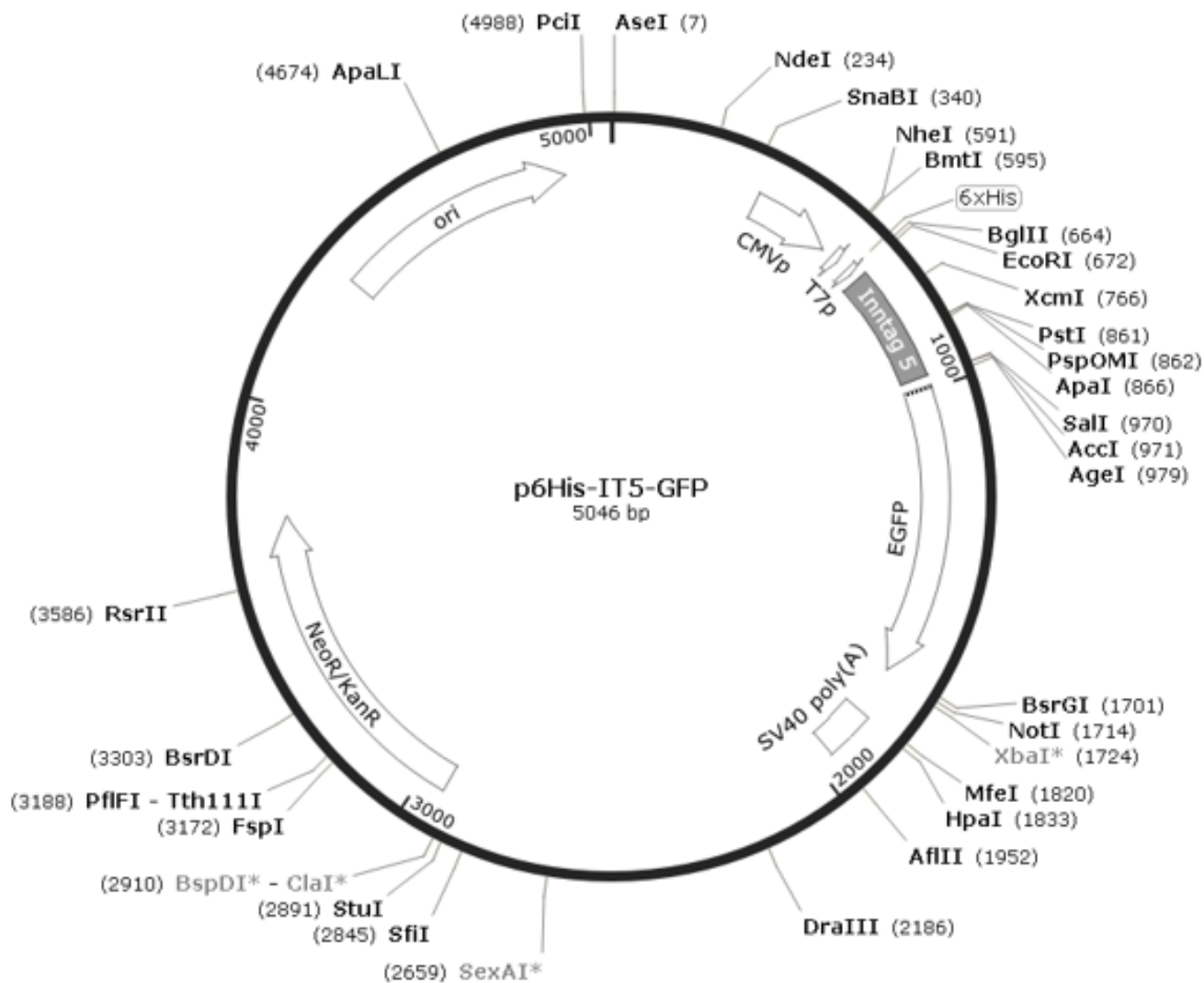


p6His-IT5-GFP

Cat # NB-19-0025

Inntag #	pdb_id	Description	prot_gi	Organism	Length (aa)
5	1WHP	Allergen Phl p 2	157834206	<i>Phleum pratense</i>	96



p6His-IT5-GFP sequence landmarks

CMVp	365..568 = 204 bp
T7p	597..615 = 19 bp
6xHis	644..661 = 183 bp
Inntag 5	680..967 = 288 bp
EGFP	992..1711 = 720 bp
SV40 poly(A)	1834..1955 = 122 bp
NeoR/KanR	2942..3736 = 795 bp
ori	4344..493 = 589 bp

p6His-IT5-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, SalI, SexAI*, SfiI, SnaBI, StuI, Tth111I, XbaI*, XcmI.

(* Blocked by Dam methylation)

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p6His-IT5-GFP cloning / expression region

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                    CMV promoter
511  CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTGG TTTAGTGAAC CGTCAGATCC NheI
                                     GCTAGCTAAT

T7 promoter
601  ACGACTCACT ATAGGICTCA TAGAAGGAGT AGCCACCATG GGTCAACACC ATCACCATCA CGCAGATCTT BglIII EcoRI
                                     M G H H H H H H A D L R I L V P K
                                     TGCCGAAAGT

Inntag 5
691  GACCTTTACC GTGGAAAAAG GCAGCAACGA AAAACATCTG GCCGTGCTGG TGAATATGA AGGCGATACC ATGGCCGAAG TGGAACTGCG
      V T F T V E K G S N E K H L A V L V K Y E G D T M A E V E L

871  CGAACATGGC AGCGATGAAT GGGTGGCCAT GACCAAAGGC GAAGGCGGCG TGTGGACCTT TGATAGCGAA GAACCGCTGC PstI ApaI
      R E H G S D E W V A M T K G E G G V W T F D S E E P L Q G P

871  TAACTTTTCG TTTCTGACCG AAAAAGGCAT GAAAACGCTG TTTGATGATG TGGTGCCGGA AAAATATACC ATTGGCGCCA CCTATGCCCC
      F N F R F L T E K G M K N V F D D V V P E K Y T I G A T Y A

961  SalI AgeI
      GGAAGAACAG TCGAGGCCAC CGGTCGCCAC CATGGTGAGC AAGGGCGAGS AGCTGTTTCC CGGGGTGGTG CCCATCTCTGG TCGAGCTGGA
      P E E 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

EGFP gene
1051 CGGCGACGTA AACGGCCACA AGTTCAGCGT GTCCGGCGAG GCGGAGGGCG 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

1141 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

1231 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

1321 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

1411 CAAGCTGGAG TACAACACAC ACAGCCACAA CGTCTATATC ATGGCCGACA AGCAGAAGAA CGGCATCAAG GTGAACCTCA 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

1501 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 P D N

1591 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

1681 CACTCTCGGC ATGGACGAGC BsrGI NotI XbaI*
      I T L G M D E L Y K *
      TGTACAAGTA AAGCGGCCGC GACTCTAGAT CATAATCAGC CATAACACAT
  
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