# pUC-GP (Zarie Eboalvirus 2014)

## Cat# ZEB-GP347

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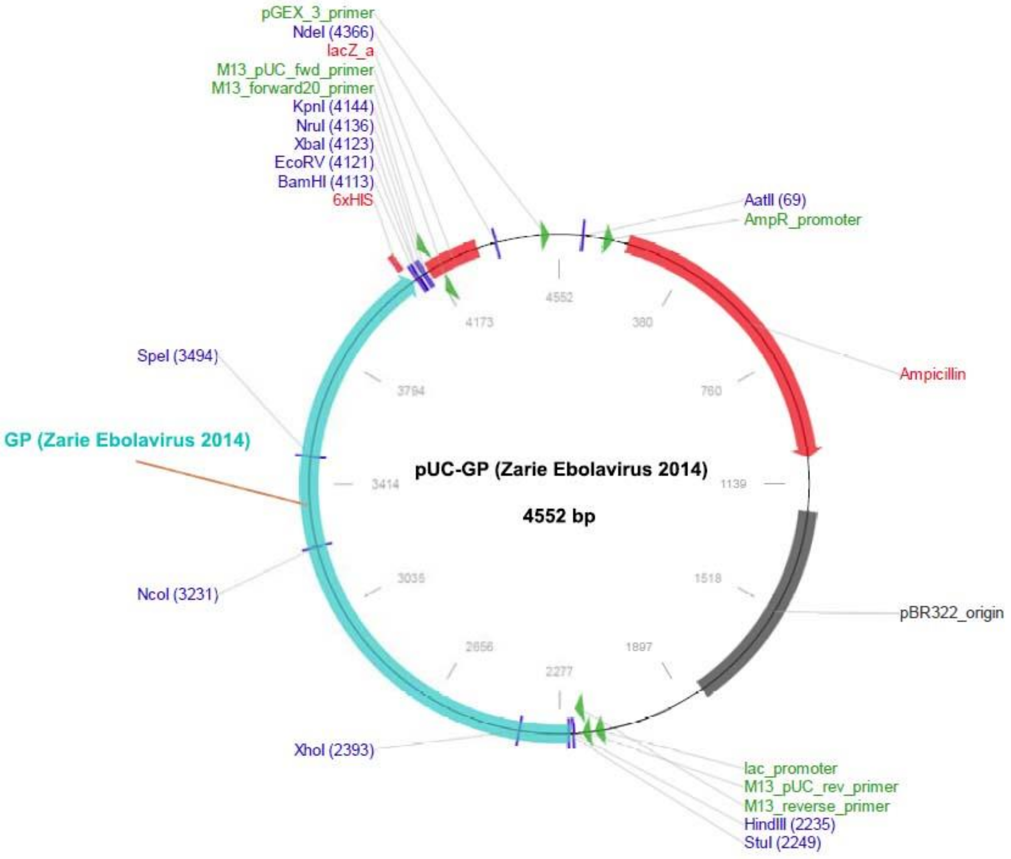
| **Gene Name** | pUC-GP (Zarie Ebolavirus 2014) |
| **Gene description:** | Codon optimized cDNA clone of Zarie Ebolavirus Glycoprotein (isolate H.sapiens wt/GIN/2014/Gueckedou-C07) for high-level expression in mammalian cells |
| **cDNA Insert Size** | 1800 bp codon optimized Zarie Ebolavirus GP (isolate H.sapiens wt/GIN/2014/Gueckedou-C07) cDNA sequence corresponding to amino acid 33-632 (Genebank No. KJ660347) |
| **Vector** | pUC57 |
| **Amount** | 10 µl (300 ng) |
| **Storage** | 4 °C |

## Construct map:



## Detailed sequence of the whole construct (pUC-NP (Zarie Ebolavirus 2014):

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   1 GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT
  81 TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA
 161 ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT
 241 TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA
 321 CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
 401 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC
 481 ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA
 561 TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC
 641 CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG
 721 ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT
 801 TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG
 881 GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT
 961 CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC
1041 TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT TTAAAACTTC ATTTTTAATT
1121 TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT
1201 CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA
1281 CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC
1361 GCAGATACCA AATACTGTTC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC
1441 TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG
1521 TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
1601 ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG
1681 GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC
1761 CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT
1841 TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA
1921 TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA
2001 GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA ATGCAGCTGG CACGACAGGT TTCCCGACTG
2081 GAAAGCGGGC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC
2161 CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTT
2241 GCATGCAGGC CTCTGCAGTC GACGGGCCCG ACGCGCGCTG TATCCCTCTG GGAGTCATCC ATAACTCCAC CCTGCAGGTG
2321 TCCGATGTGG ATAAGCTCGT GTGCAGAGAC AAGCTCTCCT CCACCAACCA GCTGAGAAGC GTGGGACTCA ACCTCGAGGG
2401 AAACGGAGTG GCAACTGACG TGCCTTCCGC TACTAAGAGA TGGGGATTCC GGTCCGGAGT GCCTCCTAAA GTGGTGAACT
2481 ACGAGGCTGG AGAATGGGCA GAGAACTGCT ACAACCTGGA GATCAAGAAG CCCGACGGGT CCGAGTGCCT CCCTGCAGCA
2561 CCTGATGGCA TTAGAGGATT CCCTAGGTGC AGGTACGTGC ATAAGGTGAG CGGAACTGGC CCTTGTGCAG GGGATTTCGC
2641 ATTCCATAAG GAGGGGGCCT TCTTCCTCTA CGACAGGCTT GCTTCCACTG TGATCTACCG GGGGACAACC TTCGCTGAGG
2721 GCGTGGTGGC TTTTCTTATC CTGCCACAGG CTAAGAAGGA CTTCTTCTCC TCCCACCCAC TGAGGGAGCC AGTGAACGCT
2801 ACCGAAGACC CATCTTCTGG CTACTACTCC ACCACAATCC GCTACCAGGC TACCGGCTTC GGGACAAACG AGACCGAATA
2881 CCTGTTCGAG GTCGACAACC TGACCTACGT CCAGCTGGAG TCCAGGTTCA CCCCACAGTT TCTCCTCCAG CTTAACGAGA
2961 CCATCTACGC CAGCGGGAAG AGGTCTAACA CCACAGGCAA GCTGATCTGG AAGGTCAACC CCGAGATCGA CACCACAATC
3041 GGGGAGTGGG CTTTTTGGGA GACCAAGAAG AACCTGACCC GGAAGATCCG GTCCGAGGAG CTTAGCTTTA CCGCCGTCTC
3121 TAACGGCCCC AAGAACATCA GCGGCCAGTC TCCAGCTAGG ACATCAAGCG ACCCAGAGAC AAACACCACA AACGAGGACC
3201 ACAAGATCAT GGCCAGCGAG AACAGCAGCG CCATGGTCCA GGTGCATAGC CAGGGGAGGA AAGCCGCCGT CTCACACCTT
3281 ACAACATTGG CCACAATCTC CACCTCACCA CAGTCCTTGA CCACCAAGCC TGGGCCAGAT AACTCAACCC ACAACACCCC
3361 CGTGTACAAG CTGGACATCA GCGAGGCCAC ACAAGTCGGC CAACACCACA GAAGGGCCGA TAATGACAGC ACCGCCAGTG
3441 ATACACCCCC CGCCACAACA GCCGCCGGGC CCTTGAAAGC CGAAAATACA AATACTAGTA AGAGTGCCGA CAGTTTGGAC
3521 CTGGCCACTA CCACAAGTCC CCAGAACTAC AGCGAGACCG CCGGGAATAA CAACACTCAC CATCAGGACA CAGGGGAAGA
3601 GAGCGCCAGC AGCGGGAAAT TGGGCTTGAT CACTAACACT ATCGCCGGGG TCGCCGGCTT GATTACAGGG GGCAGGCGGA
3681 CACGCCGCGA AGTCATTGTG AACGCCCAGC CCAAATGTAA CCCCAACCTG CACTATTGGA CTACACAGGA TGAAGGCGCC
3761 GCCATTGGGC TGGCCTGGAT TCCCTATTTT GGCCCCGCCG CCGAGGGGAT CTACACAGAG GGCCTGATGC ACAACCAGGA
3841 TGGGCTGATT TGCGGCCTGC GGCAGCTGGC CAACGAGACT ACTCAGGCCC TGCAGCTCTT TCTGCGGGCC ACTACTGAGC
3921 TCCGGACTTT TAGCATTCTC AACCGGAAAG CCATTGATTT TCTCCTGCAG CGGTGGGGGG GCACTTGCCA CATTCTGGGC
4001 CCCGATTGCT GCATTGAGCC CCACGATTGG ACAAAGAACA TTACAGATAA GATTGATCAG ATTATTCACG ATTTTGTCGA
4081 CCACCATCAC CATCACCATT GAGAATTCGA CGGGATCCGA TATCTAGATG CATTCGCGAG GTACCGAGCT CGAATTCACT
4161 GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT TGCAGCACAT CCCCCTTTCG
4241 CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCCTG
4321 ATGCGGTATT TTCTCCTTAC GCATCTGTGC GGTATTTCAC ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC
4401 CGCATAGTTA AGCCAGCCCC GACACCCGCC AACACCCGCT GACGCGCCCT GACGGGCTTG TCTGCTCCCG GCATCCGCTT
4481 ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA GAGGTTTTCA CCGTCATCAC CGAAACGCGC GA
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***Note:*** *GP sequence (2282 bp – 4081 bp) is highlighted in yellow color*

## Detailed amino acid sequence of the codon optimized cDNA clone:

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1      IPLGVIHNST LQVSDVDKLV CRDKLSSTNQ LRSVGLNLEG NGVATDVPSA TKRWGFRSGV PPKVVNYEAG EWAENCYNLE
81     IKKPDGSECL PAAPDGIRGF PRCRYVHKVS GTGPCAGDFA FHKEGAFFLY DRLASTVIYR GTTFAEGVVA FLILPQAKKD
161    FFSSHPLREP VNATEDPSSG YYSTTIRYQA TGFGTNETEY LFEVDNLTYV QLESRFTPQF LLQLNETIYA SGKRSNTTGK
241    LIWKVNPEID TTIGEWAFWE TKKNLTRKIR SEELSFTAVS NGPKNISGQS PARTSSDPET NTTNEDHKIM ASENSSAMVQ
321    VHSQGRKAAV SHLTTLATIS TSPQSLTTKP GPDNSTHNTP VYKLDISEAT QVGQHHRRAD NDSTASDTPP ATTAAGPLKA
401    ENTNTSKSAD SLDLATTTSP QNYSETAGNN NTHHQDTGEE SASSGKLGLI TNTIAGVAGL ITGGRRTRRE VIVNAQPKCN
481    PNLHYWTTQD EGAAIGLAWI PYFGPAAEGI YTEGLMHNQD GLICGLRQLA NETTQALQLF LRATTELRTF SILNRKAIDF
561    LLQRWGGTCH ILGPDCCIEP HDWTKNITDK IDQIIHDFVD
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