**pUCmu PCR simulation**

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limit: 13

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# pcr

| Component | Name | Size | Seguid |

|-------------|-----------------|--------|--------------------------------------|

| fw primer | 1786\_pUCmuf | 41 | lsseguid=xFUWQZICmCqYDARtFUhMd2A5XpQ |

| rv primer | 1785\_pUCmur | 41 | lsseguid=V72xyXJdD1NZmEpCSN-QVPP-Gjc |

| template | pUCmu | 1669 | cdseguid=jEg2G-c5DZWICcghJ\_xmafqcsTQ |

| pcr product | 1589bp\_PCR\_prod | 1589 | ldseguid=jt0r3vBO-L0OTR\_bhfPcoM8rFT0 |

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5GTTTTTCCATAGGCTC...CATGAGCGGATACATA3

||||||||||||||||

3gtactcgcctatgtatcaagactaggagctcgtagaattct5

5atgaatgtggcaatgagacaagaacgtttttccataggctc3

||||||||||||||||

3CAAAAAGGTATCCGAG...GTACTCGCCTATGTAT5

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Suggested program for Taq DNA polymerase.

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|95°C|95°C | |tmf:48.7

|\_\_\_\_|\_\_\_\_\_ 72°C|72°C|tmr:49.3

|3min|30s \ 55.7°C \_\_\_\_\_|\_\_\_\_|45s/kb

| | \\_\_\_\_\_\_/ 1:11|5min|GC 50%

| | 30s | |1589bp

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>1786\_pUCmuf lsseguid=xFUWQZICmCqYDARtFUhMd2A5XpQ (fw)

atgaatgtggcaatgagacaagaacgtttttccataggctc

>1785\_pUCmur lsseguid=V72xyXJdD1NZmEpCSN-QVPP-Gjc (rv)

tcttaagatgctcgaggatcagaactatgtatccgctcatg

>pUCmu cdseguid=jEg2G-c5DZWICcghJ\_xmafqcsTQ (template)

ACGCGTCGCGAGGCCATATGGGTTAACCCATGGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTCGGATATCCTCGAGACTAGTGGGCCCGTTTAAACACATGTGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCCTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATA

>1589bp\_PCR\_prod ldseguid=jt0r3vBO-L0OTR\_bhfPcoM8rFT0 (pcr product)

atgaatgtggcaatgagacaagaacgtttttccataggctcCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCCTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTcatgagcggatacatagttctgatcctcgagcatcttaaga

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**pYPKpw PCR simulation**

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limit: 13

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# pcr

| Component | Name | Size | Seguid |

|-------------|----------------|--------|--------------------------------------|

| fw primer | p577 | 29 | lsseguid=88tnRfbdPYGncA3mXDlzes3rcFQ |

| rv primer | p578 | 29 | lsseguid=\_jCx3g-OKiK1IiEOAAObuvg3tQE |

| template | pYPKpw | 5603 | cdseguid=xj7evEO4h83-RGFeHu8q15tL\_Qs |

| pcr product | 385bp\_PCR\_prod | 385 | ldseguid=2k0paIjddOVee40kQtRxzW-3ccI |

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5GTTCTGATCCTCGAGCATCTTAAGAATTC...ACTTATGAATGTGGCAATGAGACAAGAAC3

|||||||||||||||||||||||||||||

3tgaatacttacaccgttactctgttcttg5

5gttctgatcctcgagcatcttaagaattc3

|||||||||||||||||||||||||||||

3CAAGACTAGGAGCTCGTAGAATTCTTAAG...TGAATACTTACACCGTTACTCTGTTCTTG5

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Suggested program for Taq DNA polymerase.

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|95°C|95°C | |tmf:63.7

|\_\_\_\_|\_\_\_\_\_ 72°C|72°C|tmr:64.1

|3min|30s \ 58.9°C \_\_\_\_\_|\_\_\_\_|45s/kb

| | \\_\_\_\_\_\_/ 0:30|5min|GC 48%

| | 30s | |385bp

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>p577 lsseguid=88tnRfbdPYGncA3mXDlzes3rcFQ (fw)

gttctgatcctcgagcatcttaagaattc

>p578 lsseguid=\_jCx3g-OKiK1IiEOAAObuvg3tQE (rv)

gttcttgtctcattgccacattcataagt

>pYPKpw cdseguid=xj7evEO4h83-RGFeHu8q15tL\_Qs (template)

GTTCTGATCCTCGAGCATCTTAAGAATTCGTCCCACGGTTTGTCTAGAGCAGCCGACAATCTGGCCAATTTCCTGACGGGTAATTTTGATTTGCATGCCGTCCGGGTGAGTCATAGCGTCTGGTGACGTCATGCGCATGATATCTTCACAGGCGGTTTTCGCACGTACCCATGCGCTACGTTCCTGGCCCTCTTCAAACAGGCCCAGTTCGCCAATAAAATCACCCTGATTCAGATAGGAGAGGATCATTTCTTTACCCTCTTCGTCTTTGATCAGCACTGCCACAGAGCCTTTAACGATGTAGTACAGCGTTTCCGCTTTTTCACCCTGGTGAATAAGCGTGCTCTTGGATGGGTACTTATGAATGTGGCAATGAGACAAGAACCATTCGAGAGTAGGATCCGTTTGAGGTTTACCAAGTACCATAAGATCCTTAAATTTTTATTATCTAGCTAGATGATAATATTATATCAAGAATTGTACCTGAAAGCAAATAAATTTTTTATCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGGGGTAATAACTGATATAATTAAATTGAAGCTCTAATTTGTGAGTTTAGTATACATGCATTTACTTATAATACAGTTTTTTAGTTTTGCTGGCCGCATCTTCTCAAATATGCTTCCCAGCCTGCTTTTCTGTAACGTTCACCCTCTACCTTAGCATCCCTTCCCTTTGCAAATAGTCCTCTTCCAACAATAATAATGTCAGATCCTGTAGAGACCACATCATCCACGGTTCTATACTGTTGACCCAATGCGTCTCCCTTGTCATCTAAACCCACACCGGGTGTCATAATCAACCAATCGTAACCTTCATCTCTTCCACCCATGTCTCTTTGAGCAATAAAGCCGATAACAAAATCTTTGTCGCTCTTCGCAATGTCAACAGTACCCTTAGTATATTCTCCAGTAGATAGGGAGCCCTTGCATGACAATTCTGCTAACATCAAAAGGCCTCTAGGTTCCTTTGTTACTTCTTCTGCCGCCTGCTTCAAACCGCTAACAATACCTGGGCCCACCACACCGTGTGCATTCGTAATGTCTGCCCATTCTGCTATTCTGTATACACCCGCAGAGTACTGCAATTTGACTGTATTACCAATGTCAGCAAATTTTCTGTCTTCGAAGAGTAAAAAATTGTACTTGGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCTCCATGGAAAAATCAGTCAAAATATCCACATGTGTTTTTAGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAATTCCTTGGTGGTACGAACATCCAATGAAGCACACAAGTTTGTTTGCTTTTCGTGCATGATATTAAATAGCTTGGCAGCAACAGGACTAGGATGAGTAGCAGCACGTTCCTTATATGTAGCTTTCGACATGATTTATCTTCGTTTCCTGCAGGTTTTTGTTCTGTGCAGTTGGGTTAAGAATACTGGGCAATTTCATGTTTCTTCAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCCTTCCTTCGTTCTTCCTTCTGTTCGGAGATTACCGAATCAAAAAAATTTCAAAGAAACCGAAATCAAAAAAAAGAATAAAAAAAAAATGATGAATTGAATTGAAAAGCTAGCTTATCGATGATAAGCTGTCAAAGATGAGAATTAATTCCACGGACTATAGACTATACTAGATACTCCGTCTACTGTACGATACACTTCCGCTCAGGTCCTTGTCCTTTAACGAGGCCTTACCACTCTTTTGTTACTCTATTGATCCAGCTCAGCAAAGGCAGTGTGATCTAAGATTCTATCTTCGCGATGTAGTAAAACTAGCTAGACCGAGAAAGAGACTAGAAATGCAAAAGGCACTTCTACAATGGCTGCCATCATTATTATCCGATGTGACGCTGCAGCTTCTCAATGATATTCGAATACGCTTTGAGGAGATACAGCCTAATATCCGACAAACTGTTTTACAGATTTACGATCGTACTTGTTACCCATCATTGAATTTTGAACATCCGAACCTGGGAGTTTTCCCTGAAACAGATAGTATATTTGAACCTGTATAATAATATATAGTCTAGCGCTTTACGGAAGACAATGTATGTATTTCGGTTCCTGGAGAAACTATTGCATCTATTGCATAGGTAATCTTGCACGTCGCATCCCCGGTTCATTTTCTGCGTTTCCATCTTGCACTTCAATAGCATATCTTTGTTAACGAAGCATCTGTGCTTCATTTTGTAGAACAAAAATGCAACGCGAGAGCGCTAATTTTTCAAACAAAGAATCTGAGCTGCATTTTTACAGAACAGAAATGCAACGCGAAAGCGCTATTTTACCAACGAAGAATCTGTGCTTCATTTTTGTAAAACAAAAATGCAACGCGACGAGAGCGCTAATTTTTCAAACAAAGAATCTGAGCTGCATTTTTACAGAACAGAAATGCAACGCGAGAGCGCTATTTTACCAACAAAGAATCTATACTTCTTTTTTGTTCTACAAAAATGCATCCCGAGAGCGCTATTTTTCTAACAAAGCATCTTAGATTACTTTTTTTCTCCTTTGTGCGCTCTATAATGCAGTCTCTTGATAACTTTTTGCACTGTAGGTCCGTTAAGGTTAGAAGAAGGCTACTTTGGTGTCTATTTTCTCTTCCATAAAAAAAGCCTGACTCCACTTCCCGCGTTTACTGATTACTAGCGAAGCTGCGGGTGCATTTTTTCAAGATAAAGGCATCCCCGATTATATTCTATACCGATGTGGATTGCGCATACTTTGTGAACAGAAAGTGATAGCGTTGATGATTCTTCATTGGTCAGAAAATTATGAACGGTTTCTTCTATTTTGTCTCTATATACTACGTATAGGAAATGTTTACATTTTCGTATTGTTTTCGATTCACTCTATGAATAGTTCTTACTACAATTTTTTTGTCTAAAGAGTAATACTAGAGATAAACATAAAAAATGTAGAGGTCGAGTTTAGATGCAAGTTCAAGGAGCGAAAGGTGGATGGGTAGGTTATATAGGGATATAGCACAGAGATATATAGCAAAGAGATACTTTTGAGCAATGTTTGTGGAAGCGGTATTCGCAATGGGAAGCTCCACCCCGGTTGATAATCAGAAAAGCCCCAAAAACAGGAAGATTATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGCGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGGCATTGCTACAGGCATCGTGGTGTCACTCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATAGTGTATCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATAGATCCTGAGGATCGGGGTGATAAATCAGTCTGCGCCACATCGGGGGAAACAAAATGGCGCGAGATCTAAAAAAAAAGGCTCCAAAAGGAGCCTTTCGCGCTACCAGGTAACGCGCCACTCCGACGGGATTAACGAGTGCCGTAAACGACGATGGTTTTACCGTGTGCGGAGATCAG

>385bp\_PCR\_prod ldseguid=2k0paIjddOVee40kQtRxzW-3ccI (pcr product)

gttctgatcctcgagcatcttaagaattcGTCCCACGGTTTGTCTAGAGCAGCCGACAATCTGGCCAATTTCCTGACGGGTAATTTTGATTTGCATGCCGTCCGGGTGAGTCATAGCGTCTGGTGACGTCATGCGCATGATATCTTCACAGGCGGTTTTCGCACGTACCCATGCGCTACGTTCCTGGCCCTCTTCAAACAGGCCCAGTTCGCCAATAAAATCACCCTGATTCAGATAGGAGAGGATCATTTCTTTACCCTCTTCGTCTTTGATCAGCACTGCCACAGAGCCTTTAACGATGTAGTACAGCGTTTCCGCTTTTTCACCCTGGTGAATAAGCGTGCTCTTGGATGGGTacttatgaatgtggcaatgagacaagaac

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**pUCmupw assembly**

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limit: 13

topology: circular

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# Assembly

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-|385bp\_PCR\_prod|25

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| 25|1589bp\_PCR\_prod|25

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| 25-

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Detailed figure:

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gttctgatcctcgagcatcttaagaattcGTCCCACGGTTTGTCTAGAGCAGCCGACAATCTGGCCAATTTCCTGACGGGTAATTTTGATTTGCATGCCGTCCGGGTGAGTCATAGCGTCTGGTGACGTCATGCGCATGATATCTTCACAGGCGGTTTTCGCACGTACCCATGCGCTACGTTCCTGGCCCTCTTCAAACAGGCCCAGTTCGCCAATAAAATCACCCTGATTCAGATAGGAGAGGATCATTTCTTTACCCTCTTCGTCTTTGATCAGCACTGCCACAGAGCCTTTAACGATGTAGTACAGCGTTTCCGCTTTTTCACCCTGGTGAATAAGCGTGCTCTTGGATGGGTacttatgaatgtggcaatgagacaagaac

ATGAATGTGGCAATGAGACAAGAAC

atgaatgtggcaatgagacaagaacgtttttccataggctcCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCCTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTcatgagcggatacatagttctgatcctcgagcatcttaaga

GTTCTGATCCTCGAGCATCTTAAGA

```

Resulting sequence:

```

> name circular

gttctgatcctcgagcatcttaagaattcGTCCCACGGTTTGTCTAGAGCAGCCGACAATCTGGCCAATTTCCTGACGGGTAATTTTGATTTGCATGCCGTCCGGGTGAGTCATAGCGTCTGGTGACGTCATGCGCATGATATCTTCACAGGCGGTTTTCGCACGTACCCATGCGCTACGTTCCTGGCCCTCTTCAAACAGGCCCAGTTCGCCAATAAAATCACCCTGATTCAGATAGGAGAGGATCATTTCTTTACCCTCTTCGTCTTTGATCAGCACTGCCACAGAGCCTTTAACGATGTAGTACAGCGTTTCCGCTTTTTCACCCTGGTGAATAAGCGTGCTCTTGGATGGGTacttatgaatgtggcaatgagacaagaacgtttttccataggctcCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCCTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTcatgagcggatacata

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limit: 13

topology: circular

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# Assembly

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-|385bp\_PCR\_pro\_rc|25

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| 25|1589bp\_PCR\_pr\_rc|25

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| 25-

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Detailed figure:

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gttcttgtctcattgccacattcataagtACCCATCCAAGAGCACGCTTATTCACCAGGGTGAAAAAGCGGAAACGCTGTACTACATCGTTAAAGGCTCTGTGGCAGTGCTGATCAAAGACGAAGAGGGTAAAGAAATGATCCTCTCCTATCTGAATCAGGGTGATTTTATTGGCGAACTGGGCCTGTTTGAAGAGGGCCAGGAACGTAGCGCATGGGTACGTGCGAAAACCGCCTGTGAAGATATCATGCGCATGACGTCACCAGACGCTATGACTCACCCGGACGGCATGCAAATCAAAATTACCCGTCAGGAAATTGGCCAGATTGTCGGCTGCTCTAGACAAACCGTGGGACgaattcttaagatgctcgaggatcagaac

TCTTAAGATGCTCGAGGATCAGAAC

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GTTCTTGTCTCATTGCCACATTCAT

```

Resulting sequence:

```

> name circular

gttcttgtctcattgccacattcataagtACCCATCCAAGAGCACGCTTATTCACCAGGGTGAAAAAGCGGAAACGCTGTACTACATCGTTAAAGGCTCTGTGGCAGTGCTGATCAAAGACGAAGAGGGTAAAGAAATGATCCTCTCCTATCTGAATCAGGGTGATTTTATTGGCGAACTGGGCCTGTTTGAAGAGGGCCAGGAACGTAGCGCATGGGTACGTGCGAAAACCGCCTGTGAAGATATCATGCGCATGACGTCACCAGACGCTATGACTCACCCGGACGGCATGCAAATCAAAATTACCCGTCAGGAAATTGGCCAGATTGTCGGCTGCTCTAGACAAACCGTGGGACgaattcttaagatgctcgaggatcagaactatgtatccgctcatgAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAGGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGgagcctatggaaaaac

```

LOCUS pUCmupw 1924 bp DNA circular 03-JUN-2025

DEFINITION .

ACCESSION .

VERSION .

KEYWORDS .

SOURCE .

ORGANISM . .

COMMENT Annotated with pLannotate v1.2.2

COMMENT

COMMENT ApEinfo:methylated:1

COMMENT ApEinfo:cdseguid=VMelzsmrEmbkWKrn7\_JGg9Nt6ik

FEATURES Location/Qualifiers

CDS complement(1001..1860)

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/database="snapgene"

/identity="99.7"

/match\_length="99.9"

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/other="CDS"

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/label="AmpR (fragment)"

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/ApEinfo\_fwdcolor="#e9d024"

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/ApEinfo\_graphicformat="arrow\_data {{0 0.5 0 1 2 0 0 -1 0

-0.5} {0 .5 .1 .5 .1 -.5 0 -.5} 0} width 5 offset 0"

promoter complement(1861..1924)

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rep\_origin complement(389..977)

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/ApEinfo\_graphicformat="arrow\_data {{0 0.5 0 1 2 0 0 -1 0

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CDS complement(join(1910..1924,1..384))

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/ApEinfo\_fwdcolor="#e9d024"

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-0.5} {0 .5 .1 .5 .1 -.5 0 -.5} 0} width 5 offset 0"

ncRNA 832..936

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/ApEinfo\_graphicformat="arrow\_data {{0 0.5 0 1 2 0 0 -1 0

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61 ctggccaatt tcctgacggg taattttgat ttgcatgccg tccgggtgag tcatagcgtc

121 tggtgacgtc atgcgcatga tatcttcaca ggcggttttc gcacgtaccc atgcgctacg

181 ttcctggccc tcttcaaaca ggcccagttc gccaataaaa tcaccctgat tcagatagga

241 gaggatcatt tctttaccct cttcgtcttt gatcagcact gccacagagc ctttaacgat

301 gtagtacagc gtttccgctt tttcaccctg gtgaataagc gtgctcttgg atgggtactt

361 atgaatgtgg caatgagaca agaacgtttt tccataggct ccgcccccct gacgagcatc

421 acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg

481 cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat

541 acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt

601 atctcagttc ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa ccccccgttc

661 agcccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg

721 acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg

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841 gtatctgcgc tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg

901 gcaaacaaac caccgctggt agcggtggtt tttttgtttg caagcagcag attacgcgca

961 gaaaaaaagg atctcaagaa gatcctttga tcttttctac taccaatgct taatcagtga

1021 ggcacctatc tcagcgatct gtctatttcg ttcatccata gttgcctgac tccccgtcgt

1081 gtagataact acgatacggg agggcttacc atctggcccc agtgctgcaa tgataccgcg

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1201 gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag tctattaatt gttgccggga

1261 agctagagta agtagttcgc cagttaatag tttgcgcaac gttgttgcca ttgctacagg

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1501 taattctcct actgtcatgc catccgtaag atgcttttct gtgactggtg agtactcaac

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1801 aggaaggcaa aatgccgcaa aaaagggaat aagggcgaca cggaaatgtt gaatactcat

1861 actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata

1921 cata

//

Uma imagem com diagrama, captura de ecrã, texto, Gráfico

Os conteúdos gerados por IA podem estar incorretos.

**pUCmupw**

**PCR simulations for plasmid identity**

**pUCmupw PCR simulation**

| Component   | Name           | Size   | Seguid                               |

|-------------|----------------|--------|--------------------------------------|

| fw primer   | 577            | 29     | lsseguid=88tnRfbdPYGncA3mXDlzes3rcFQ |

| rv primer   | 461            | 29     | lsseguid=gbK1-SUgatJgfJhi5sCybhg0YUU |

| template    | pUCmupw        | 1924   | ldseguid=UL4ttTXmJBuIJrqK-ycfsvtPQDA |

| pcr product | 776bp\_PCR\_prod | 776    | ldseguid=OoPIcFRk7\_0RhRf3K6MikwvY9Zo |

```

5gttctgatcctcgagcatcttaagaattc...gtaacaggattagcagagcgaggtatgta3

                                 |||||||||||||||||||||||||||||

                                3CATTGTCCTAATCGTCTCGCTCCATACAT5

5gttctgatcctcgagcatcttaagaattc3

 |||||||||||||||||||||||||||||

3caagactaggagctcgtagaattcttaag...cattgtcctaatcgtctcgctccatacat5

```

Suggested program for Taq DNA polymerase.

```

|95°C|95°C               |    |tmf:63.7

|\_\_\_\_|\_\_\_\_\_          72°C|72°C|tmr:65.9

|3min|30s  \ 60.8°C \_\_\_\_\_|\_\_\_\_|45s/kb

|    |      \\_\_\_\_\_\_/ 0:34|5min|GC 53%

|    |       30s         |    |776bp

```

**pYPKpw PCR simulation**

| Component   | Name            | Size   | Seguid                               |

|-------------|-----------------|--------|--------------------------------------|

| fw primer   | 577             | 29     | lsseguid=88tnRfbdPYGncA3mXDlzes3rcFQ |

| rv primer   | 461             | 29     | lsseguid=gbK1-SUgatJgfJhi5sCybhg0YUU |

| template    | pYPKpw          | 5603   | ldseguid=ll40AVxWtuevkihH0ihR007E8Fk |

| pcr product | 1179bp\_PCR\_prod | 1179   | ldseguid=uFE6DzKHbI7OM9r0YTf\_XQ0MXjA |

```

5GTTCTGATCCTCGAGCATCTTAAGAATTC...GTAACAGGATTAGCAGAGCGAGGTATGTA3

                                 |||||||||||||||||||||||||||||

                                3CATTGTCCTAATCGTCTCGCTCCATACAT5

5gttctgatcctcgagcatcttaagaattc3

 |||||||||||||||||||||||||||||

3CAAGACTAGGAGCTCGTAGAATTCTTAAG...CATTGTCCTAATCGTCTCGCTCCATACAT5

```

Suggested program for Taq DNA polymerase.

```

|95°C|95°C               |    |tmf:63.7

|\_\_\_\_|\_\_\_\_\_          72°C|72°C|tmr:65.9

|3min|30s  \ 60.3°C \_\_\_\_\_|\_\_\_\_|45s/kb

|    |      \\_\_\_\_\_\_/ 0:53|5min|GC 50%

|    |       30s         |    |1179bp