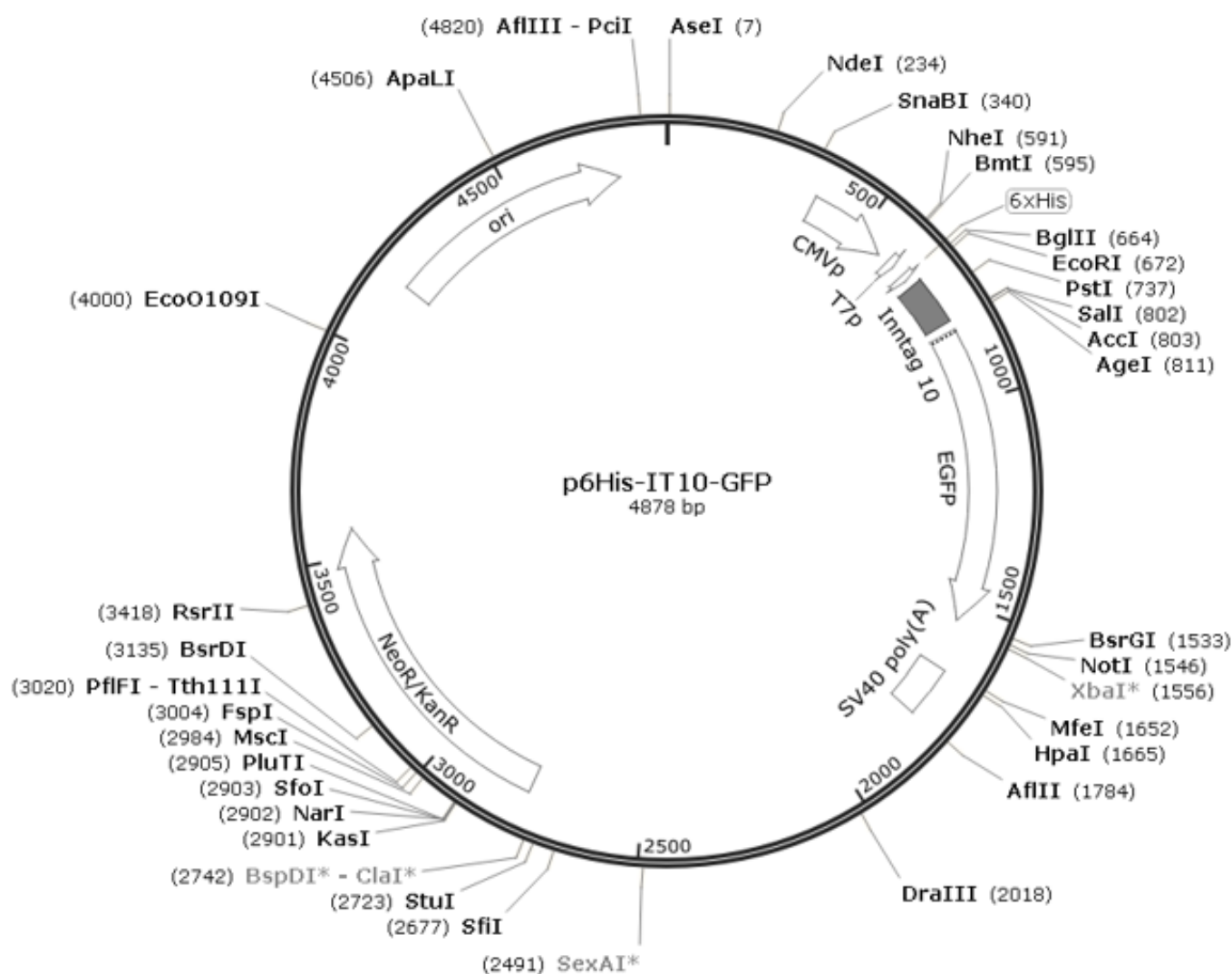


p6His-IT10-GFP

Cat # NB-19-0029

Inntag #	pdb_id	Description	prot_gi	Organism	Length (aa)
10	3BBG	Pollen allergen 5	159164870	<i>Ambrosia trifida</i>	40



p6His-IT10-GFP sequence landmarks

CMVp	365..568 = 204bp
T7p	597..615 = 19 bp
6xHis	644..661 = 18 bp
Inntag 10	680..799 = 120 bp
EGFP	824..1543 = 720 bp
SV40 poly(A)	1666..1787 = 122 bp
NeoR/KanR	2774..3568 = 795 bp
ori	4176..4764 = 589 bp

p6His-IT10-GFP unique restriction enzymes

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

(* Blocked by Dam methylation)

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p6His-IT10-GFP cloning / expression region

523 CMV promoter → AATGGGCGGT AGGCGGTGAC GGTGGGAGGT CTATATAAGC AGAGCTGGTT TAGTGAACCG TCAGATCCGC NheI TAGCTAATAC T7 promoter GACTCACTAT

613 → AGGTCTCATA GAAGGAGTAG CCACCATGGG 6xHis TCATCACCAT CACCATCACG BglIII EcoRI CAGATCTTCG AATTCCTGGAT GATGGCCTGT GCTATGAAGG
 M G H H H H H H A D L R I L D D G L C Y E

703 CACCAACTGC GGCAAAGTGG GCAAATATTG PstI Inntag 10 CTGCAGCCCG ATTGGCAAAT ATTGCGTGTG CTATGATAGC AAAGCCATTT GCAACAAAAA
 G T N C G K V G K Y C C S P I G K Y C V C Y D S K A I C N K

793 CTGCACCCAG SalI AgeI EGFP gene TCGACGCCAC CCGTCCGCCAC CATGGTGAGC AAGGGCGAGG AGCTGTTTAC CGGGGTGGTG CCCATCTCGG TCGAGCTGGA
 N C T Q S T P P V A T M V S K G E E L F T G V V P I L V E L

883 CGGCGACGTA AACGGCCACA AGTTCAGCGT GTCCGGCGAG GGCGAGGGCG 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

973 CACCGGCAAG CTGCCCGTGC CCTGGCCAC CCTCGTGACC ACCCTGACCT ACGGCGTGCA GTGCTTCAGC CGCTACCCCG ACCACATGAA
 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

1063 GCAGCAGCAC 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

1153 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

1243 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

1333 CAACATCGAG GACGGCAGCG TGCAGCTCGC CGACCACTAC CAGCAGAACA CCCCATCGG CGACGGCCCC GTGCTGCTGC CCGACACCA
 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 P D N

1423 CTACCTGAGC ACCCAGTCCG CCCTGAGCAA 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

1513 BsrGI NotI XbaI*
 CACTCTCGGC ATGGACGAGC TGTACAAGTA AAGCGGCCGC GACTCTAGAT CATAATCAGC CATACCACAT ATTTGTAGAG GTTTTACTTG
 I T L G M D E L Y K *

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