAGCCCGGAT CATAACTGCC AGAGCAAAC T
      L C P D N L C C S Q W G W C G S T D E Y C S P D H N C Q S N

802  Sali AgeI EGFP gene
      CAAAGATCAG TCGACGCCAC CGGTGCGCCAC CATGGTGAGC AAGGGCGAGG AGCTGTTTAC CGGGGTGGTG CCCATCCTGG TCGAGCTGGA
      C K D Q S T P E V A T M V S K G E E L F T G V V P I L V E L

892  CGGCGACGTA AACGGCCACA AGTTCAGCGT GTCCGGCGAG GGCAGGGGCG ATGCCACCTA CGGCAAGCTG ACCCTGAAGT TCATCTGCAC
      D G D V N G H K F S V S G E G E G D A T Y G K L T L K F I C

982  CACCGGCAAG CTGCCCGTGC CCTGGCCAC CCTCGTGACC ACCCTGACCT ACGGCGTGCA GTGCTTCAGC CGCTACCCCG ACCCATGAA
      T T G K L P V P W P T L V T T L T Y G V Q C F S R Y P D H M

1072 GCAGCAGGAC TTCTTCAAGT CCGCCATGCC CGAAGGCTAC GTCCAGGAGC GCACCATCTT CTTCAAGGAC GACGGCAACT ACAAGACCCG
      K Q H D F F K S A M P E G Y V Q E R T I F F K D D G N Y K T

1162 CGCCGAGGTG AAGTTCGAGG GCGACACCCT GGTGAACCGC ATCGAGCTGA AGGGCATCGA CTTCAAGGAG GACGGCAACA TCCTGGGGCA
      R A E V K F E G D T L V N R I E L K G I D F K E D G N I L G

1252 CAAGCTGGAG TACAAC TACA ACAGCCACAA CGTCTATATC ATGGCCGACA AGCAGAAGAA CGGCATCAAG GTGAACTTCA AGATCCGCCA
      H K L E Y N Y N S H N V Y I M A D K Q K N G I K V N F K I R

1342 CAACATCGAG GACGGCAGCG TGCAGCTCGC CGACCACTAC CAGCAGAACA CCCCATCGG CGACGGCCCC GTGCTGCTGC CCGACAACCA
      H N I E D G S V Q L A D H Y Q Q N T P I G D G P V L L L P D N

1432 CTACCTGAGC ACCCAGTCCG CCTGAGCAA AGACCCCAAC GAGAAGCGCG ATCACATGGT CCTGCTGGAG TTCGTGACCG CCGCCGGGAT
      H Y L S T Q S A L S K D P N E K R D H M V L L E F V T A A G

1522 BarGI XbaI*
      CACTCTCGGC ATGGACGAGC TGTACAAGTA AAGCGGCCGC GACTCTAGAT CATAATCAGC CATAACCAT
      I T L G M D E L Y K *
  
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