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siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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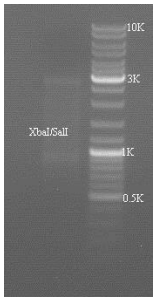
pUC-HCV E2 (subtype 1a)

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 ^{o}C.

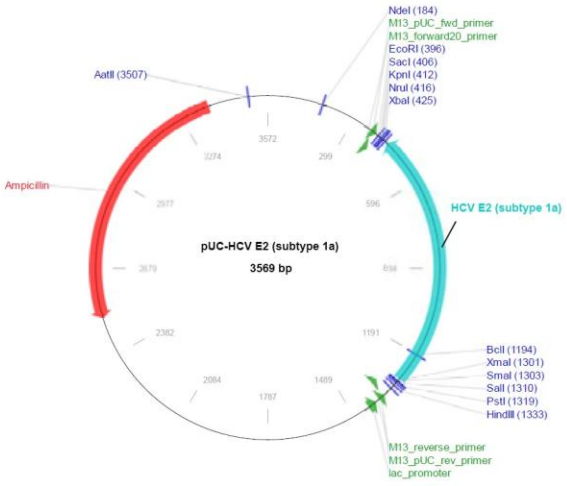
Quality Control



Restriction Enzyme Digestion:

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

Construct map:



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

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  1   AETHVTGGSA GRTTAGLVGL LTPGAKQNIQ LINTNGSWHI NSTALNCNES LNTGWLAGLF YQHKFNSSGC
 71   PERLASCRRL TDFAQGWGPI SYANGSGLDE RPYCWHYPPR PCGIVPAKSV CGPVYCFTPS PVVVGTTDRS
141   GAPTYSWGAN DTDVFVLNNT RPPLGNWFGC TWMNSTGFTK VCGAPPCVIG GVGNNTLLCP TDCFRKHPEA
211   TYSRCGSGPW ITPRCMVDYP YRLWHYPCTI NYTIFKVRMY VGGVEHRLEA ACNWTRGERC DLEDRDRSEL
281   S
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Detailed sequence of the whole construct (pUC-HCV E2 (subtype 1a)):

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1      TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
81     GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGA
161    GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC
241    ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
321    GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATT
401    CGAGCTCGGTACCTCGCGAATGCATCTAGATATCGGATCCCGTC***GCTCAGTTCGCTCCGATCCCGATCTTCCAGATCACA***
481    ***CCGCTCGCCCCGTGTCCAGTTGCAGGCGGCCTCCAGCCTGTGCTCCACGCCGCCGACGTACATGCGGACCTTAAAAATAG***
561    ***TGTAGTTAATAGTACAGGGGTAGTGCCAGAGCCGATAGGGGTAATCCACCATACACCTGGGTGTAATCCAGGGGCCGCTC***
641    ***CCGCACCTGCTGTATGTGGCCTCGGGGTGCTTGCGAAAACAGTCTGTGGGGCACAGCAATGTGTTATTGCCCACCCCCCC***
721    ***GATCACGCAGGGGGGGGCGCCGCAGACCTTTGTAAACCCAGTGCTGTTCATCCATGTGCACCCAAACCAGTTGCCCAGTG***
801    ***GGGGCCGAGTGTTGTTCAACACGAACACGTCAGTATCATTGGCGCCCCAGCTGTATGTTGGGGCCCCACTCCTGTCTGTA***
881    ***GTGCCCACCACCACAGGACTTGGGGTGAAGCAATAGACTGGGCCGCACACTGATTTGGCTGGGACGATCCCGCAAGGCCT***
961    ***AGGGGGGTAATGCCAGCAGTAAGGTCTCTCGTCCAACCCAGACCCGTTGGCGTAAGAAATAGGGCCCCACCCTTGGGCGA***
1041   ***AGTCGGTCAGTCTTCTGCATGAGGCGAGCCTCTCAGGGCACCCGCTGGAGTTGAACTTGTGCTGGTAGAAGAGCCCTGCC***
1121   ***AGCCAGCCGGTGTTGAGGGACTCGTTGCAGTTCAGGGCGGTGGAGTTGATGTGCCAGGACCCGTTGGTGTTGATCAGCTG***
1201   ***GATGTTCTGCTTTGCTCCTGGGGTGAGAAGTCCCACAAGTCCAGCTGTGGTTCTTCCAGCGGATCCTCCGGTGACATGGG***
1281   ***TCTCAGC***ATCGGATCCCGGGCCCGTCGACTGCAGAGGCCTGCATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCT
1361   GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG
1441   AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAAT
1521   GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG
1601   GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
1681   AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCC
1761   GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG
1841   TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC
1921   GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG
2001   TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC
2081   TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
2161   GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG
2241   TTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA
2321   AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT
2401   TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTA
2481   TATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCA
2561   TCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
2641   ACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC
2721   CTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTG
2801   CGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCA
2881   ACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA
2961   GTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGC
3041   TTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTC
3121   AATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT
3201   CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTC
3281   ACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAAT
3361   ACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
3441   TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATC
3521   ATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
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