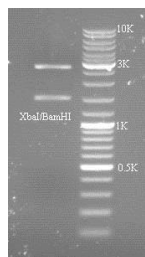


pUC-gp120 (ADA)(HIV-1/Clade B)

Cat# HIV-0023

Gene Name	pUC-gp120 (ADA)(HIV-1/Clade B)
Gene description:	Codon optimized cDNA clone of HIV-1 gp120 (ADA)(Clade B) for high-level expression in mammalian cells
cDNA Insert Size	1455 bp codon optimized HIV-1 gp120 (ADA)(Clade B) cDNA, corresponding to amino acid 34-518 (Gene accession# M60472) inserted at EcoRV site of pUC57 vector
Vector	pUC57
Cloning Site	EcoRV
Storage	4 °C.

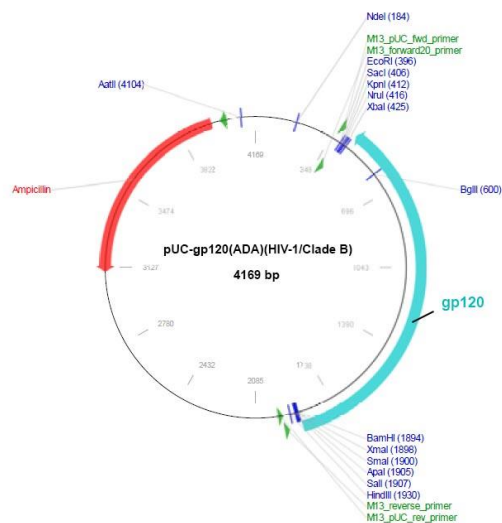
Quality Control



Restriction Enzyme Digestion:

Lane 1, digested with BamHI and XbaI
Lane 2, DNA ladder

Construct map:



Detailed amino acid sequence of the HIV-1 gp120 (ADA)(Clade B) cDNA clone:

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1      WVTVYYGVVPVWKEATTTLFCASDAKAYDTEVHNWVATHACVPTDPNPQEVVLENVTFENFMWKNMVEQMHEDIISLWDQ
81     SLKPCVKLTPLCVTLNCTDLRNVNTINNSSEGMERGEIKNCSFNITTSIRDVKVKDYALFYRLDVVPIDNDNTSYRLINCN
161    TSTITQACPKVSFEPIPIHYCTPAGFAILKCKDKKFNGTGPKCNVSTVQCTHGIRPVVSTQLLLNGSLAEDEVIRSSNF
241    TDNAKNIIVQLKESVEINCTRPNNNTRKSIHIGPGRIFYTTGEIIGDIRQAHCNISRTKWNNTLNQIATKLKEQFGNNKT
321    IVFNQSSGGDEPEIVMHSFNCGGEFFYCNSTQLFNSTWNFNNGTWNLTQSNTEGNDTITLPCRIKQIINMWQEVGKAMYAP
401    PIRGQIRCSSNITGLILTRDGGTNSGSEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTAKRRRVQREKRAVGTIG
481    AMFLG

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Detailed sequence of the whole construct (pUC-gp120(ADA)(HIV-1/Clade B):

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1      TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
81     GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTTCGCGGGCTTAACTATGCGGCATCAGA
161    GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCC
241    ATTCGCCATTACAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
321    GGATGTGCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGGTTTTCCAGTCACGACGTTGTAAACGACGGCCAGTGAATT
401    CGAGCTCGGTACCTCGCAATGCATCTAGATGAAAGCCCAGGAACATGGCGCCGATGGTGCCACGGCTCTCTCTCTCT
481    CTGCACCACTCTTCTCTTGGCCTTGGTGGGGGCCACGCCAGGGCTCGATCTTCACCACCTTGTACTTGTACAGCTCGC
561    TTCTCCAGTTGTCTCTCATGTGCGCCGCCCGGGTCTGAAGATCTCGCTGCCGCTGCTGTTGGTGCCGCCGCTCTCTGGTC
641    AGGATCAGGCCGGTGATGTTGCTGCTGCTGATCTGATCTGGCCTCTGATGGGGGGGGCGTACATGGCCTTCCCACTCTCTG
721    CCACATGTTGATGATCTGCTGATTTCTGTCAGGCGAGGGTGTGGTGTGCTTGCCTTCGGTGGCCTTGTCTGGGTTCAGGT
801    TCCAGGTGCCGTTGAAGTTCCAGGTGCTGTTGAACAGCTGGGTGCTGTTGCAGTAGAAGAACTCGCCGCCGCGAGTTGAAG
881    CTGTGCATCACGATCTCGGGTGCAGCGCGCTGCTCTGGTTGAACACGATGGTCTTGTGTTGTCGGAAGTCTCTCTTCAG
961    CTTGGTGGCGATCTGGTTTCAGGGTGTGTTTCCACTTGGTTCTGCTGATGTTGCAGTGGGCTGTCTGATGTCGCCGATGA
1041   TCTCGCCGGTGGTGTAGAAGGCTCTGCCGGGGCCGATGTGGATGCTCTTCTGGTGTGTTGTTGGGTCTGGTGCAGTTG
1121   ATCTCCACGCTCTCTCTTCAGCTGCAGATGATGTTCTTGGCGTTGTGGTGAAGTTGCTGCTTCTGATCACCACTCTCTC
1201   CTCGGCCAGGCTGCCGTTTCAGCAGCAGCTGGGTGCTCACCCAGGGTCTGATGCGGTGGGTGCACTGCACGGTGTCTCAGT
1281   TCTTGCAGGGGCCGGTGGCCTTGAAGTTCTTGTCTTGCCTTGCCTTGCAGTTCAGGATGGCGAAGCCGGCGGGGGTGCAGTAGTGGATG
1361   GGGATGGGCTCGAAGCTCACCTTGGGGCAGGCTGGGTGATGGTGTGCTGGTGTGTCAGTTGATCAGTCTGTAGCTGGTGTG
1441   GTGCTTGTGATGGGCACCACTCCAGTCTGTAGAAGAGGGCGTAGTCTTCTTACCTTGTCTCTGATGCTGGTGGTGA
1521   TGTTGAAGCTGCAGTTCTTGTATCTCGCCTCTCATGCCCTCGCTGCTGTTGTTGATGTTGGTTCAGTCTTCTCAGGTTCGGTG
1601   CAGTTTCAGGGTCACGCACAGGGGGGTTCAGTTTCACGCAGGGCTTCAGGCTCTGGTCCCACAGGCTGATGATGCTCTCGTG
1681   CATCTGCTCCACCATGTTGTTCTTCCACATGTTGAAGTTCTCGGTTCAGTTCTCCAGCACCACCTCTCTGGGGGTGGGGT
1761   CGGTGGGCACGCAGGCGTGGGTGGCCACACGTTGTGTCACCTCGGTGCTGATGGCCTTGGCGCTCGCTGGCGCAGAACAGG
1841   GTGGTGGTGGCCTCTCTTCCACAGGGGCACGCCGTAGTACACGGTCAACCAATCGGATCCCGGGCCCGTGCAGTGCAGAGG
1921   CCTGCATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATCCACACAACA
2001   TACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG
2081   CCCGCTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCATTAATGAATCGGCCAACCGCGCGGGGAGAGGCGGTTTGCATAT
2161   TGGGCGCTCTTCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCGGTGCTGCGCTGCGGCGAGCGGTATCAGCTCACTCAA
2241   AGCGGTAATACGGTTATCCACAGAATCAGGGGATAACCGCAGGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG
2321   AACCGTAAAGAGCCGCGCTTGTGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCCAGCCTCAAG
2401   TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTCTGTTT
2481   CGACCTTCCGCTTACCGGATACCTGTCCGCTTCTCTCTTCCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGG
2561   TATCTCAGTTCCGTGTAGGTGCTTCCGCTCCAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCCGACCGCTGCGCCTT
2641   ATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA
2721   GCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT
2801   GGTATCTGCGCTGTGCTGAAGCGAGTTACCTTCCGAAAGAGTGTGGTAGTCTTGTATCCGGCAACAAACACCGCTGG
2881   TAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTA
2961   CGGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTCACTAG
3041   ATCCTTTTAAATTAATAAAGTGTAAATCAATCTAAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTT
3121   AATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCTGTTTCATCCATAGTTGCGCTGACTCCCCGCTCGTGTAGATAACTA
3201   CGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCA
3281   GCAATAAACGACGACCGGGAAGGGCGGACGCGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTATTTG
3361   TTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTAAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGT
3441   CACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCACACGATCAAGGCGAGTTACATGATCCCCATGTTGTGTC
3521   AAAAAAGCGGTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTTATGGC
3601   AGCACTGCATAATTCTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTACTCAACCAAGTCATTCT
3681   GAGAATAGTGATGCGGCGACCGAGTTGCTCTTGGCCGCGCTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTA
3761   AAAGTGCTCATATTGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTA
3841   ACCCACTGTGCACCAACTGATCTTCAGCATCTTTTACTTTCACGAGCTTCTGGGTGAGCAAAAAACAGGAAGGCAAA
3921   ATGCCGCAAAAAAGGAATAAGGGCGACACGGAATGTTGAATACTACTACTCTTCTTTTCAATATTATTGAAGCATT
4001   TATCAGGGTTATGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAACAAATAGGGGTTCGCGCACATT

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4081 TCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGC
4161 CCTTTCGTC