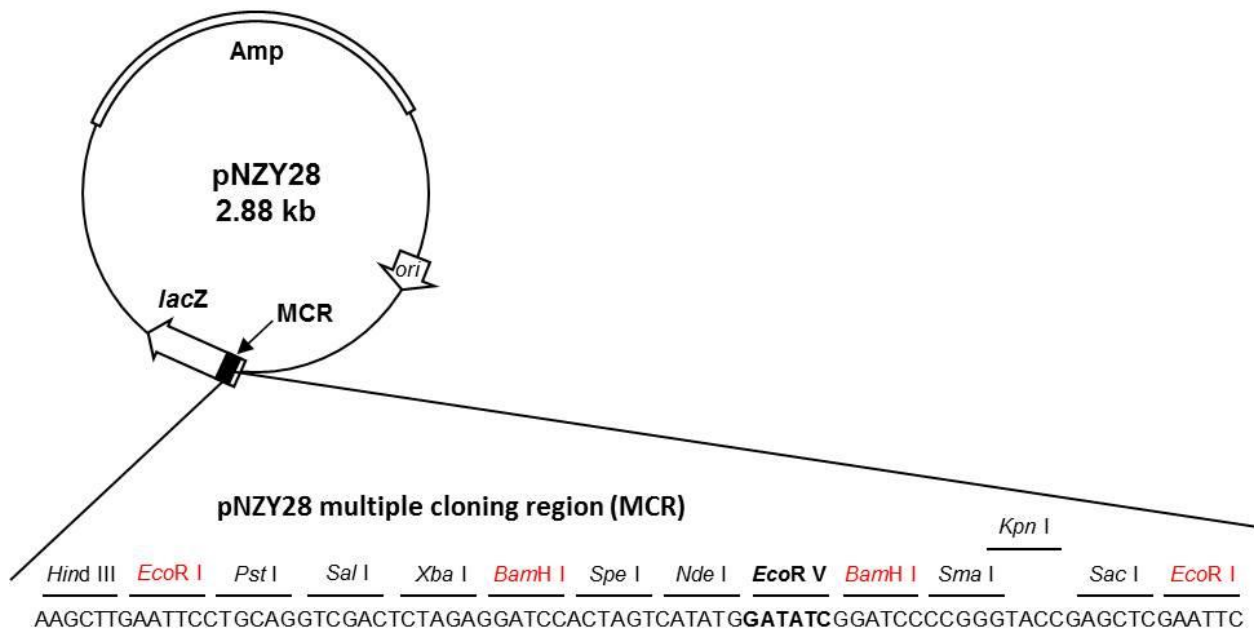


pNZY28- Vector Map



pNZY28 Vector Sequence reference points:

Base pairs	2886
lacZ start codon	1
T7 RNA polymerase promoter	24-44
T7 promoter sequencing primer binding site	24-39
Multiple cloning region	45-126
M13/pUC U19-mer sequencing primer binding site	144-161
phage f1 region	283-737
pUC/M13 Reverse Sequencing Primer binding site	2855-2878

T7 promoter sequencing primer	5'-(TAATACGACTCACTATAGGG)-3'
M13/pUC U19-mer sequencing primer	5'-(GTTTTCCCAGTCACGACGT)-3'
M13/pUC Reverse Sequencing primer	5'-(GAGCGGATAACAATTTTCACACAGG)-3'

Sequence (2886 bp):

ATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTTGAATTCCTGCAGGTCGACTCT
AGAGGATCCACTAGTCATATGGATATCGGATCCCCGGGTACCGAGCTCGAATTCCTGGCCGTCGTTTTAC
AACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGC
TGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAA
ATTGTAAGCGTTAATATTTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATA
GGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTT
GGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGAT
GGCCCACTACGTGAACCATCACCCATAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAA
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AAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCC
GCGCTTAATGCGCCGCTACAGGGCGGCTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTG
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GGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTTCGCCCGAAGAACGTTTTCCAA
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CTTCATTTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAAATCCCTAACG
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CTACCAACTCTTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTA
GCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTAC
CAGTGGCTGCTGCCAGTGGCGATAAGTTCGTGTCTTACCGGGTTGACTCAAGACGATAGTTACCGGATAAG
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GAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAAGCGGACAGGTATCCGG
TAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
CCTGTGCGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATG
GAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCCTGGCCTTTTTGCTGGCCTTTTTGCTCACATGTTCTTTTC
CTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGC
CGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCC
CGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCA
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TTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCT