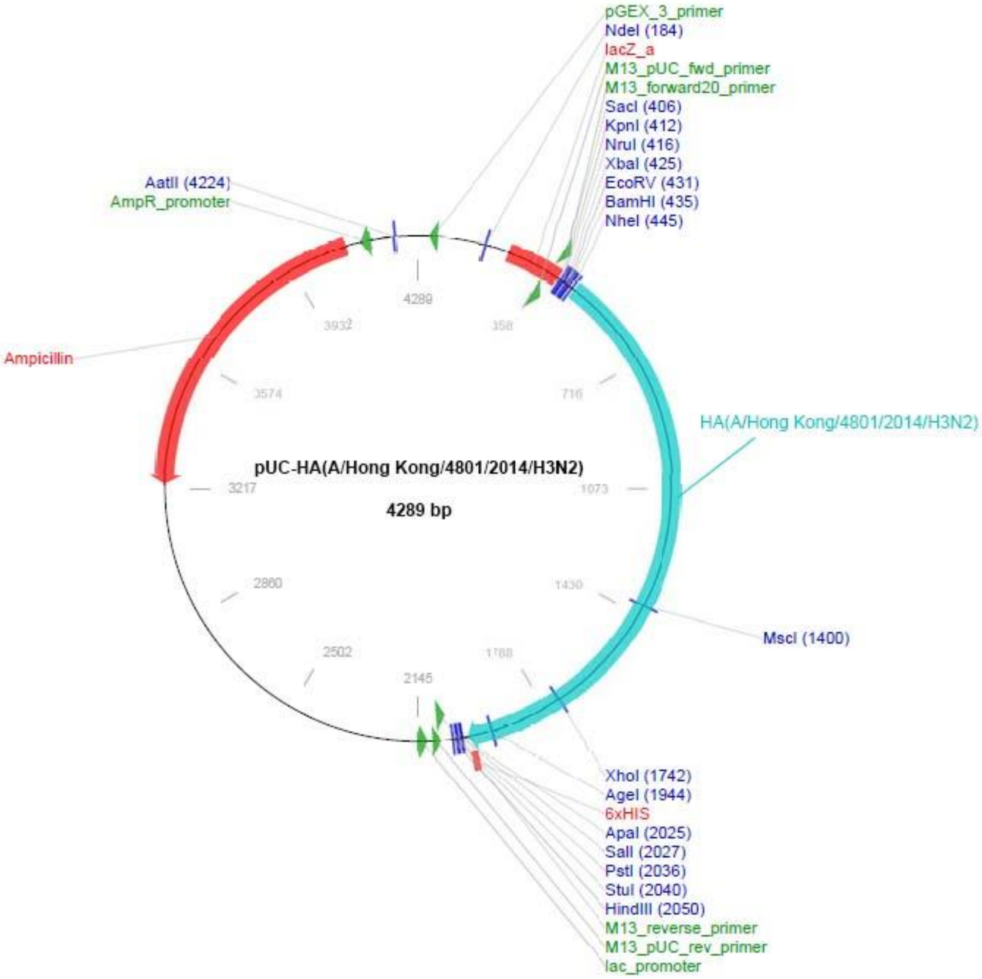
pUC-HA (A/Hong Kong/4801/2014/H3N2)

Cat# HA-HK3214

Gene Name	pUC-HA (A/Hong Kong/4801/2014/H3N2)
Gene description	Codon optimized cDNA clone of influenza A hemagglutinin (aa 17-529) (A/ Hong Kong/4801/2014)(H3N2) for high-level expression in mammalian cells
cDNA Insert Size	1509 bp codon optimized influenza A hemagglutinin (A/ Hong Kong/4801/2014)(H3N2) cDNA sequence corresponding to amino acid 17-529 (Accession# EPI653201)
Vector	pUC57
Storage	4 ºC

Construct map



Detailed sequence of the whole construct (pUC-HA(A/ Hong Kong/4801/2014/H3N2):

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   1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT
  81 GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
 161 GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC
 241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT TACGCCAGCT GGCGAAAGGG
 321 GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGAATT
 401 CGAGCTCGGT ACCTCGCGAA TGCATCTAGA TATCGGATCC CGACGCTAGC TCAAAAAATC CCCGGCAATG ACAACAGCAC
 481 TGCAACCCTC TGTCTCGGAC ATCACGCAGT CCCAAACGGA ACAATCGTGA AGACCATCAC AAACGACCGC ATCGAGGTGA
 561 CCAACGCAAC CGAGCTTGTG CAGAACTCCA GTATCGGAGA GATCTGTGAC TCCCCACACC AAATCCTCGA CGGAGAAAAC
 641 TGCACCCTTA TCGACGCTCT TCTGGGAGAC CCTCAATGTG ACGGATTCCA GAACAAGAAG TGGGACCTGT TCGTGGAGCG
 721 CTCTAAGGCT TACTCTAACT GCTACCCTTA CGACGTGCCA GACTACGCTT CCCTTAGAAG CCTCGTGGCT TCATCCGGAA
 801 CATTGGAGTT CAACAACGAG TCCTTCAACT GGACCGGGGT CACACAGAAC GGCACATCAT CTGCTTGCAT CAGAAGGTCC
 881 AGCAGCTCCT TCTTCTCCCG GTTGAACTGG CTGACCCACT TGAACTACAC GTACCCCGCT CTGAACGTGA CCATGCCAAA
 961 CAACGAGCAG TTCGACAAGC TGTACATCTG GGGGGTCCAC CATCCTGGGA CCGATAAGGA CCAGATCTTC CTGTACGCCC
1041 AGTCGTCAGG CAGAATCACT GTGTCCACCA AGAGATCCCA GCAGGCCGTG ATTCCTAACA TCGGCTCCAG ACCAAGGATC
1121 AGGGACATCC CCAGTAGGAT CAGTATCTAC TGGACCATCG TCAAGCCTGG GGACATCTTG CTGATCAACA GCACCGGGAA
1201 CTTGATCGCC CCCAGGGGCT ATTTTAAGAT CAGGAGTGGG AAGAGCAGCA TTATGAGGAG CGACGCCCCC ATTGGCAAAT
1281 GCAAGAGCGA ATGCATTACT CCCAACGGGA GCATTCCCAA CGACAAGCCC TTTCAGAACG TCAACAGGAT TACATACGGC
1361 GCCTGCCCCA GGTATGTCAA GCACAGCACA CTGAAGCTGG CCACAGGGAT GCGGAATGTG CCCGAAAAAC AGACTCGGGG
1441 GATTTTTGGC GCCATTGCCG GCTTTATCGA AAATGGCTGG GAAGGGATGG TGGATGGGTG GTATGGCTTC CGGCATCAGA
1521 ATAGCGAAGG GCGCGGCCAG GCCGCCGATC TGAAAAGCAC TCAGGCCGCC ATTGATCAGA TTAATGGAAA ACTGAACCGG
1601 CTGATTGGCA AAACAAACGA GAAATTTCAC CAGATTGAGA AAGAGTTTTC CGAGGTCGAG GGGCGGATTC AGGATCTGGA
1681 GAAGTACGTC GAGGATACTA AGATTGATCT GTGGAGCTAC AACGCCGAGC TGCTGGTGGC CCTCGAGAAC CAGCACACAA
1761 TTGATCTGAC AGATAGCGAG ATGAACAAGC TCTTTGAGAA GACTAAGAAG CAGCTCCGCG AGAACGCCGA GGATATGGGC
1841 AACGGGTGCT TTAAGATCTA CCACAAGTGC GATAACGCCT GCATTGGCTC CATTCGGAAC GGGACATACG ATCACAATGT
1921 GTACCGGGAT GAGGCCCTCA ACAACCGGTT TCAGATTAAG GGCGTCGAGC TGAAGTCCGG CTACAAGGAT CACCACCACC
2001 ACCACCACTG AGAATTCGAC GGGCCCGTCG ACTGCAGAGG CCTGCATGCA AGCTTGGCGT AATCATGGTC ATAGCTGTTT
2081 CCTGTGTGAA ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT GGGGTGCCTA
2161 ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA CCTGTCGTGC CAGCTGCATT
2241 AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC
2321 TCGGTCGTTC GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC
2401 AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
2481 TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG
2561 GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC
2641 TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT
2721 GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC
2801 GACTTATCGC CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
2881 GTGGTGGCCT AACTACGGCT ACACTAGAAG AACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAAAA
2961 GAGTTGGTAG CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGC
3041 AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG
3121 GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTTAAA TCAATCTAAA
3201 GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT
3281 TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT
3361 GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG
3441 GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT
3521 TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC
3601 CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA
3681 GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA
3761 TGCTTTTCTG TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC
3841 GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC
3921 TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT
4001 TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG
4081 AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTTGAAT
4161 GTATTTAGAA AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA AACCATTATT
4241 ATCATGACAT TAACCTATAA AAATAGGCGT ATCACGAGGC CCTTTCGTC
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Note: *HA sequence (452 bp – 2008 bp) is highlighted in yellow color*

Detailed amino acid sequence of the codon optimized cDNA clone:

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 17                     QKIP GNDNSTATLC LGHHAVPNGT IVKTITNDRI EVTNATELVQ NSSIGEICDS PHQILDGENC
 81   TLIDALLGDP QCDGFQNKKW DLFVERSKAY SNCYPYDVPD YASLRSLVAS SGTLEFNNES FNWTGVTQNG TSSACIRRSS
161   SSFFSRLNWL THLNYTYPAL NVTMPNNEQF DKLYIWGVHH PGTDKDQIFL YAQSSGRITV STKRSQQAVI PNIGSRPRIR
241   DIPSRISIYW TIVKPGDILL INSTGNLIAP RGYFKIRSGK SSIMRSDAPI GKCKSECITP NGSIPNDKPF QNVNRITYGA
321   CPRYVKHSTL KLATGMRNVP EKQTRGIFGA IAGFIENGWE GMVDGWYGFR HQNSEGRGQA ADLKSTQAAI DQINGKLNRL
401   IGKTNEKFHQ IEKEFSEVEG RIQDLEKYVE DTKIDLWSYN AELLVALENQ HTIDLTDSEM NKLFEKTKKQ LRENAEDMGN
481   GCFKIYHKCD NACIGSIRNG TYDHNVYRDE ALNNRFQIKG VELKSGYKD
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