

Mycobacterium tuberculosis

NCBI

LOCUS NR_102810 1532 bp rRNA linear

>NR_102810.2 Mycobacterium tuberculosis strain H37Rv 16S ribosomal RNA, complete sequence
TGTTTGGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGA
AAGGTCTCTTCGGAGATACTCGAGTGCCGAACGGGTGAGTAACACGTGGGTGATCTGCCCTGCACTTCGG
GATAAGCCTGGGAACTGGGTCTAATACCGGATAGGACCACGGGATGCATGTCTTGTGGTGGAAAGCGCT
TTAGCGGTGTGGGATGAGCCCGCGGCTATCAGCTTGTTGGTGGGTGACGGCCTACCAAGGCGACGACG
GGTAGCCGGCCTGAGAGGGTGTCCGGCCACACTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAG
CAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCTGGGGGATGACGGCCTTCGG
GTTGTAAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGGATTGACGGTAGGTGGAGAAGAAGCA
CCGGCCAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTACTGGGCGTA
AAGAGCTCGTAGGTGGTTTGTCTCGCTTGTTCGTGAAATCTCACGGCTTAAGTGTGAGCGTGCGGGCGATA
CGGGCAGACTAGAGTACTGCAGGGGAGACTGGAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGA
GGAACACCGGTGGCGAAGGCGGGTCTCTGGGCAGTAAGTACGCTGAGGAGCGAAAGCGTGGGGAGCGAA
CAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGTACTAGGTGTGGGTTTCCTTCCTTGGGAT
CCGTGCCGTAGCTAACGCATTAAGTACCCCGCCTGGGGAGTACGGCCGCAAGGCTAAACTCAAAGGAAT
TGACGGGGGCCCCGCACAAGCGGCGGAGCATGTGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGGT
TTGACATGCACAGGACGCGTCTAGAGATAGGCGTTCCCTTGTGGCCTGTGTGCAGGTGGTGCATGGCTGT
CGTCAGCTCGTGTCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCTCATGTTGCCAGC
ACGTAATGGTGGGACTCGTGAGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCA
TCATGCCCCCTTATGTCCAGGGCTTCACACATGCTACAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGG
TTAAGCGAATCCTTAAAGCCGGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTGAAGTCGGAGT
CGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGACACACCGCCCGTCACG
TCATGAAAGTCGGTAACACCCGAAGCCAGTGGCCTAACCTCGGGAGGGAGCTGTGGAAGGTGGGATCGG
CGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCTGGATCACCTCCTTT

Primer 3 Output

No mispriming library specified
Using 1-based sequence positions
OLIGO [start](#) [len](#) [tm](#) [gc%](#) [any](#) [3' seq](#)
LEFT PRIMER 185 20 59.97 45.00 6.00 0.00 ATGCATGTCTTGTGGTGGAA
RIGHT PRIMER 368 20 59.96 50.00 6.00 0.00 GTGCAATATTCCTCCACTGCT
SEQUENCE SIZE: 1532
INCLUDED REGION SIZE: 1532

PRODUCT SIZE: 184, PAIR ANY COMPL: 6.00, PAIR 3' COMPL: 2.00

1 TGT TTGGAGAGTTT GATCCTGGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGC

61 GTCGAACGGAAGGTCTCTTCGGAGATACTCGAGTGGCGAACGGGTGAGTAACACGTGG

121 TGATCTGCCCTGCACTTCGGGATAAGCCTGGGAAACTGGGTCTAATACCGGATAGGACCA

181 CGGGATGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGATGAGCCCGCGGCCTAT
>>>>>>>>>>>>>>>>>>

241 CAGCTTGTTGGTGGGGTGACGGCCTACCAAGGCACGACGGGTAGCCGGCCTGAGAGGGT

301 GTCCGGCCACACTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAA
<<<<<<<<<<<<<<<<<<

361 TATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGGGGGATGACGGCCTTCGG
<<<<<<<<

421 GTTGTA AACCTCTTTCACCATCGACGAAGGTCCGGGTTCCTCGGATTGACGGTAGGTGG

481 AGAAGAAGCACCGGCCAACTACGTGCCAGCAGCCGCGTAATACGTAGGGTGCGAGCGTT

541 GTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGTGGTTTTGTCGCGTTGTTTCGTGAAATCT

601 CACGGCTTA ACTGTGAGCGTGCGGGCGATACGGGCAGACTAGAGTACTGCAGGGGAGACT

661 GGAATTCTCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGC

721 GGGTCTCTGGGCAGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGA

781 TACCCTGGTAGTCCACGCCGTAAACGGTGGGTACTAGGTGTGGGTTCCTTCCTTGGGAT

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841 CCGTGCCGTAGCTAACGCATTAAGTACCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAC
901 TCAAAGGAATTGACGGGGGCCCCGACAAAGCGGCGGAGCATGTGGATTAATTCGATGCAAC
961 GCGAAGAACCTTACCTGGGTTTGACATGCACAGGACGCGTCTAGAGATAGGCGTTCCTT
1021 GTGGCCTGTGTGCAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCTGTGAGATGTTGGGTTA
1081 AGTCCCGCAACGAGCGCAACCCTTGCTCATGTTGCCAGCACGTAATGGTGGGGACTCGT
1141 GAGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGCCCCCT
1201 TATGTCCAGGGCTTCACACATGCTACAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGG
1261 TTAAGCGAATCCTTAAAAGCCGGTCTCAGTTCGGATCGGGGTCTGCAACTCGACCCCGTG
1321 AAGTCGGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCT
1381 TGTACACACCGCCCGTCACGTCATGAAAGTCGGTAACACCCGAAGCCAGTGGCCTAACCC
1441 TCGGGAGGGAGCTGTCTGAAGGTGGGATCGGCGATTGGGACGAAGTCGTAACAAGGTAGCC
1501 GTACCGGAAGGTGCGGCTGGATCACCTCCTTT

```

KEYS (in order of precedence):

>>>>> left primer

<<<<< right primer

Primer Show

Paste the raw or FASTA sequence into the text area below.

```

>NR_102810.2 Mycobacterium tuberculosis strain H37Rv 16S ribosomal RNA,
complete sequence
TGTTTGGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGCGTGCCTTAACACA
TGCAAGTCGAACGGA
AAGGTCTCTCGGAGATACTCGAGTGCGCAACGGTGAGTAACACGTGGGTGATC
TGCCCTGCACCTCGG

```

Enter the patterns in the 5' to 3' direction. An example pattern is: `/ac[gt]agcct/ (My pattern's name)`. The two slashes mark the boundary of the pattern and the round brackets surround the name of the pattern. The square brackets surround possible bases at a degenerate site. You can enter multiple patterns separated by commas. Primer Show automatically constructs a reverse-complement version of each primer sequence so that matches on the reverse strand can be shown. Incorrect entry of the patterns may produce errors.

```

/GTGCAATATCCCCACTGCT/ (Right primer),
/ATGCATGCTCTGTGTGAA/ (Left primer),
/AGAGTTTGATCCTGGCTCAG/ (Forward primer),
/ACGGCTACCTTGTACGACTT/ (Reverse primer),
/attaacctcaactaag/ (T3 primer),
/cgaggtcgacggtatcg/ (KS primer),

```

SUBMIT CLEAR

- Show 60 bases per line.
- Show the translation for none
- Show the DNA sequence as single-stranded DNA.

The Sequence Manipulation Suite: Primer Show

Results for 1532 residue sequence "NR_102810.2 Mycobacterium tuberculosis strain H37Rv 16S ribosomal RNA, complete sequence" starting "TGTTTGGAGA".

```

1      AGAGTTTGATCCTGGCTCAG 3' Forward primer
1  TGTTTGGAGAGTTTGTATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAA
61  GTCGAACGGAAAGGTCTCTTCGGAGATACTCGAGTGGCGAACGGGTGAGTAACACGTGGG
121 TGATCTGCCCTGCACCTTCGGGATAAGCCTGGGAACTGGTCTAATACCGGATAGGACCA
181  ATGCATGTCTTGTGGTGGAA 3' Left primer
181 CGGGATGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGATGAGCCCCGGGCCTAT
241 CAGCTTGTGTGGGTGGGTGACGGCTACCAAGGCGACGCGGTAGCCGGCTGAGAGGGT
301  TCGTCACCCCTT
301 GTCCGGCCACACTGGGACTGAGATACGGCCAGACTCTACGGGAGGCAGAGTGGGGAA
361 ATAACGTG 5' Right primer
361 TATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCTGGGGGATGACGGCCTTCGG
421 GTTGTAACCTCTTTCACCATCGACGAAGTCCGGGTCTCTCGGATTGACGGTAGGTGG
481 AGAAGAAGCACCGGCCAACTACGTGCCAGCAGCCGCGTAATACGTAGGGTGCGAGCGTT
541 GTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGTGGTTTGTCCGCTGTTCGTGAAATCT
601 CACGGCTTAATGTGAGCGTGCAGCGATACGGGCACTAGAGTACTGACGGGGAGACT
661 GGAATTCCTGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGC
721 GGGTCTCTGGGCAGTAACGACGCTGAGGAGCGAAAGCGTGGGAGCGCAACAGGATTAGA
781 TACCCTGGTAGTCCACGCCGTAAACGGTGGGTACTAGGTGTGGGTTTCCTTCCCTGGGAT
841 CCGTGCCGTAGCTAACGCATTAAAGTACCCCGCTGGGGAGTACGGCCGCAAGGCTAAAC
901 TCAAAGGAATTGACGGGGGCCGACAAAGCGCGGAGCATGTGGATTAATTCGATGCAAC
961 GCGAAGAACCCTTACCTGGGTTTGACATGCACAGGACGCGTCTAGAGATAGGCGTCCCTT
1021 GTGGCCTGTGTGCAGTGGTGCATGGCTGTCTCAGCTCGTGTCTGAGATGTTGGGTTA
1081 AGTCCCGCAACGAGCGCAACCTTGTCTCATGTTGCCAGCACGTAATGGTGGGACTCGT
1141 GAGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGCCCTT
1201 TATGTCCAGGGCTTCACACATGCTACAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGG
1261 TTAAGCGAATCCTTAAAGCCGGTCTCAGTTCGGATCGGGTCTGCAACTCGACCCCGTG
1321 AAGTCGGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGCCT
1381 TGTACACACCCCGTCACGTCATGAAAGTCGGTAACACCCGAAGCCAGTGGCCTAACCC
1441  TTCAGCATTTGTTCCATCGG
1441 TCGGGAGGGAGCTGTCTGAAGGTGGGATCGGCGATTGGGACGAAGTCGTAACAAGGTAGCC
1501 CA 5' Reverse primer
1501 GTACCGGAAGGTGCGGCTGGATCACCTCCTTT

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	Sequência	Tamanho Amplicon	Tm	Ta
Primer Forward	AGAGTTTGATCCTGGCTCAG	8 - 1502	60°C (56°C)	56°C
Primer Reverse	ACGGCTACCTTGTTACGACTT	8 - 1502	62°C (60°C)	58°C
Right Primer	GTGCAATATTCCCCACTGCT	185 - 368	56°C (58°C)	52°C
Left Primer	ATGCATGTCTTGTGGTGGAA	185 - 368	58°C (56°C)	54°C

→ tamanho do gene que codifica o 16S ribossomal do procarioto selecionado: 1532bp

→ os primers universais apresentam homologia

Alunos:

Carolinne T. Fogagnolo

Débora Akemi Endo Colodete

Larissa Andrade

Marlon Fortes

Yurie Sato