pmirGLO Vector

pmirGLO Vector sequence reference points:

Base pairs 7350

SV40 late polyadenylation region 106-327

SV40 early enhancer/promoter 426-844

hRluc-neo fusion protein coding region 889-2664

Synthetic polyadenylation region 2728-2776

Beta-lactamase (Ampr) coding region 3037-3897

ColE1-derived plasmid origin of replication 4052-4088

Human phosphoglycerate kinase promoter 5094-5609

luc2 reporter gene 5645-7297

Multiple cloning region 7306-7350

..

1 CATGCAAGCT GATCCGGCTG CTAACAAAGC CCGAAAGGAA GCTGAGTTGG

51 CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG GGCGGCCGCT

101 TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA

3’-A TGTAACTACT CAAACCTG-5’ 🡨Reverse Primer

151 GAATGCAGTG AAAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT

201 TTATTTGTAA CCATTATAAG CTGCAATAAA CAAGTTAACA ACAACAATTG

251 CATTCATTTT ATGTTTCAGG TTCAGGGGGA GATGTGGGAG GTTTTTTTAA

301 GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGAATTTTA ACAAAATATT

351 AACGCTTACA ATTTCCTGAT GCGGTATTTT CTCCTTACGC ATCTGTGCGG

401 TATTTCACAC CGCATACGCG GATCTGCGCA GCACCATGGC CTGAAATAAC

451 CTCTGAAAGA GGAACTTGGT TAGGTACCTT CTGAGGCGGA AAGAACCAGC

501 TGTGGAATGT GTGTCAGTTA GGGTGTGGAA AGTCCCCAGG CTCCCCAGCA

551 GGCAGAAGTA TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCAGGTGTGG

601 AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC ATGCATCTCA

651 ATTAGTCAGC AACCATAGTC CCGCCCCTAA CTCCGCCCAT CCCGCCCCTA

701 ACTCCGCCCA GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATTTTTTT

751 TATTTATGCA GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT

801 AGTGAGGAGG CTTTTTTGGA GGCCTAGGCT TTTGCAAAAA GCTTGATTCT

851 TCTGACACAA CAGTCTCGAA CCAAAGGCTG GAGCCACCAT GGCTTCCAAG

901 GTGTACGACC CCGAGCAACG CAAACGCATG ATCACTGGGC CTCAGTGGTG

951 GGCTCGCTGC AAGCAAATGA ACGTGCTGGA CTCCTTCATC AACTACTATG

1001 ATTCCGAGAA GCACGCCGAG AACGCCGTGA TTTTTCTGCA TGGTAACGCT

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1101 TAGATGCATC ATCCCTGATC TGATCGGAAT GGGTAAGTCC GGCAAGAGCG

1151 GGAATGGCTC ATATCGCCTC CTGGATCACT ACAAGTACCT CACCGCTTGG

1201 TTCGAGCTGC TGAACCTTCC AAAGAAAATC ATCTTTGTGG GCCACGACTG

1251 GGGGGCTTGT CTGGCCTTTC ACTACTCCTA CGAGCACCAA GACAAGATCA

1301 AGGCCATCGT CCATGCTGAG AGTGTCGTGG ACGTGATCGA GTCCTGGGAC

1351 GAGTGGCCTG ACATCGAGGA GGATATCGCC CTGATCAAGA GCGAAGAGGG

1401 CGAGAAAATG GTGCTTGAGA ATAACTTCTT CGTCGAGACC ATGCTCCCAA

1451 GCAAGATCAT GCGGAAACTG GAGCCTGAGG AGTTCGCTGC CTACCTGGAG

1501 CCATTCAAGG AGAAGGGCGA GGTTAGACGG CCTACCCTCT CCTGGCCTCG

1551 CGAGATCCCT CTCGTTAAGG GAGGCAAGCC CGACGTCGTC CAGATTGTCC

1601 GCAACTACAA CGCCTACCTT CGGGCCAGCG ACGATCTGCC TAAGATGTTC

1651 ATCGAGTCCG ACCCTGGGTT CTTTTCCAAC GCTATTGTCG AGGGAGCTAA

1701 GAAGTTCCCT AACACCGAGT TCGTGAAGGT GAAGGGCCTC CACTTCAGCC

1751 AGGAGGACGC TCCAGATGAA ATGGGTAAGT ACATCAAGAG CTTCGTGGAG

1801 CGCGTGCTGA AGAACGAGCA GACCGGTGGT GGGAGCGGAG GTGGCGGATC

1851 AGGTGGCGGA GGCTCCGGAG GGATTGAACA AGATGGATTG CACGCAGGTT

1901 CTCCGGCCGC TTGGGTGGAG AGGCTATTCG GCTATGACTG GGCACAACAG

1951 ACAATCGGCT GCTCTGATGC CGCCGTGTTC CGGCTGTCAG CGCAGGGGCG

2001 CCCGGTTCTT TTTGTCAAGA CCGACCTGTC CGGTGCCCTG AATGAACTGC

2051 AGGACGAGGC AGCGCGGCTA TCGTGGCTGG CCACGACGGG CGTTCCTTGC

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2251 CCGGCTACCT GCCCATTCGA CCACCAAGCG AAACATCGCA TCGAGCGAGC

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2751 ACATCTGTGT GTTGGTTTTT TGTGTGAATC GATAGCGATA AGGATCCTCT

2801 TTGCGCTTGC GTTTTCCCTT GTCCAGATAG CCCAGTAGCT GACATTCATC

2851 CGGGGTCAGC ACCGTTTCTG CGGACTGGCT TTCTACGTAA TGGTTTCTTA

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3001 TGATAAATGC TTCAATAATA TTGAAAAAGG AAGAGTATGA GTATTCAACA

3051 TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC CTTCCTGTTT

3101 TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG

3151 GGTGCACGAG TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT

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3901 GAAATGACCG ACCAAGCGAC GCCCAACCGG TATCAGCTCA CTCAAAGGCG

3951 GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG

4001 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG

4051 CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC

4101 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT

4151 TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA

4201 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT

4251 AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT

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4551 GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT

4601 TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATTT CAAGAAGATC

4651 CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT

4701 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT

4751 TTTATAGTCC GGAAATACAG GAACGCACGC TGGATGGCCC TTCGCTGGGA

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4851 TGGCCTGTAC CCTCTGGTTG CATAGGTATT CATACGGTTA AAATTTATCA

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5651 GATGCCAAAA ACATTAAGAA GGGCCCAGCG CCATTCTACC CACTCGAAGA

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5751 TGCCCGGCAC CATCGCCTTT ACCGACGCAC ATATCGAGGT GGACATTACC

5801 TACGCCGAGT ACTTCGAGAT GAGCGTTCGG CTGGCAGAAG CTATGAAGCG

5851 CTATGGGCTG AATACAAACC ATCGGATCGT GGTGTGCAGC GAGAATAGCT

5901 TGCAGTTCTT CATGCCCGTG TTGGGTGCCC TGTTCATCGG TGTGGCTGTG

5951 GCCCCAGCTA ACGACATCTA CAACGAGCGC GAGCTGCTGA ACAGCATGGG

6001 CATCAGCCAG CCCACCGTCG TATTCGTGAG CAAGAAAGGG CTGCAAAAGA

6051 TCCTCAACGT GCAAAAGAAG CTACCGATCA TACAAAAGAT CATCATCATG

6101 GATAGCAAGA CCGACTACCA GGGCTTCCAA AGCATGTACA CCTTCGTGAC

6151 TTCCCATTTG CCACCCGGCT TCAACGAGTA CGACTTCGTG CCCGAGAGCT

6201 TCGACCGGGA CAAAACCATC GCCCTGATCA TGAACAGTAG TGGCAGTACC

6251 GGATTGCCCA AGGGCGTAGC CCTACCGCAC CGCACCGCTT GTGTCCGATT

6301 CAGTCATGCC CGCGACCCCA TCTTCGGCAA CCAGATCATC CCCGACACCG

6351 CTATCCTCAG CGTGGTGCCA TTTCACCACG GCTTCGGCAT GTTCACCACG

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6501 TGCTGGTGCC CACACTATTT AGCTTCTTCG CTAAGAGCAC TCTCATCGAC

6551 AAGTACGACC TAAGCAACTT GCACGAGATC GCCAGCGGCG GGGCGCCGCT

6601 CAGCAAGGAG GTAGGTGAGG CCGTGGCCAA ACGCTTCCAC CTACCAGGCA

6651 TCCGCCAGGG CTACGGCCTG ACAGAAACAA CCAGCGCCAT TCTGATCACC

6701 CCCGAAGGGG ACGACAAGCC TGGCGCAGTA GGCAAGGTGG TGCCCTTCTT

6751 CGAGGCTAAG GTGGTGGACT TGGACACCGG TAAGACACTG GGTGTGAACC

6801 AGCGCGGCGA GCTGTGCGTC CGTGGCCCCA TGATCATGAG CGGCTACGTT

6851 AACAACCCCG AGGCTACAAA CGCTCTCATC GACAAGGACG GCTGGCTGCA

6901 CAGCGGCGAC ATCGCCTACT GGGACGAGGA CGAGCACTTC TTCATCGTGG

6951 ACCGGCTGAA GAGCCTGATC AAATACAAGG GCTACCAGGT AGCCCCAGCC

7001 GAACTGGAGA GCATCCTGCT GCAACACCCC AACATCTTCG ACGCCGGGGT

7051 CGCCGGCCTG CCCGACGACG ATGCCGGCGA GCTGCCCGCC GCAGTCGTCG

Forward Primer

7101 TGCTGGAACA CGGTAAAACC ATGACCGAGA AGGAGATCGT GGACTATGTG

7151 GCCAGCCAGG TTACAACCGC CAAGAAGCTG CGCGGTGGTG TTGTGTTCGT

7201 GGACGAGGTG CCTAAAGGAC TGACCGGCAA GTTGGACGCC CGCAAGATCC

7251 GCGAGATTCT CATTAAGGCC AAGAAGGGCG GCAAGATCGC CGTGTAATTC

7301 TAGTTGTTTA AACGAGCTCG CTAGCCTCGA GTCTAGAGTC GACCTGCAGG