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## Lampiran 1. Gen Pengkode Rpf-D pada *Mycobacterium tuberculosis* H37Rv


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### Mycobacterium tuberculosis H37Rv, complete genome

NCBI Reference Sequence: NC\_000962.3  
[GenBank](#) [Graphics](#)

```

>NC_000962.3:c2683712-2683248 Mycobacterium tuberculosis H37Rv, complete genome
ATGACACC6GGTTTGCTTACTACTGCGGGTGTGCGCCGACCAGTGTGACAGGTGCGCCAGGATCGTATGCA
CGGTGTTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTGGGTCTGCCACATCAAGCTC
GAAAGCCGACGACATGATTGGGACCCATCGCGCAATGCGAATCCGCGCGCAATTGGGCGCCCAACACC
GGTAACGGGTATACGGTGGTCTGCAGATCAGCCAGGCGAGCGTGGGATTCACACGGTGGTGTGCGGGTGG
CGCGCGCCGCGAGTCCCAGCAACAGATCGAGGTGCGCAGCAACATTATGAAAACCCAAAGCCGGGTGG
GTGGCCGAAATGTAGTCTTGTAGTCAAGGAGACGACCCGCTGGGCTCGCTCACCCACATCTGACGTTT
CTGCGGCCGAGACTGGAGGTTGTTGCGGGAGCAGGGACGATTGA

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**Change region shown**

- Whole sequence
- Selected region

from:  to:

[Update View](#)

**Customize view**

Display options

- Show reverse complement
- Show gap features

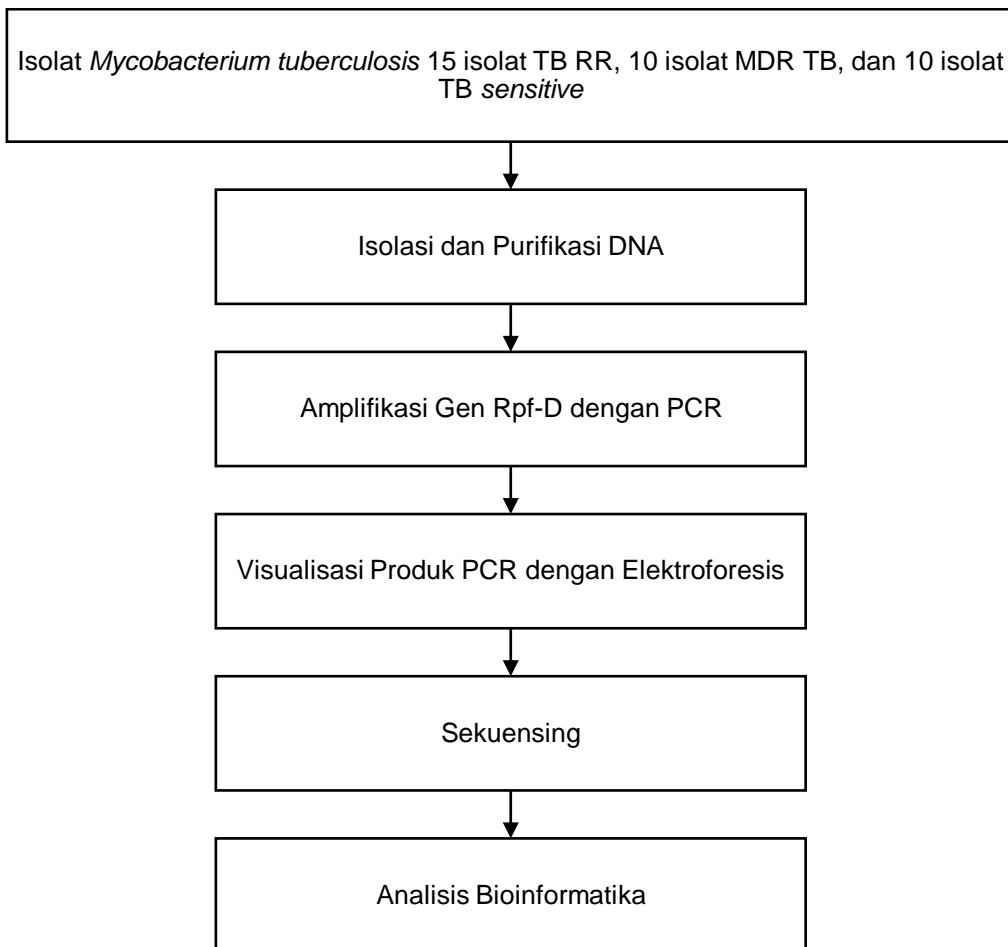
[Update View](#)

**Analyze this sequence**

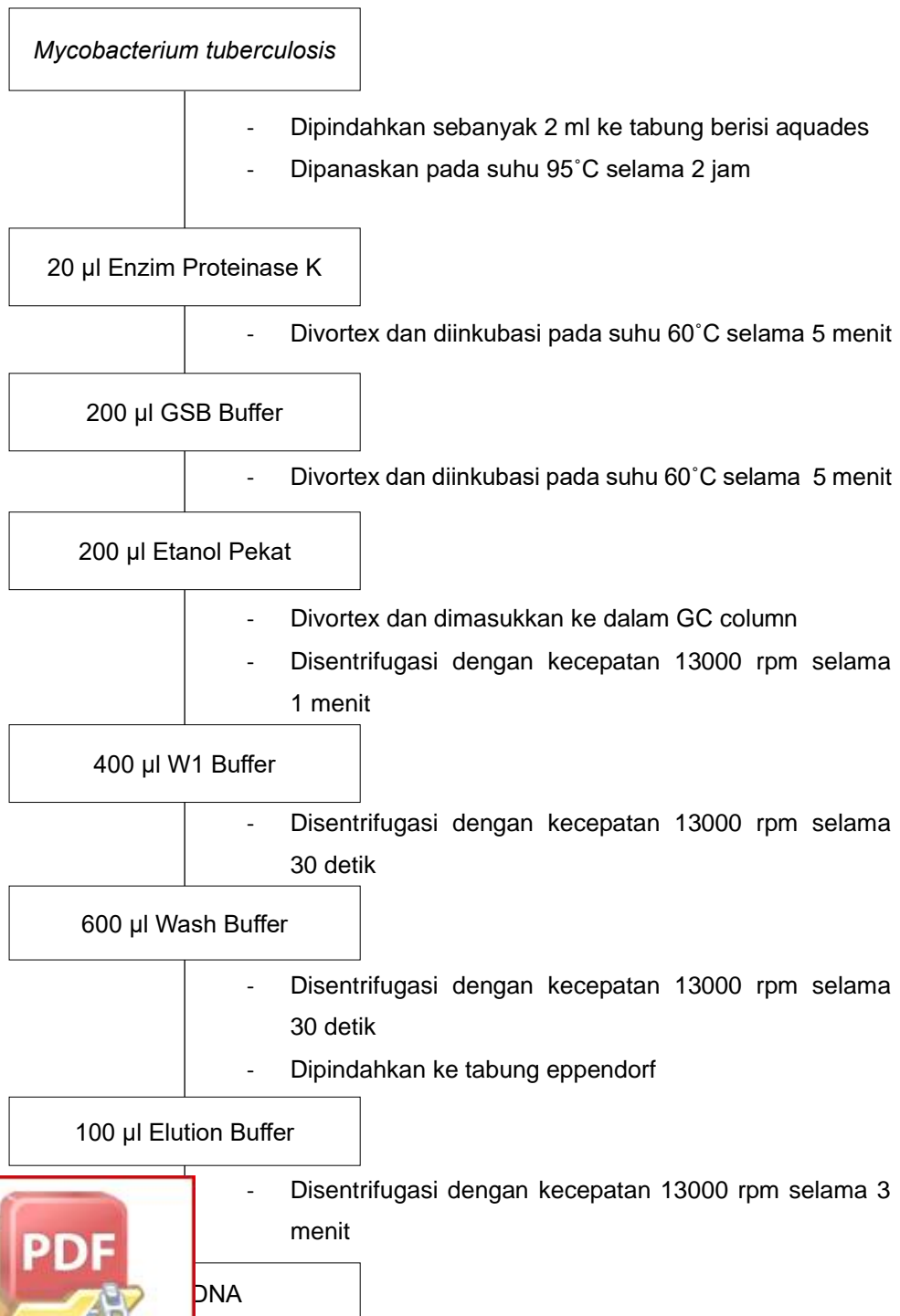
Run BLAST

[Pick Primers](#) [Activate Windows](#)

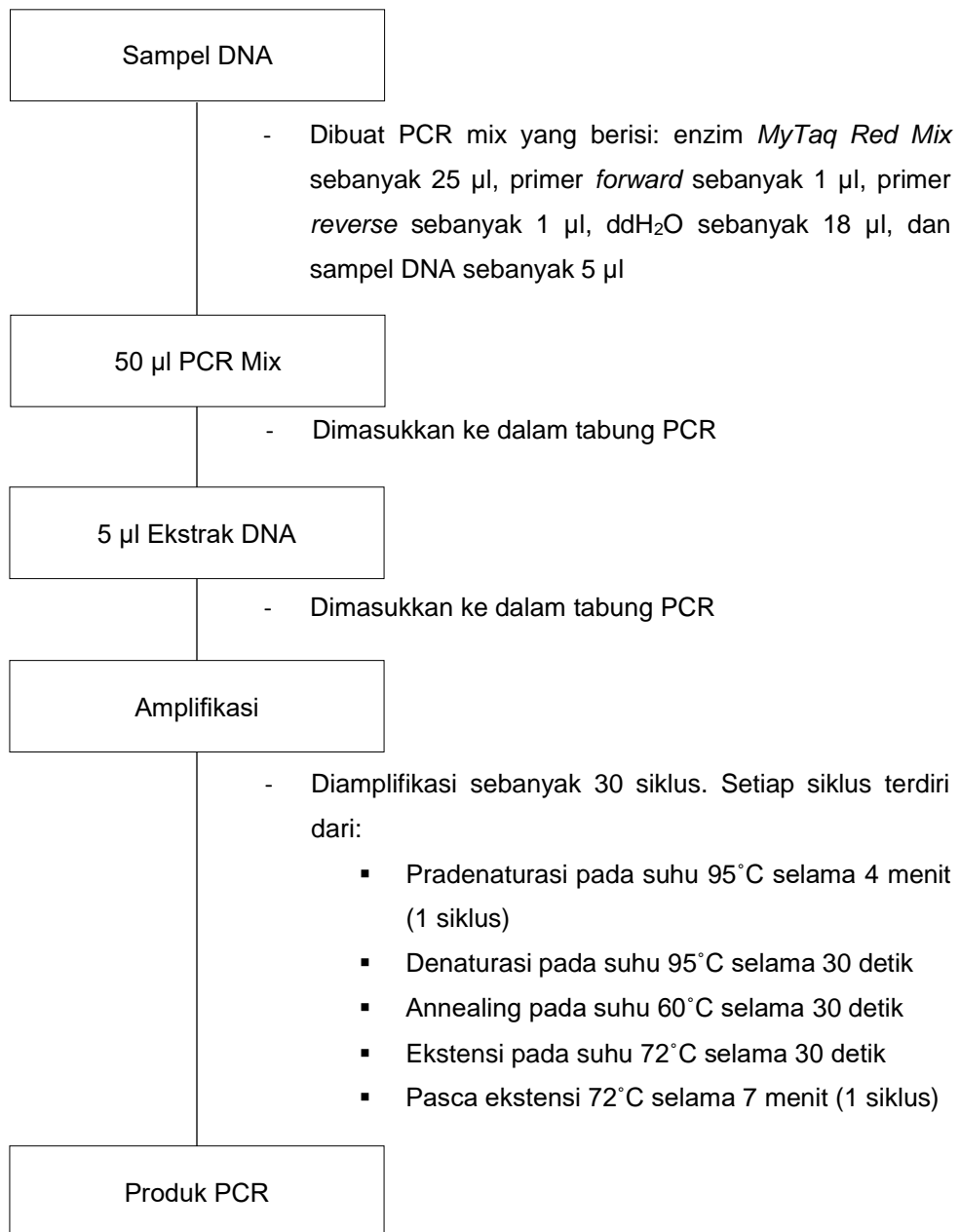


**Lampiran 2. Skema Kerja**

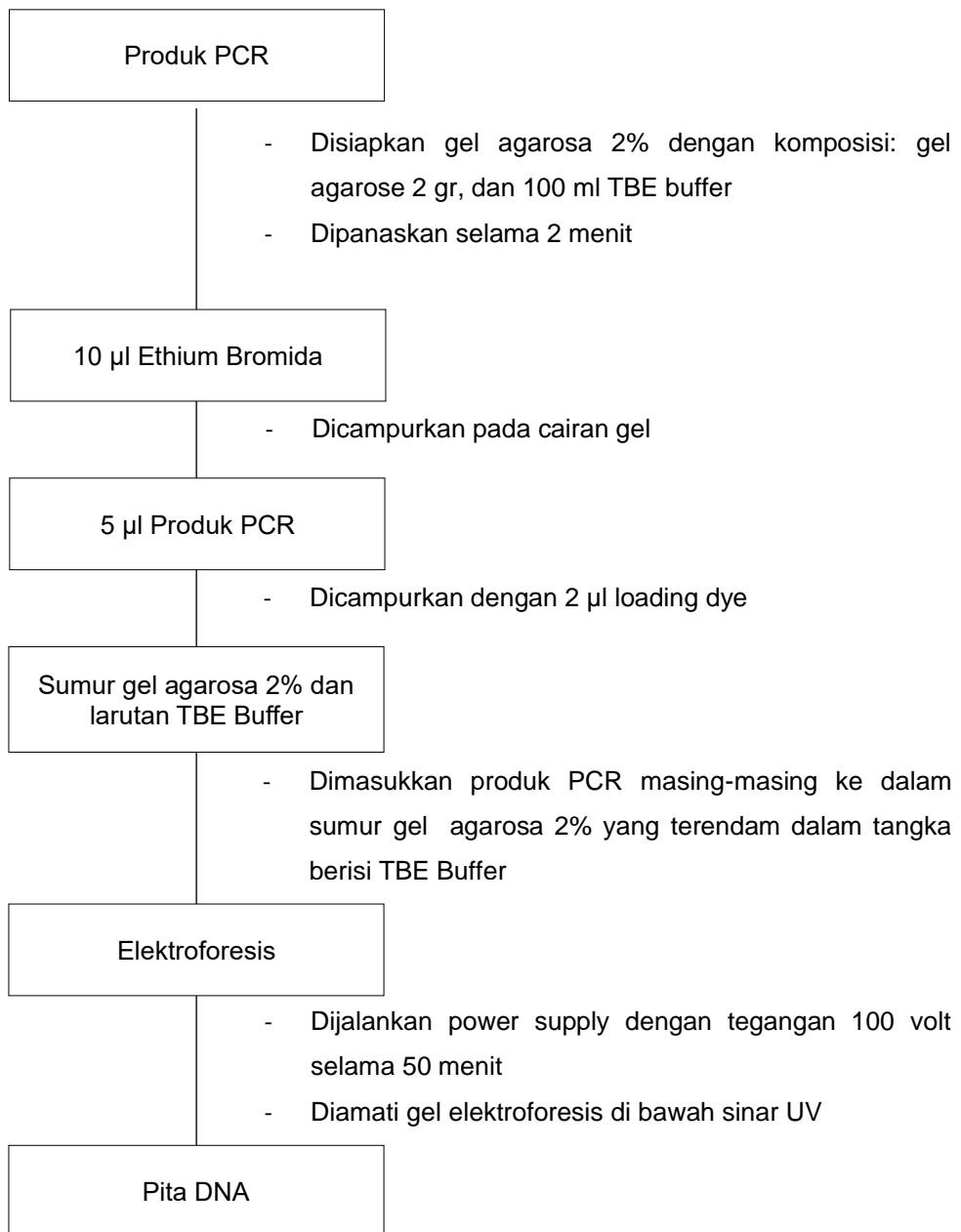
### A. Isolasi DNA *Mycobacterium tuberculosis*



## B. Amplifikasi DNA dengan PCR

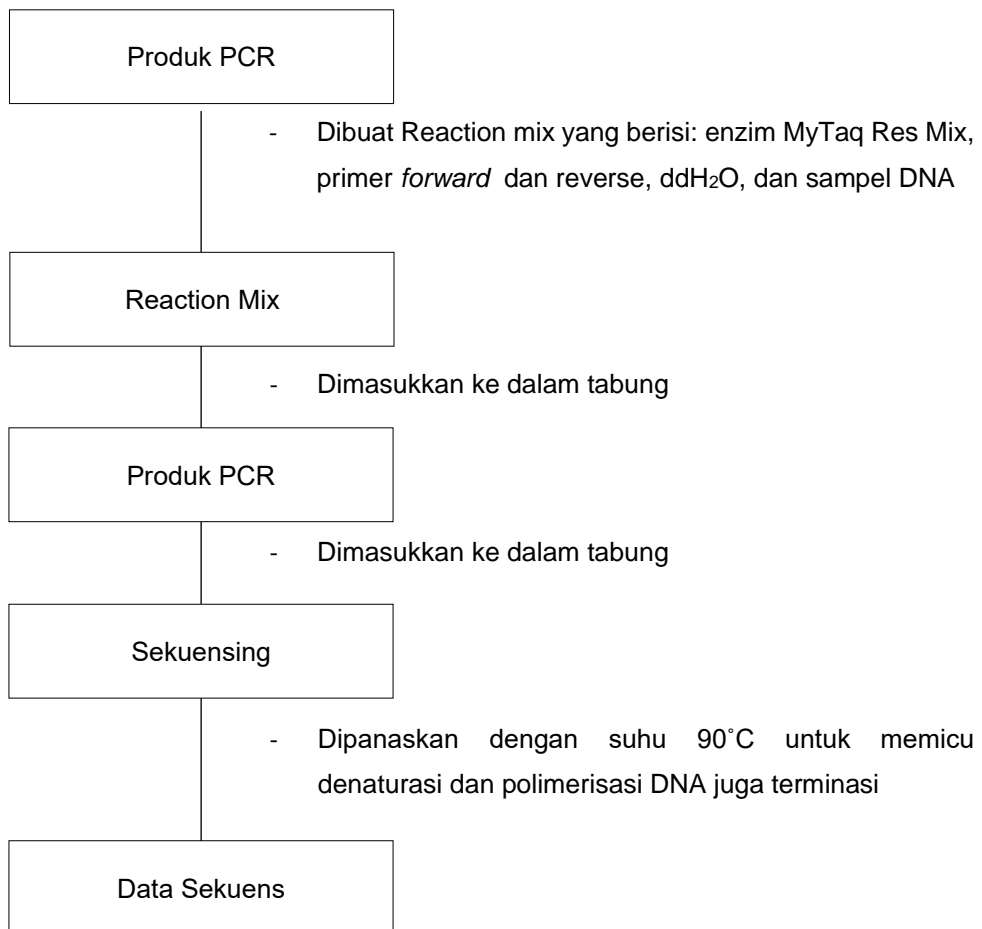


### C. Deteksi Produk PCR dengan Elektroforesis





#### D. Sekuensing Produk PCR



## Lampiran 3. Hasil Analisis BLAST

### A. Hasil BLAST Sampel A1

#### Nukleotida Kontrol

Sequence ID: **Query\_34251** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGTTTGTCTACTACTGCGGGTGTGCCCACACGTGACAGTGCGCCAGG      | 50            |           |           |
| Sbjct 1       | ATGACACCGGTTTGTCTACTACTGCGGGTGTGCCCACACGTGACAGTGCGCCAGG      | 50            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTCCGCTTGTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTCCGCTTGTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCCAAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCCAAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAAACGGGTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAAACGGGTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTCACCGTGGTGTCTGGGTCGCCGGCGGCCGGAGTCCCAG    | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTCACCGTGGTGTCTGGGTCGCCGGCGGCCGGAGTCCCAG    | 300           |           |           |
| Query 301     | CAACAGATCGAGTGCAGACAAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGTGCAGACAAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTACCCACATCTTGACGTTTC   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTACCCACATCTTGACGTTTC   | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                | 465           |           |           |

### B. Hasil BLAST Sampel A2

#### Nukleotida Kontrol

Sequence ID: **Query\_3214673** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
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| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGTTTGTCTACTACTGCGGGTGTGCCCACACGTGACAGTGCGCCAGG      | 60            |           |           |
| Sbjct 1       | ATGACACCGGTTTGTCTACTACTGCGGGTGTGCCCACACGTGACAGTGCGCCAGG      | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTCCGCTTGTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTCCGCTTGTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCCAAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCCAAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAAACGGGTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAAACGGGTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTCACCGTGGTGTCTGGGTCGCCGGCGGCCGGAGTCCCAG    | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTCACCGTGGTGTCTGGGTCGCCGGCGGCCGGAGTCCCAG    | 300           |           |           |
| Query 301     | CAACAGATCGAGTGCAGACAAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGTGCAGACAAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 421     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTACCCACATCTTGACGTTTC   | 420           |           |           |
| Sbjct 421     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTACCCACATCTTGACGTTTC   | 420           |           |           |
| Query 465     | AGCTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                          | 465           |           |           |
| Sbjct 465     | AGCTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                          | 465           |           |           |



## C. Hasil BLAST Sampel A4

### Nukleotida Kontrol

Sequence ID: **Query\_593123** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCGTTGTCCGGACCATGTTGTCGCGTTGTTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCGTTGTCCGGACCATGTTGTCGCGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTCACACGGTGGTGTCCGGTCCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTCACACGGTGGTGTCCGGTCCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGCAGACAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGCAGACAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Query 361     | TGTAGTTCTTGTAGTCAGGGAGACGCACCGTGGGTCGCTCACCCACATCTGACGTTTC   | 420           |           |           |
| Sbjct 361     | TGTAGTTCTTGTAGTCAGGGAGACGCACCGTGGGTCGCTCACCCACATCTGACGTTTC   | 420           |           |           |
| Query 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA               | 465           |           |           |
| Sbjct 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA               | 465           |           |           |

## D. Hasil BLAST Sampel A5

### Nukleotida Kontrol

Sequence ID: **Query\_3266753** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

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| Sbjct 1       | ATGACACCGGGTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
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| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCGTTGTCCGGACCATGTTGTCGCGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
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| Query 421     | TGTAGTCAGGGAGACGCACCGTGGGTCGCTCACCCACATCTGACGTTTC            | 420           |           |           |
| Sbjct 421     | TGTAGTCAGGGAGACGCACCGTGGGTCGCTCACCCACATCTGACGTTTC            | 420           |           |           |
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| Sbjct 465     | AGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                         | 465           |           |           |



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## E. Hasil BLAST Sampel A6

### Nukleotida Kontrol

Sequence ID: **Query\_926993** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
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| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 188           |           |           |
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| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAACGGGTTATACGGTGGTCTGCAGATC   | 248           |           |           |
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| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGGGTGCGCGCGCCGCGAGTCCCAG      | 308           |           |           |
| Query 301     | CAACAGATCGAGTCCGACAGCAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 368           |           |           |
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| Query 361     | TGTAGTTCTTGTAGTCAGGGAGACGCCCTGGGTCGCTCACCACATCCTGACGTTTC      | 428           |           |           |
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| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTCCGGGGAGCAGGGACGATTGA                 | 465           |           |           |

## F. Hasil BLAST Sampel A7

### Nukleotida Kontrol

Sequence ID: **Query\_9137** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
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| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTCCGCTTGTG   | 128           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 188           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 188           |           |           |
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| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAACGGGTTATACGGTGGTCTGCAGATC   | 248           |           |           |
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| Query 301     | CAACAGATCGAGTCCGACAGCAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 368           |           |           |
| Sbjct 301     | CAACAGATCGAGTCCGACAGCAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 368           |           |           |
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|               | TAGTCAGGGAGACGCCCTGGGTCGCTCACCACATCCTGACGTTTC                 | 428           |           |           |
|               | GACTGGAGGTTGTTCCGGGGAGCAGGGACGATTGA                           | 465           |           |           |
|               | GACTGGAGGTTGTTCCGGGGAGCAGGGACGATTGA                           | 465           |           |           |



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## G. Hasil BLAST Sampel A8

### Nukleotida Kontrol

Sequence ID: **Query\_914855** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACC GCCGTGTGTCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACC GCCGTGTGTCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGCTGTGCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGCTGTGCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACGACAACATTATGAAAACCC AAGGCCCGGGTGCCTGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACGACAACATTATGAAAACCC AAGGCCCGGGTGCCTGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Query 421     | CTCGCGGCCGAGACTGGAGGTTGTTGCGGGAGCAGGGACGATTGA                | 465           |           |           |
| Sbjct 421     | CTCGCGGCCGAGACTGGAGGTTGTTGCGGGAGCAGGGACGATTGA                | 465           |           |           |

## H. Hasil BLAST Sampel A9

### Nukleotida Kontrol

Sequence ID: **Query\_127129** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACC GCCGTGTGTCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACC GCCGTGTGTCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGCTGTGCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGCTGTGCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGTAAACGGTTATACGGTGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACGACAACATTATGAAAACCC AAGGCCCGGGTGCCTGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACGACAACATTATGAAAACCC AAGGCCCGGGTGCCTGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Query 421     | GACTGGAGGTTGTTGCGGGAGCAGGGACGATTGA                           | 465           |           |           |
| Sbjct 421     | GACTGGAGGTTGTTGCGGGAGCAGGGACGATTGA                           | 465           |           |           |



## I. Hasil BLAST Sampel A10

### Nukleotida Kontrol

Sequence ID: **Query\_3532067** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG    | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG    | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTGCGGTTGTTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTGCGGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCAAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCAAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTCCAACGGTGGTGTGGGTCGCCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTCCAACGGTGGTGTGGGTCGCCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGACAACATTATGAAAACCCAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGACAACATTATGAAAACCCAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCCTGGGCTCGCTCACCCACATCCTGACGTTG    | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCCTGGGCTCGCTCACCCACATCCTGACGTTG    | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                 | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                 | 465           |           |           |

## J. Hasil BLAST Sampel A11

### Nukleotida Kontrol

Sequence ID: **Query\_96379** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG    | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG    | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTGCGGTTGTTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGGACCATGTTTGTGCGGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCAAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCAAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC   | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTCCAACGGTGGTGTGGGTCGCCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTCCAACGGTGGTGTGGGTCGCCGCGGCCGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGACAACATTATGAAAACCCAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGACAACATTATGAAAACCCAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCCTGGGCTCGCTCACCCACATCCTGACGTTG    | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCCTGGGCTCGCTCACCCACATCCTGACGTTG    | 420           |           |           |
| Query 421     | GACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                           | 465           |           |           |
| Sbjct 421     | GACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                           | 465           |           |           |



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## K. Hasil BLAST Sampel A12

**Nukleotida Kontrol**  
 Sequence ID: **Query\_858043** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#) [\(Next Match\)](#) [Previous Match](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGTTTGCTTACTACTGCGGGTGTG6CCGACCACGTGACAGGTGCGCCAGG      | 68            |           |           |
| Sbjct 1       | ATGACACCGGTTTGCTTACTACTGCGGGTGTG6CCGACCACGTGACAGGTGCGCCAGG      | 68            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGCACCATGTTTGTGCGGTTGTTG     | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGCACCATGTTTGTGCGGTTGTTG     | 120           |           |           |
| Query 121     | GGTCGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC     | 180           |           |           |
| Sbjct 121     | GGTCGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC     | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCCGCGAGTCCCAG       | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCCGCGAGTCCCAG       | 300           |           |           |
| Query 301     | CAACAGATCGAGGTGCGACAGCAACATTATGAAAACCC AAGGCCCGGGTGC GTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGACAGCAACATTATGAAAACCC AAGGCCCGGGTGC GTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTTCCTTGTAGTCAGGGAGACGACCGCTGGGTCGCTCACCACATCCTGACGTTT      | 420           |           |           |
| Sbjct 361     | TGTAGTTCCTTGTAGTCAGGGAGACGACCGCTGGGTCGCTCACCACATCCTGACGTTT      | 420           |           |           |
| Query 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                  | 465           |           |           |
| Sbjct 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                  | 465           |           |           |

## L. Hasil BLAST Sampel A13

**Nukleotida Kontrol**  
 Sequence ID: **Query\_3484339** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#) [\(Next Match\)](#) [Previous Match](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGTTTGCTTACTACTGCGGGTGTG6CCGACCACGTGACAGGTGCGCCAGG      | 68            |           |           |
| Sbjct 1       | ATGACACCGGTTTGCTTACTACTGCGGGTGTG6CCGACCACGTGACAGGTGCGCCAGG      | 68            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGCACCATGTTTGTGCGGTTGTTG     | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTGCGCACCATGTTTGTGCGGTTGTTG     | 120           |           |           |
| Query 121     | GGTCGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC     | 180           |           |           |
| Sbjct 121     | GGTCGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC     | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCCGCGAGTCCCAG       | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCCGCGAGTCCCAG       | 300           |           |           |
| Query 301     | CAACAGATCGAGGTGCGACAGCAACATTATGAAAACCC AAGGCCCGGGTGC GTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGACAGCAACATTATGAAAACCC AAGGCCCGGGTGC GTGGCCGAAA | 360           |           |           |
| Query 421     | TGTAGTTCCTTGTAGTCAGGGAGACGACCGCTGGGTCGCTCACCACATCCTGACGTTT      | 420           |           |           |
| Sbjct 421     | TGTAGTTCCTTGTAGTCAGGGAGACGACCGCTGGGTCGCTCACCACATCCTGACGTTT      | 420           |           |           |
| Query 465     | GACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                             | 465           |           |           |
| Sbjct 465     | GACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA                             | 465           |           |           |



## M. Hasil BLAST Sampel B1

### Nukleotida Kontrol

Sequence ID: **Query\_47319** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

[View Map](#) [Previous Match](#)

| Score         | Expect   | Identifies    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATCCAAACGGTGGTGTGCGGTGCGCGCGGCCGCGAGTCCCAG   | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATCCAAACGGTGGTGTGCGGTGCGCGCGGCCGCGAGTCCCAG   | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCCAAAGGCCGGGTGCGTGCCGAAA  | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCCAAAGGCCGGGTGCGTGCCGAAA  | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGAGCGACCCTGGGCTCGCTCACCCACATCTGACGTTTC   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGAGCGACCCTGGGCTCGCTCACCCACATCTGACGTTTC   | 420           |           |           |
| Query 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA 465           |               |           |           |
| Sbjct 421     | CTCGCGGCCGAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA 465           |               |           |           |

## N. Hasil BLAST Sampel B2

### Nukleotida Kontrol

Sequence ID: **Query\_3448161** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

[View Map](#) [Previous Match](#)

| Score         | Expect   | Identifies    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGCGCCGACCACGTGACAGGTGCGCCAGG | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACCCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATCCAAACGGTGGTGTGCGGTGCGCGCGGCCGCGAGTCCCAG   | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATCCAAACGGTGGTGTGCGGTGCGCGCGGCCGCGAGTCCCAG   | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCCAAAGGCCGGGTGCGTGCCGAAA  | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCCAAAGGCCGGGTGCGTGCCGAAA  | 360           |           |           |
| Query 421     | TGTAGTCAGGGAGAGCGACCCTGGGCTCGCTCACCCACATCTGACGTTTC           | 420           |           |           |
| Sbjct 421     | TGTAGTCAGGGAGAGCGACCCTGGGCTCGCTCACCCACATCTGACGTTTC           | 420           |           |           |
| Query 465     | GAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA 465                    |               |           |           |
| Sbjct 465     | GAGACTGGAGGTTGTTCTGGGGAGCAGGGACGATTGA 465                    |               |           |           |



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## O. Hasil BLAST Sampel B3

### Nukleotida Kontrol

Sequence ID: **Query\_810721** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCCTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCCTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGCTTGTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGCTTGTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCGGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCGGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGTCGACAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGTCGACAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGTCGCTCACCCACATCCTGACGTTT    | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGTCGCTCACCCACATCCTGACGTTT    | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTCGGGGAGCAGGGACGATTGA                   | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTCGGGGAGCAGGGACGATTGA                   | 465           |           |           |

## P. Hasil BLAST Sampel B5

### Nukleotida Kontrol

Sequence ID: **Query\_799363** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCCTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCCTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG   | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGCTTGTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGCTTGTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC  | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCGGCGAGTCCCAG     | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACGGTGGTGTGCGGTCGCCGCGCGGCGAGTCCCAG     | 300           |           |           |
| Query 301     | CAACAGATCGAGTCGACAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGTCGACAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 421     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGTCGCTCACCCACATCCTGACGTTT    | 420           |           |           |
| Sbjct 421     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGTCGCTCACCCACATCCTGACGTTT    | 420           |           |           |
| Query 465     | GAGACTGGAGGTTGTCGGGGAGCAGGGACGATTGA                           | 465           |           |           |
| Sbjct 465     | GAGACTGGAGGTTGTCGGGGAGCAGGGACGATTGA                           | 465           |           |           |



### Q. Hasil BLAST Sampel C1

#### Nukleotida Kontrol

Sequence ID: **Query\_3406465** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGGTTACTACTGCGGGTGC TGGCCGACACGTGACAGGTGCGCCAGG | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGGTTACTACTGCGGGTGC TGGCCGACACGTGACAGGTGCGCCAGG | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCAAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCAAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTCGCCGGCGCCGCGAGTCCCAG   | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTCGCCGGCGCCGCGAGTCCCAG   | 300           |           |           |
| Query 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCGGGTGCGTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCGGGTGCGTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTTCTTGTAGTCAGGGAGACGACCCGTTGGGTCGCTACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 361     | TGTAGTTCTTGTAGTCAGGGAGACGACCCGTTGGGTCGCTACCCACATCCTGACGTTT   | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTTCCGGGAGCAGGGACGATTGA                 | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTCCGGGAGCAGGGACGATTGA                 | 465           |           |           |

### R. Hasil BLAST Sampel C2

#### Nukleotida Kontrol

Sequence ID: **Query\_3388939** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect   | Identities   | Gaps      | Strand    |
|---------------|--|--------------|-----------|-----------|
| 854 bits(462) | 0.0  | 464/465(99%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGGTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 60           |           |           |
| Sbjct 1       | ATGACACCGGGTTTGGTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 60           |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120          |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120          |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCAATTGGGACGCCATCGCGCAATGC | 180          |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCAATTGGGACGCCATCGCGCAATGC | 180          |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGCCAAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240          |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGCCAAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240          |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTCGCCGGCGCCGCGAGTCCCAG   | 300          |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTCGCCGGCGCCGCGAGTCCCAG   | 300          |           |           |
| Query 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCGGGTGCGTGGCCGAAA | 360          |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCGGGTGCGTGGCCGAAA | 360          |           |           |
| Query 421     | TGTAGTCAGGGAGACGACCCGTTGGGTCGCTACCCACATCCTGACGTTT            | 420          |           |           |
| Sbjct 421     | TGTAGTCAGGGAGACGACCCGTTGGGTCGCTACCCACATCCTGACGTTT            | 420          |           |           |
| Query 465     | TGAGACTGGAGGTTGTTCCGGGAGCAGGGACGATTGA                        | 465          |           |           |
| Sbjct 465     | TGAGACTGGAGGTTGTTCCGGGAGCAGGGACGATTGA                        | 465          |           |           |



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## S. Hasil BLAST Sampel C3

### Nukleotida Kontrol

Sequence ID: **Query\_93185** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

[Next Match](#) [Previous Match](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG  | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG  | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGGTCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGGTCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTACCCACATCCTGACGTTT   | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTTGGGGAGCAGGGACGATTGA                  | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTGGGGAGCAGGGACGATTGA                  | 465           |           |           |

## T. Hasil BLAST Sampel C4

### Nukleotida Kontrol

Sequence ID: **Query\_76685** Length: **465** Number of Matches: **1**

Range 1: 1 to 465 [Graphics](#)

[Next Match](#) [Previous Match](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 859 bits(465) | 0.0  | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG  | 60            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCTTACTACTGCGGGTGTGGCCGACCACGTGACAGGTGCGCCAGG  | 60            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTTGTCGCGACCATGTTTGTGCGGTTGTTG | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC | 180           |           |           |
| Query 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Sbjct 181     | GAATCCGGCGGCAATTGGGCGGCCAACACCGGTAACGGGTTATACGGTGGTCTGCAGATC | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGGTCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGGTCGCCGGCCGCGAGTCCCAG    | 300           |           |           |
| Query 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTCGACAGCAACATTATGAAAACCAAGGCCCGGGTGCCTGGCCGAAA  | 360           |           |           |
| Query 421     | TGTAGTCAGGGAGACGCACCGCTGGGCTCGCTACCCACATCCTGACGTTT           | 420           |           |           |
| Sbjct 421     | TGTAGTCAGGGAGACGCACCGCTGGGCTCGCTACCCACATCCTGACGTTT           | 420           |           |           |
| Query 465     | GAGACTGGAGGTTGTTGGGGAGCAGGGACGATTGA                          | 465           |           |           |
| Sbjct 465     | GAGACTGGAGGTTGTTGGGGAGCAGGGACGATTGA                          | 465           |           |           |



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## U. Hasil BLAST Sampel C5

### Nukleotida Kontrol

Sequence ID: Query\_711007 Length: 465 Number of Matches: 1

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 68            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 68            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTCGCGACCATGTTTGTCCGGTTGTTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTCGCGACCATGTTTGTCCGGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Sbjct 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCCGGCGCCGCGAGTCCCCAG  | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCCGGCGCCGCGAGTCCCCAG  | 300           |           |           |
| Query 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 361     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Query 421     | CTCGCGCCGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                 | 465           |           |           |
| Sbjct 421     | CTCGCGCCGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                 | 465           |           |           |

## V. Hasil BLAST Sampel C6

### Nukleotida Kontrol

Sequence ID: Query\_3310785 Length: 465 Number of Matches: 1

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect  | Identities    | Gaps      | Strand    |
|---------------|---|---------------|-----------|-----------|
| 859 bits(465) | 0.0   | 465/465(100%) | 0/465(0%) | Plus/Plus |
| Query 1       | ATGACACCGGGTTTGCCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 68            |           |           |
| Sbjct 1       | ATGACACCGGGTTTGCCTTACTACTGCGGGTGTGGCCGACACGTGACAGGTGCGCCAGG   | 68            |           |           |
| Query 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTCGCGACCATGTTTGTCCGGTTGTTG   | 120           |           |           |
| Sbjct 61      | ATCGTATGCACGGTGTTCATCGAAACCGCCGTGTCGCGACCATGTTTGTCCGGTTGTTG   | 120           |           |           |
| Query 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Sbjct 121     | GGTCTGTCCACCATCAGCTCGAAAGCCGACGACATCGATTGGGACGCCATCGCGCAATGC  | 180           |           |           |
| Query 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Sbjct 181     | GAATCCGGCGCAATTGGGCGCCAAACCCGGTAACGGTTATACGGTGGTCTGCAGATC     | 240           |           |           |
| Query 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCCGGCGCCGCGAGTCCCCAG  | 300           |           |           |
| Sbjct 241     | AGCCAGGCGACGTGGGATTC AACCGTGGTGTGCGGTGCGCCGGCGCCGCGAGTCCCCAG  | 300           |           |           |
| Query 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Sbjct 301     | CAACAGATCGAGGTGCGAGACAACATTATGAAAACCCAAAGGCCCGGGTGCCTGGCCGAAA | 360           |           |           |
| Query 421     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Sbjct 421     | TGTAGTCTTGTAGTCAGGGAGACGCACCGCTGGGCTCGCTCACCCACATCCTGACGTTT   | 420           |           |           |
| Query 465     | CGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                        | 465           |           |           |
| Sbjct 465     | CGAGACTGGAGGTTGTTTCGGGGAGCAGGGACGATTGA                        | 465           |           |           |



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## W. Hasil BLAST Sampel C7

### Nukleotida Kontrol

Sequence ID: Query\_3294481 Length: 465 Number of Matches: 1

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect           | Identities       | Gaps             | Strand               |
|---------------|------------------|------------------|------------------|----------------------|
| 859 bits(465) | 0.0              | 465/465(100%)    | 0/465(0%)        | Plus/Plus            |
| Query 1       | ATGACACCGGGTTTGC | TTACTACTGCGGGTGT | TGGCCGACCACGTGAC | AGGTGCGCCAGG 60      |
| Sbjct 1       | ATGACACCGGGTTTGC | TTACTACTGCGGGTGT | TGGCCGACCACGTGAC | AGGTGCGCCAGG 60      |
| Query 61      | ATCGTATGCACGGTGT | CATCGAAACCGCCGT  | TGTCGCGACCATGTT  | TGTCGCGTTGTTG 120    |
| Sbjct 61      | ATCGTATGCACGGTGT | CATCGAAACCGCCGT  | TGTCGCGACCATGTT  | TGTCGCGTTGTTG 120    |
| Query 121     | GGTCTGTCCACCATC  | AGCTCGAAAGCCGAC  | GACATCGATTGGGAC  | GCCATCGCGCAATGC 180  |
| Sbjct 121     | GGTCTGTCCACCATC  | AGCTCGAAAGCCGAC  | GACATCGATTGGGAC  | GCCATCGCGCAATGC 180  |
| Query 181     | GAATCCGGCGCAATT  | TGGCGGCCAACACCG  | GTAAACGGGTTATAC  | GGTGGTCTGCAGATC 240  |
| Sbjct 181     | GAATCCGGCGCAATT  | TGGCGGCCAACACCG  | GTAAACGGGTTATAC  | GGTGGTCTGCAGATC 240  |
| Query 241     | AGCCAGGCGACGTGG  | GATTCAACGGTGGT   | GTCGGGTCGCCGGC   | GGCCGCGAGTCCCCAG 300 |
| Sbjct 241     | AGCCAGGCGACGTGG  | GATTCAACGGTGGT   | GTCGGGTCGCCGGC   | GGCCGCGAGTCCCCAG 300 |
| Query 301     | CAACAGATCGAGGTC  | GACAGAACATTATG   | AAAAACCAAGGCCCG  | GGGTGCGTGGCCGAAA 360 |
| Sbjct 301     | CAACAGATCGAGGTC  | GACAGAACATTATG   | AAAAACCAAGGCCCG  | GGGTGCGTGGCCGAAA 360 |
| Query 361     | TGTAGTTCCTTAGT   | CAGGGAGACGCCACC  | GCTGGGCTCGCTACC  | CACATCTGACGTTCC 420  |
| Sbjct 361     | TGTAGTTCCTTAGT   | CAGGGAGACGCCACC  | GCTGGGCTCGCTACC  | CACATCTGACGTTCC 420  |
| Query 421     | CTCGCGGCCGAGACT  | TGGAGGTTGTTCTG   | GGGAGCAGGGACGAT  | TGA 465              |
| Sbjct 421     | CTCGCGGCCGAGACT  | TGGAGGTTGTTCTG   | GGGAGCAGGGACGAT  | TGA 465              |

## X. Hasil BLAST Sampel C8

### Nukleotida Kontrol

Sequence ID: Query\_640285 Length: 465 Number of Matches: 1

Range 1: 1 to 465 [Graphics](#)

| Score         | Expect           | Identities       | Gaps             | Strand               |
|---------------|------------------|------------------|------------------|----------------------|
| 859 bits(465) | 0.0              | 465/465(100%)    | 0/465(0%)        | Plus/Plus            |
| Query 1       | ATGACACCGGGTTTGC | TTACTACTGCGGGTGT | TGGCCGACCACGTGAC | AGGTGCGCCAGG 60      |
| Sbjct 1       | ATGACACCGGGTTTGC | TTACTACTGCGGGTGT | TGGCCGACCACGTGAC | AGGTGCGCCAGG 60      |
| Query 61      | ATCGTATGCACGGTGT | CATCGAAACCGCCGT  | TGTCGCGACCATGTT  | TGTCGCGTTGTTG 120    |
| Sbjct 61      | ATCGTATGCACGGTGT | CATCGAAACCGCCGT  | TGTCGCGACCATGTT  | TGTCGCGTTGTTG 120    |
| Query 121     | GGTCTGTCCACCATC  | AGCTCGAAAGCCGAC  | GACATCGATTGGGAC  | GCCATCGCGCAATGC 180  |
| Sbjct 121     | GGTCTGTCCACCATC  | AGCTCGAAAGCCGAC  | GACATCGATTGGGAC  | GCCATCGCGCAATGC 180  |
| Query 181     | GAATCCGGCGCAATT  | TGGCGGCCAACACCG  | GTAAACGGGTTATAC  | GGTGGTCTGCAGATC 240  |
| Sbjct 181     | GAATCCGGCGCAATT  | TGGCGGCCAACACCG  | GTAAACGGGTTATAC  | GGTGGTCTGCAGATC 240  |
| Query 241     | AGCCAGGCGACGTGG  | GATTCAACGGTGGT   | GTCGGGTCGCCGGC   | GGCCGCGAGTCCCCAG 300 |
| Sbjct 241     | AGCCAGGCGACGTGG  | GATTCAACGGTGGT   | GTCGGGTCGCCGGC   | GGCCGCGAGTCCCCAG 300 |
| Query 301     | CAACAGATCGAGGTC  | GACAGAACATTATG   | AAAAACCAAGGCCCG  | GGGTGCGTGGCCGAAA 360 |
| Sbjct 301     | CAACAGATCGAGGTC  | GACAGAACATTATG   | AAAAACCAAGGCCCG  | GGGTGCGTGGCCGAAA 360 |
| Query 361     | TGTAGTTCCTTAGT   | CAGGGAGACGCCACC  | GCTGGGCTCGCTACC  | CACATCTGACGTTCC 420  |
| Sbjct 361     | TGTAGTTCCTTAGT   | CAGGGAGACGCCACC  | GCTGGGCTCGCTACC  | CACATCTGACGTTCC 420  |
| Query 421     | CTCGCGGCCGAGACT  | TGGAGGTTGTTCTG   | GGGAGCAGGGACGAT  | TGA 465              |
| Sbjct 421     | CTCGCGGCCGAGACT  | TGGAGGTTGTTCTG   | GGGAGCAGGGACGAT  | TGA 465              |



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## Lampiran 4. Komposisi Bahan

### A. Komposisi Reagen Ekstraksi DNA

|                       |         |
|-----------------------|---------|
| Sampel Isolat         | : 200µl |
| Enzim Proteinase K    | : 20µl  |
| GSB <i>buffer</i>     | : 200µl |
| Etanol absolut        | : 200µl |
| W1 <i>buffer</i>      | : 400µl |
| Wash <i>buffer</i>    | : 600µl |
| Elusion <i>buffer</i> | : 100µl |

### B. Komposisi Larutan Stok Primer

#### a. Primer *Forward*

Massa primer kering : 18,4 nmol

Volume ddH<sub>2</sub>O : 184 µl

**Konsentrasi stok : 100 µl (184 µl)**

Pengenceran larutan stok:

$$V_1 N_1 = V_2 N_2$$

$$V_1 \cdot 100 = 100 \mu\text{l} \cdot 10$$

$$V_1 = 10 \mu\text{l} \rightarrow \text{Volume ddH}_2\text{O} = 90 \mu\text{l}$$

#### b. Primer *Reverse*

Massa primer kering : 20,6 nmol

Volume ddH<sub>2</sub>O : 206 µl

**Konsentrasi stok : 100 µl (206 µl)**

Pengenceran larutan stok:

$$V_1 N_1 = V_2 N_2$$

$$V_1 \cdot 100 = 100 \mu\text{l} \cdot 10$$

$$V_1 = 10 \mu\text{l} \rightarrow \text{Volume ddH}_2\text{O} = 90 \mu\text{l}$$



**D. Komposisi PCR Mix**

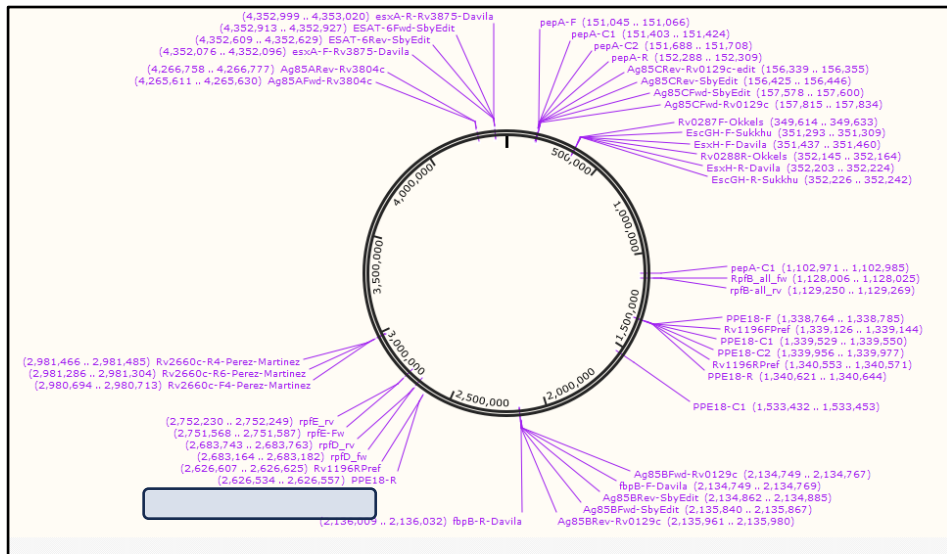
|                        |                               |
|------------------------|-------------------------------|
| Enzim <i>mytaq red</i> | : 25 $\mu$ l                  |
| Primer <i>forward</i>  | : 1 $\mu$ l                   |
| Primer <i>reverse</i>  | : 1 $\mu$ l                   |
| ddH <sub>2</sub> O     | : 13 $\mu$ l                  |
| Sampel DNA             | : 10 $\mu$ l                  |
| <b>Volume Total</b>    | <b>: 50 <math>\mu</math>l</b> |

**E. Komposisi Gel Agarosa**

|                          |          |
|--------------------------|----------|
| Berat agarosa            | : 2 gram |
| Volume TBE <i>buffer</i> | : 100 ml |



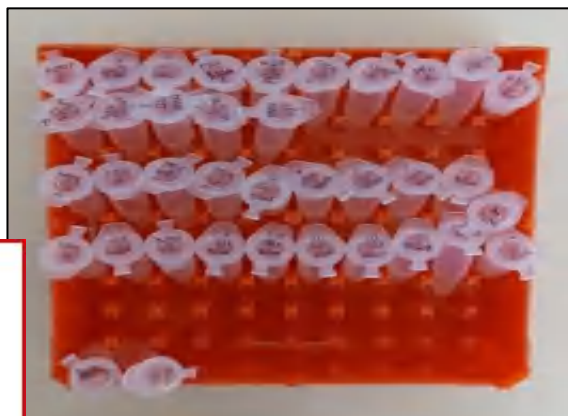
### Lampiran 5. Posisi Primer Rpf-D pada Genom *Mycobacterium tuberculosis* H37Rv



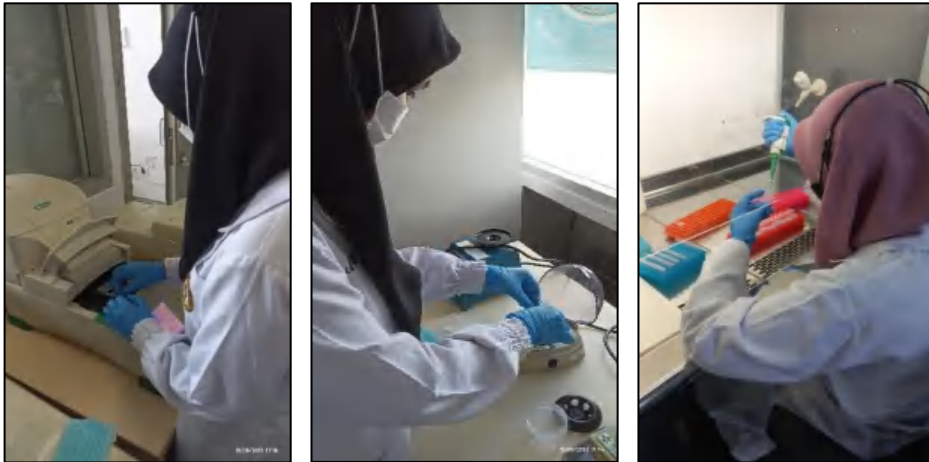


## Lampiran 6. Dokumentasi Penelitian

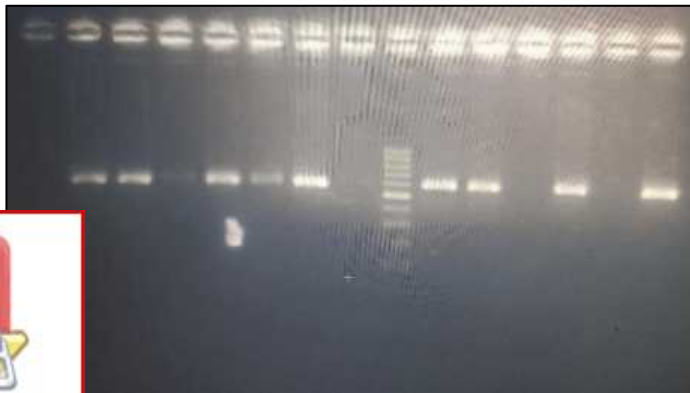
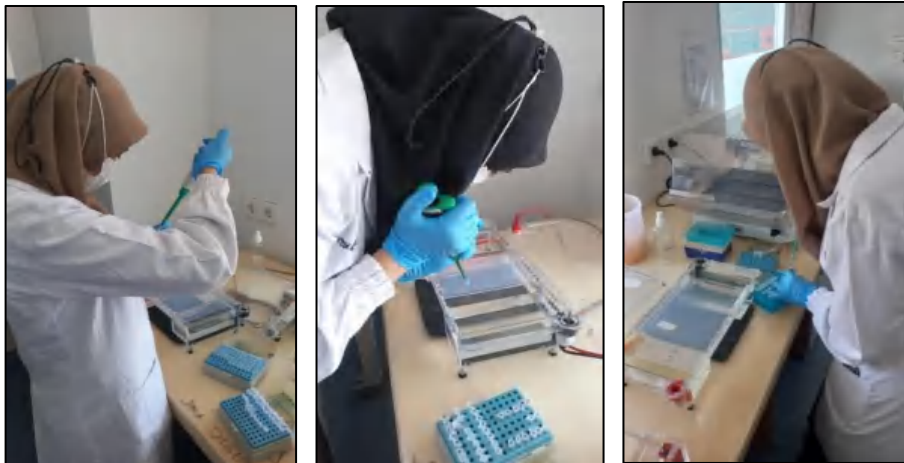
### A. Ekstraksi DNA



### B. Amplifikasi Gen RpfD



### C. Elektroforesis



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