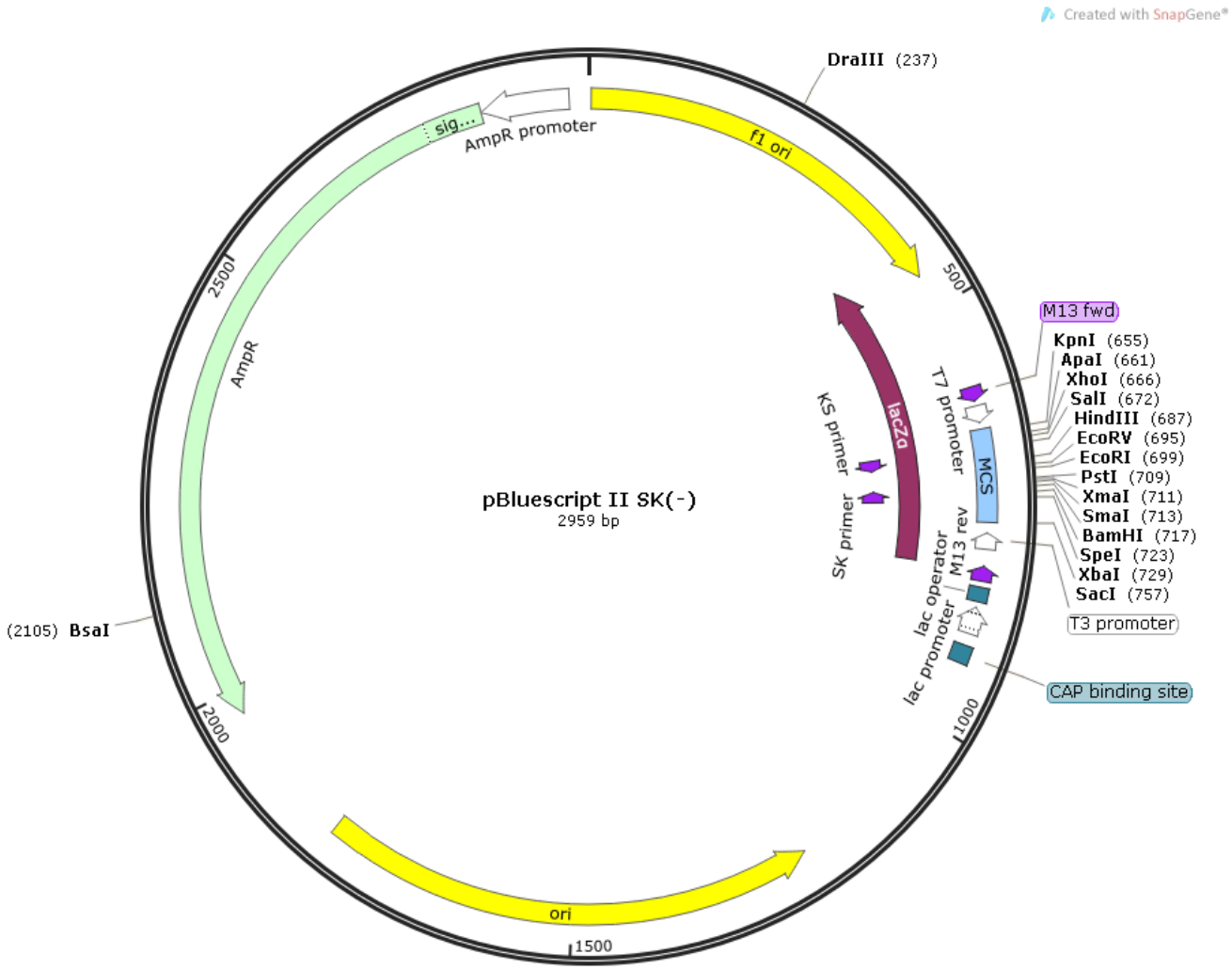
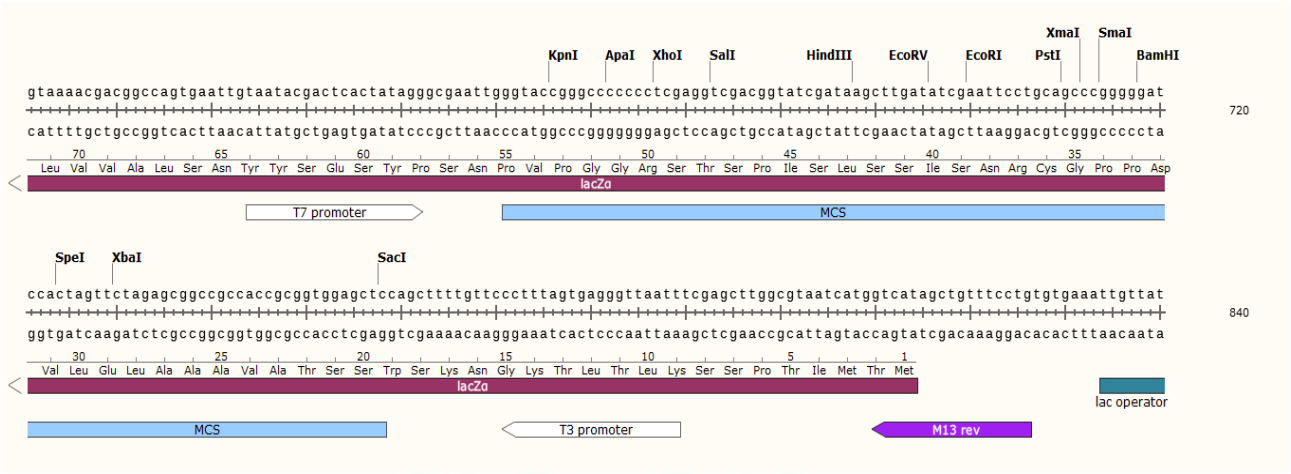
pBluescript II SK(-) Vector Information



载体名称:	pBluescript II SK(-)
质粒类型:	克隆载体
表达水平:	高拷贝
启动子:	T3 promoter，T7 promoter
克隆方法:	多克隆位点，限制性内切酶
克隆位点:	MCS
载体大小:	2959bp
5’测序引物及序列:	pUC344 :GTGCTGCAAGGCGATTAAGT
3’测序引物及序列:	pUC510R: TTCCGGCTCGTATGTTGTGT
载体标签:	--
载体抗性:	Amp
筛选标记:	--
产品目录号:	
稳定性:	瞬时表达 Transient
组成型/诱导型:	非组成型
病毒/非病毒:	非病毒
克隆菌株:	DH5α / Match-T1

MCS 区：

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LOCUS       Exported 2959bp ds-DNA circular SYN 21-APR-2019
DEFINITION  synthetic circular DNA
ACCESSION   .
VERSION     .
KEYWORDS    pBluescript II SK(-)
SOURCE      synthetic DNA construct
  ORGANISM  synthetic DNA construct
REFERENCE   1  (bases 1 to 2959)
  AUTHORS   Trial User
  TITLE     Direct Submission
  JOURNAL   Exported Saturday, May 25, 2019 from SnapGene 3.2.1
            http://www.snapgene.com
FEATURES             Location/Qualifiers
     source          1..2959
                     /organism="synthetic DNA construct"
                     /mol_type="other DNA"
     rep_origin      4..459
                     /direction=RIGHT
                     /note="f1 ori"
                     /note="f1 bacteriophage origin of replication; arrow
                     indicates direction of (+) strand synthesis"
     CDS             complement(410..814)
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                     /gene="lacZ fragment"
                     /product="LacZ-alpha fragment of beta-galactosidase"
                     /note="lacZ-alpha"
                     /translation="MTMITPSSKLTLTKGNKSWSSTAVAAALELVDPPGCRNSISSLSI
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     primer_bind     601..617
                     /note="M13 fwd"
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	/note="common sequencing primer, one of multiple similar variants"
promoter	624..642
	/note="T7 promoter"
	/note="promoter for bacteriophage T7 RNA polymerase"
misc_feature	651..758
	/note="MCS"
	/note="pBluescript multiple cloning site"
primer_bind	668..684
	/note="KS primer"
	/note="common sequencing primer, one of multiple similar variants"
primer_bind	complement(718..734)
	/note="SK primer"
	/note="common sequencing primer, one of multiple similar variants"
promoter	complement(771..789)
	/note="T3 promoter"
	/note="promoter for bacteriophage T3 RNA polymerase"
primer_bind	complement(810..826)
	/note="M13 rev"
	/note="common sequencing primer, one of multiple similar variants"
protein_bind	834..850
	/bound_moiety="lac repressor encoded by lacI"
	/note="lac operator"
	/note="The lac repressor binds to the lac operator to inhibit transcription in E. coli. This inhibition can be relieved by adding lactose or isopropyl-beta-D-thiogalactopyranoside (IPTG)."
promoter	complement(858..888)
	/note="lac promoter"
	/note="promoter for the E. coli lac operon"
protein_bind	903..924
	/bound_moiety="E. coli catabolite activator protein"
	/note="CAP binding site"
	/note="CAP binding activates transcription in the presence of cAMP."
rep_origin	complement(1212..1800)
	/direction=LEFT
	/note="ori"
	/note="high-copy-number ColE1/pMB1/pBR322/pUC origin of replication"
CDS	complement(1971..2831)
	/codon_start=1
	/gene="bla"

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                      ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVEYS
                      PVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRW
                      EPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSA
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                      LIKHW"
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                     /gene="bla"
                     /note="AmpR promoter"
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       61 CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG
      121 CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTTCCGAT
      181 TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGTG
      241 GGCCATCGCC CTGATAGACG GTTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA
      301 GTGGACTCTT GTTCCAAACT GGAACAACAC TCAACCCTAT CTCGGTCTAT TCTTTTGATT
      361 TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTTAAAAAA TGAGCTGATT TAACAAAAAT
      421 TTAACGCGAA TTTTAACAAA ATATTAACGC TTACAATTTG CCATTCGCCA TTCAGGCTGC
      481 GCAACTGTTG GGAAGGGCGA TCGGTGCGGG CCTCTTCGCT ATTACGCCAG CTGGCGAAAG
      541 GGGGATGTGC TGCAAGGCGA TTAAGTTGGG TAACGCCAGG GTTTTCCCAG TCACGACGTT
      601 GTAAAACGAC GGCCAGTGAA TTGTAATACG ACTCACTATA GGGCGAATTG GGTACCGGGC
      661 CCCCCCTCGA GGTCGACGGT ATCGATAAGC TTGATATCGA ATTCCTGCAG CCCGGGGGAT
      721 CCACTAGTTC TAGAGCGGCC GCCACCGCGG TGGAGCTCCA GCTTTTGTTC CCTTTAGTGA
      781 GGGTTAATTT CGAGCTTGGC GTAATCATGG TCATAGCTGT TTCCTGTGTG AAATTGTTAT
      841 CCGCTCACAA TTCCACACAA CATACGAGCC GGAAGCATAA AGTGTAAAGC CTGGGGTGCC
      901 TAATGAGTGA GCTAACTCAC ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA
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     1141 GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG
     1201 TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA
     1261 AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC
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     1501 TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA
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     1681 AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT
     1741 GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA
     1801 GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA
     1861 GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA
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     1921 TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TTACCAATGC
     1981 TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA
     2041 CTCCCCGTCG TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTGCA
     2101 ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC
     2161 GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT
     2221 TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA CGTTGTTGCC
     2281 ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT
     2341 TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT GCAAAAAAGC GGTTAGCTCC
     2401 TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG
     2461 GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT
     2521 GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG CTCTTGCCCG
     2581 GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT CATCATTGGA
     2641 AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC CAGTTCGATG
     2701 TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG
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//
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