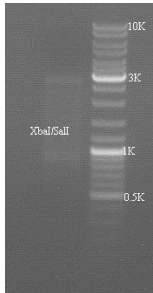


pUC-HCV E2 (subtype 1a)

Cat# HCV-E21a

Gene Name	pUC-HCV E2 (subtype 1a)
Gene description:	Codon optimized cDNA clone of HCV E2 subtype 1a
cDNA Insert Size	843 bp codon optimized HCV E2 (subtype 1a) cDNA, corresponding to amino acid 383-663 (Gene accession# AF009606) inserted at EcoRV site of pUC57 vector
Vector	pUC57
Cloning Site	EcoRV
Storage	4 °C.

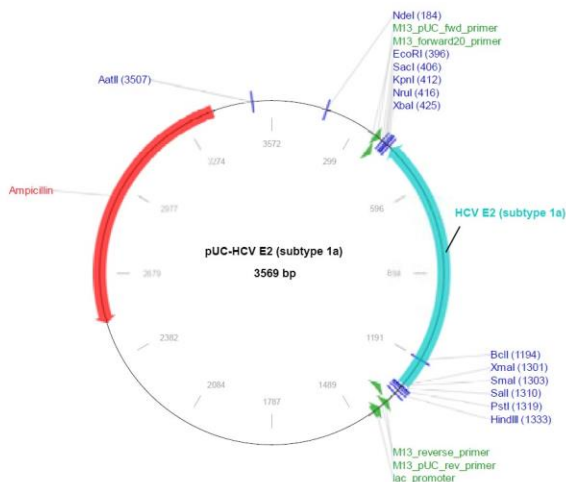
Quality Control



Restriction Enzyme Digestion:

Lane 1, digested with Sall and XhoI
Lane 2, DNA ladder

Construct map:



Detailed amino acid sequence of the HCV E2 (subtype 1a) cDNA clone:

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1  AETHVTGSSA GRRTAGLVGL LTPGAKQNIQ LINTNGSWHI NSTALNCNES LNTGWLGLF YQHKFNSSGC
71  PERLASCRRL TDFAQGWGPI SYANGSLDE RPYCWHYPPR PCGIVPAKSV CGPVYCFTPS PVVVGTDRS
141 GAPTYSWGAN DTDVFLNNT RPPLGNWFGC TWMNSTGFTK VCGAPPCVIG GVMNNTLLCP TDCFRKHPEA
211 TYSRCGSGPW ITPRCMVDYP YRLWHYPCTI NYTIFKVRMY VGGVEHRLEA ACNWTRGERC DLEDNRSEL
281 S
  
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Detailed sequence of the whole construct (pUC-HCV E2 (subtype 1a)):

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1      TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
81     GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCTGGCTTAACTATGCGGCATCAGA
161    GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC
241    ATTCCGCAATTCAGGTCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
321    GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAAAACGACGCGCCAGTGAATT
401    CGAGCTCGGTACCTCGGAATGCATCTAGATATCGGATCCCGTCGCTCAGTTCGCTCCGATCCCGATCTTCCAGATCACA
481    CCGCTCGCCCCGTGTCCAGTTGCAGGCGGCCTCCAGCCTGTGCTCCACGCCGCGACGTACATGCGGACCTTAAAAATAG
561    TGTAGTTAATAGTACAGGGGTAGTGCAGAGCCGATAGGGGTAATCCACCATACACTGGGTGTAATCCAGGGGCGGCTC
641    CCGCACCTGCTGTATGTGGCCTCGGGGTGCTTGGCAAAAACAGTCTGTGGGGCACAGCAATGTGTTATTGCCACCCCCC
721    GATCACCGAGGGGGGGCGCCGACAGCTTTGTAACCCAGTGTTCATCCATGTGCACCCAAACAGTTGCCAGTG
801    GGGGCCAGGTGTTGTTCAACACGAAACCGTCAATGTTGGCGCCAGCTGTATGTTGGGGCCCACTCTCTGTATA
881    GTGCCACCACCACAGCACTTGGGGTGAAGCAATAGACTGGGCCGACACTGATTTGGCTGGGACGATCCCGCAAGGCC
961    AGGGGGGTAATGCCAGCAGTAAGTCTCTCGTCCAACCCAGACCCGTTGGCGTAAGAAAATAGGGCCCCACCCTGGGCGA
1041   AGTCGGTCAGTCTTCTGCATGAGGCGAGCCTCTCAGGGCACCCGCTGGAGTTGAACTTGTGCTGGTAGAAGAGCCCTGCC
1121   AGCCAGCCGGTGTGAGGGACTCGTTGCAGTTCAGGGCGGTGGAGTTGATGTGCCAGGACCCGTTGGTGTGATCAGCTG
1201   GATGTTCTGCTTTGCTCCTGGGGTGAGAAAGTCCCAAGTCCAGCTGTGGTTCTTCCAGCGGATCTCCGGTGACATGGG
1281   TCTCAGCATTCGGATCCCGGGCCCGTCGACTGCAGAGGCGCTGCATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCT
1361   GTGTGAAATTGTTATCCGCTCACAAATCCACACAAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATG
1441   AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCATTAAT
1521   GAATCGGCCAACGCGCGGGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCG
1601   GTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
1681   AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCCGCTGTGCTGGCGTTTTTCCATAGCTCC
1761   GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG
1841   TTTCCCCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCTTCCGCTTACCGGATACCTGTCCGCTTCTCCCTTC
1921   GGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGCTGTAGTTCGTTCCGCTCCAAGCTGGGCTGTG
2001   TGCACGAACCCCGCTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC
2081   TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTG
2161   GTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG
2241   TTGGTAGCTCTTGATCCGGCAAACAAACCCCGCTGGTAGCGGTGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGA
2321   AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGAT
2401   TTTGGTCATGAGATTATCAAAAAGGATCTTCCACTAGACTCTTTTAAATTAATAAATAAAGTTTTAAATCAATCTAAAGTA
2481   TATATGAGTAAACTTGGTCTGACAGTTACCAATGCCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCTGTTCA
2561   TCCATAGTTGCTGACTCCCCGTCGTGATAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
2641   ACCGCGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC
2721   CTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTG
2801   CGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTATGGCTTCATTCAGCTCCGGTTCCCA
2881   ACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTCAGAA
2961   GTAAGTGGCCCGCAGTGTATCACTCATGTTATGCGACAGCTGCATAAATCTTACTGTCTATGCTATCCGTAAGATGC
3041   TTTTCTGTGACTGGTGTACTCAACCAAGTCACTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCGCGTC
3121   AATACGGGATAAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATATTGAAAAACGTTCTTCGGGGCGAAAACCTCT
3201   CAAGGATCTTACCCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTT
3281   ACCAGCGTTTCTGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACAGGAAATGTTGAAT
3361   ACTCATACTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
3441   TTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGCTAAGAAACCATTATTATC
3521   ATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTC
  
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