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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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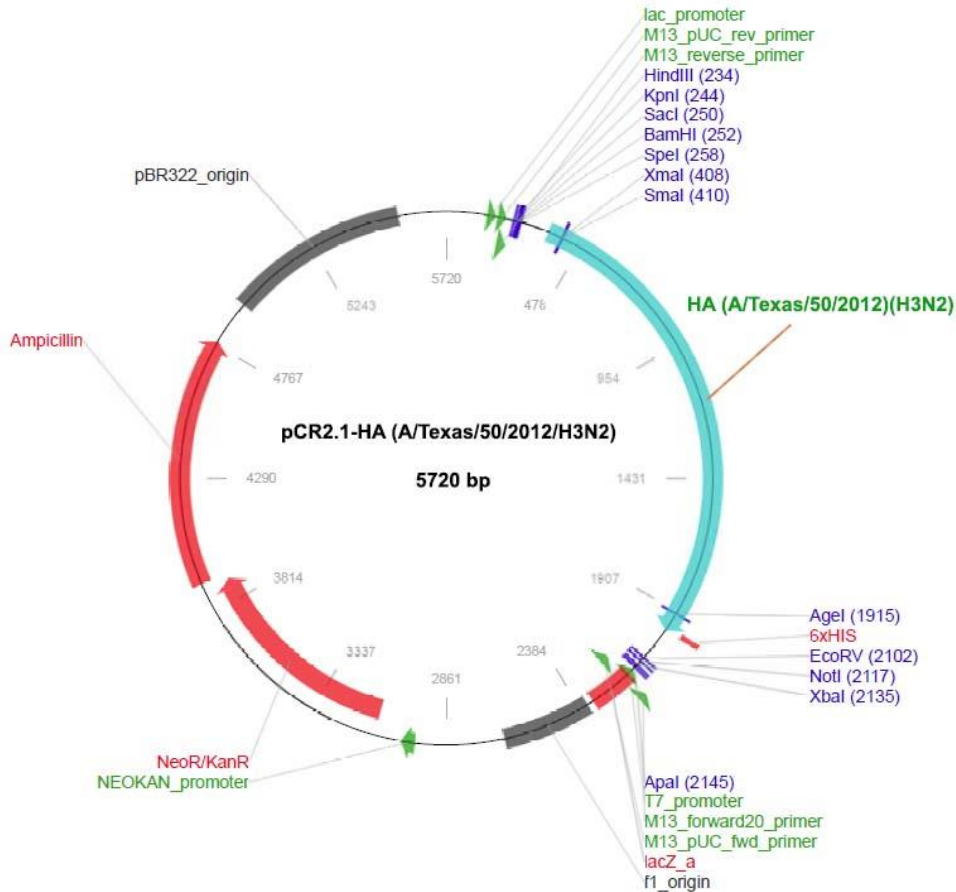
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pCR2.1-HA (A/Texas/50/2012/H3N2)

Cat# HA-T219

Gene Name	pCR2.1-HA (A/Texas/50/2012)(H3N2)
Gene description:	Codon optimized cDNA clone of influenza A hemagglutinin (aa 17-529) (A/Texas/50/2012)(H3N2) for high-level expression in mammalian cells
cDNA Insert Size	1599 bp codon optimized influenza B hemagglutinin (A/Texas/50/2012)(H3N2) cDNA with a Kozak consensus sequence(GACATGA), corresponding to amino acid 17-529 (Gene accession# AGL06219).
Vector	pCR2.1
Storage	4 °C

Construct map:



Detailed sequence of the whole construct (pCR2.1-HA (A/Texas/50/2012/H3N2):

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1   AGCGCCCAAT  ACGCAAACCG  CCTCTCCCCG  CGCGTTGGCC  GATTCATTAA  TGCAGCTGGC  ACGACAGGTT
71  TCCCGACTGG  AAAGCGGGCA  GTGAGCGCAA  CGCAATTAAT  GTGAGTTAGC  TCACTCATT  GGCACCCAG
141 GCTTTACTACT  TTATGCTTCC  GGCTCGTATG  TTGTGTGGAA  TTGTGAGCGG  ATAACAATTT  CACACAGGAA
211 ACAGCTATGA  CCATGATTAC  GCCAAGCTTG  GTACCGAGCT  CGGATCCACT  AGTAACGGCC  GCCAGTGTGC
281 TGGTAACGGC  CGCCAGTGTG  CTGGAATTCG  CCCTTTCCTT  TCCTGGGTCT  TTTCTGCAGG  CACCGTCGCC
351 GCCACCATGG  ACATGAGGGT  CCCCGCTCAG  CTCTGGGGC  TCCTGCTGCT  CTGGCTCCCC  GGGGCGCGCT
421 GTCAAAAACT  GCCC GGCAAT  GACAACAGCA  CTGCAACCCT  CTGTCTCGGA  CATCACGCAG  TCCCAAACGG
491 AACAATCGTG  AAGACCATCA  CAAACGACCG  CATCGAGGTG  ACCAACGCAA  CCGAGCTTGT  GCAGAACTCC
561 AGTATCGGAG  AGATCTGTGA  CTCCCCACAC  CAAATCCTCG  ACGGAGAAAA  CTGCACCCTT  ATCGACGCTC
631 TTCTGGGAGA  CCTCAATGT  GACGGATTCC  AGAACAAGAA  GTGGGACCTG  TTCGTGGAGC  GCTCTAAGGC
701 TTACTCTAAC  TGCTACCCTT  ACGACGTGCC  AGACTACGCT  TCCCTTAGAA  GCCTCGTGGC  TTCATCCGGA
771 ACATTGGAGT  TCAACAACGA  GTCCTTCAAC  TGGAACGGGG  TCACACAGAA  CGGCACATCA  TCTGCTTGCA
841 TCAGAAAGGTC  CAACAACCTC  TTCTTCTCCC  GGTGAACTG  GCTGACCCAC  TTGAACTTCA  AGTACCCCGC
911 TCTGAACGTG  ACCATGCCAA  ACAACGAGCA  GTTCGACAAG  CTGTACATCT  GGGGGGTCCA  CCATCCTGTG
981 ACCGATAAAG  ACCAGATCTT  CCTGTACGCC  CAGCCGTCAG  GCAGAATCAC  TGTGTCCACC  AAGAGATCCC
1051 AGCAGGCCGT  GATTCTAAC  ATCGGCTTCA  GACCAAGGAT  CAGGAACATC  CCCAGTAGGA  TCAGTATCTA
1121 CTGGACCATC  GTC AAGCCTG  GGGACATCTT  GCTGATCAAC  AGCACCGGGA  ACTTGATCGC  CCCCAGGGGC
1191 TATTTTAAGA  TCAGGAGTGG  GAAGAGCAGC  ATTATGAGGA  GCGACGCCCC  CATTGGCAAA  TGCAAGACCG
1261 AATGCATTAC  TCCCAACGGG  AGCATTTCCA  ACGAAAGCC  CTTTCAGAAC  GTC AAGAGGA  TTACATACGG
1331 CGCTTGCCCC  AGGTATGTCA  AGCAGAGCAC  ACTGAAGCTG  GCCACAGGGA  TCGGGAATGT  GCCC GAAAAA
1401 CAGACTGCGG  GGATTTTGG  CGCCATTGCC  GGCTTTATCG  AAAATGGCTG  GGAAGGGATG  GTGGATGGGT
1471 GGTATGGCTT  CCGGCATCAG  AATAGCGAAG  GGCGCGGCCA  GGCCGCCGAT  CTGAAAAGCA  CTCAGGCCGC
1541 CATTGATCAG  ATTAATGGGA  AACTGAACCG  GCTGATTTGG  AAAACAAACG  AGAAATTTCA  CCAGATTGAG
1611 AAAGAGTTTT  CCGAGGTCTG  GGGGCGGATT  CAGGATCTGG  AGAAGTACGT  CGAGGATACT  AAGATTGATC
1681 TGTGGAGCTA  CAACGCCGAG  CTGCTGGTGG  CCCTCGAGAA  CCAGCACACA  ATTGATCTGA  CAGATAGCGA
1751 GATGAACAAG  CTCTTTGAGA  AGACTAAGAA  GCAGCTCCGC  GAGAACGCCG  AGGATATGGG  CAACGGGTGC
1821 TTTAAGATCT  ACCACAAGTG  CGATAACGCC  TGCATTGGCT  CCATTCGGAA  CGGGACATAC  GATCACGATG
1891 TGTACCGGGA  TGAGGCCCTC  AACAACCGGT  TTCAGATTAA  GGGCGTCGAG  CTGAAGTCCG  GCTACAAGGA
1961 TCACCACCAC CACCACCACT GAGAATTCAT  TGATCATTAA  TCAGCCATAC  CACATTTGTA  GAGGTTTTAC
2031 TTGCTTTAAA  AAACCTCCCA  CACCTCCCCC  TGAACCTGAA  ACATAAAAATG  AATAAGGGCG  AATTCTGCAG
2101 ATATCCATCA  CACTGGCGGC  CGCTCGAGCA  TGCATCTAGA  GGGCCCAATT  CGCCCTATAG  TGAGTCGTAT
2171 TACAATTAC  TGGCCGTCTG  TTTACAACGT  CGTGACTGGG  AAAACCTTGG  CGTTACCCAA  CTTAATCGCC
2241 TTGCAGCACA  TCCCCCTTTC  GCCAGCTGGC  GTAATAGCGA  AGAGGCCCGC  ACCGATCGCC  CTTCCCAACA
2311 GTTGCGCAGC  CTGAATGGCG  AATGGACGCG  CCCTGTAGCG  GCGCATTAA  CGCGGCGGGT  GTGGTGGTTA
2381 CGCGCAGCGT  GACCCTACA  CTTGCCAGCG  CCCTAGCGCC  CGCTCCTTTC  GCTTCTTTC  CTTCTTTCT
2451 CGCCACGTT  GCCGGCTTTC  CCCGTCAAGC  TCTAAATGAT  GGGCTCCCTT  TAGGGTTCCG  ATTTAGTGCT
2521 TTACCGCAC  TCGACCCCAA  AAAACTTGAT  TAGGTGATG  GTTCACGTAG  TGGGCCATCG  CCTGATAGA
2591 CGGTTTTTTC  CCTTTGACG  TTGGAGTCCA  CGTCTTTTAA  TAGTGGACTC  TTGTTCCAAA  CCTGGAACAAC
2661 ACTCAACCTT  ATCTCGGTCT  ATTCTTTTGA  TTTATAAGGG  ATTTTGCCGA  TTTGCGCCTA  TTGGTTAAAA
2731 AATGAGCTGA  TTTAACAATA  ATTTAACGCG  AATTTTAAAC  AAATTCAGGG  CGCAAGGGCT  GCTAAAGGAA
2801 GCGGAACACG  TAGAAAAGCA  GTCCGAGAAA  ACGGTGCTGA  CCCC GGATGA  ATGTCAGCTA  CTGGGCTATC
2871 TGGACAAGGG  AAAACGCAAG  CGCAAAGAGA  AAGCAGGTAG  CTTGCAGTGG  GCTTACATGG  CGATAGCTAG
2941 ACTGGGCGGT  TTTATGGACA  GCAAGCGAAC  CGGAATTGCC  AGCTGGGGCG  CCCTCTGGTA  AGGTTGGGAA
3011 GCCCTGCAA  GTAAACTGGA  TGGCTTTCTT  GCCGCCAAGG  ATCTGATGGC  GCAGGGGATC  AAGATCTGAT
3081 CAAGAGACAG  GATGAGGATC  GTTTCGCATG  ATTGAACAAG  ATGGATTGCA  CGCAGGTTCT  CCGGCCGCTT
3151 GGGTGGAGAG  GCTATTCGGC  TATGACTGGG  CACAACAGAC  AATCGGCTGC  TCTGATGCCG  CCGTGTTCG
3221 GCTGTCAGCG  CAGGGGCGCC  CGGTTCTTTT  TGTC AAGACC  GACCTGTCCG  GTGCCCTGAA  TGAAGTGCAG
3291 GACGAGGCAG  CGCGGCTATC  GTGGCTGGCC  ACGACGGGCG  TTCCTTGCGC  AGCTGTGCTC  GACGTTGTCA
3361 CTGAAGCGGG  AAGGGACTGG  CTGCTATTGG  GCGAAGTGCC  GGGGCAGGAT  CTCCTGTGAT  CCCACCTTGC
3431 TCCTGCCGAG  AAAGTATCCA  TCATGGCTGA  TGCAATGCGG  CGGCTGCATA  CGCTTGATCC  GGCTACCTGC
3501 CCATTCGACC  ACCAAGCGAA  ACATCGCATC  GAGCGAGCAC  GACTCGGAT  GGAAGCCGGT  CTTGTGATC
3571 AGGATGATCT  GGACGAAGAG  CATCAGGGGC  TCGCGCCAGC  CGAACTGTT  GCCAGGCTCA  AGGCGCGCAT
3641 GCCCGACGGC  GAGGATCTCG  TCGTGACCCA  TGGCGATGCC  TGCTTGCCGA  ATATCATGGT  GGAAAATGGC
3711 CGCTTTTCTG  GATTCATCGA  CTGTGGCCGG  CTGGGTGTGC  CGGACCGCTA  TCAGGACATA  GCGTTGGCTA
3781 CCCGTGATAT  TGCTGAAGAG  CTTGGCGGCG  AATGGGCTGA  CCGCTTCTC  GTGCTTTACG  GTATCGCCGC

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3851 TCCCGATTTCG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT GAATTGAAAA AGGAAGAGTA
3921 TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCCTTCTG TTTTTGCTCA
3991 CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG
4061 GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA
4131 AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA
4201 CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA
4271 AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG
4341 GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA
4411 ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG
4481 TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG
4551 CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG
4621 AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA
4691 GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCTT
4761 CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACCTCA
4831 TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAATCCC TTAACGTGAG
4901 TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC
4971 GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT
5041 ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTTCT TCTAGTGTA
5111 CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC
5181 CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA
5251 GGCGCAGCGG TCGGGCTGAA CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
5321 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC
5391 CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA
5461 TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG GGGGCGGAGC
5531 CTATGAAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT
5601 TCTTCTCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG
5671 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG

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Note: signal peptide (361 bp -422 bp) is highlighted in green color; HA sequence (423 bp – 1961 bp) is highlighted in yellow color.

Detailed amino acid sequence of the codon optimized cDNA clone:

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1 MRVPAQLLGL LLLWLPGARC QKLPGNDNST ATLCGLHHAV PNGTIVKTIT NDRIEVTNAT ELVQNSSIGE
71 ICDSPHQILD GENCTLIDAL LGDPQCDGFQ NKKWDLFVER SKAYSNCYPY DVPDYASLRS LVASSGTLEF
141 NNESFNWNGV TQNGTSSACI RRSNNSFFSR LNWLTHLNFK YPALNVTMPN NEQFDKLYIW GVHHPVTDKD
211 QIFLYAQPSG RITVSTKRSQ QAVIPNIGFR PRIRNIPSRI SIYWTIVKPG DILLINSTGN LIAPRGYFKI
281 RSGKSSIMRS DAPIGKCKSE CITPNGSIPN DKPFQNVNRI TYGACPRYVK QSTLKLATGM RNVPEKQTRG
351 IFGAIAGFIE NGWEGMVDGW YGFRHQNSEG RGQAADLKST QAAIDQINGK LNRLIGKTNE KFHQIEKEFS
421 EVEGRIQDLE KYVEDTKIDL WSYNAELLVA LENQHTIDLT DSEMKNLFEK TKKQLRENAE DMGNCGFKIY
491 HKCDNACIGS IRNGTYDHDV YRDEALNNRF QIKGVELKSG YKDHSHHHH

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