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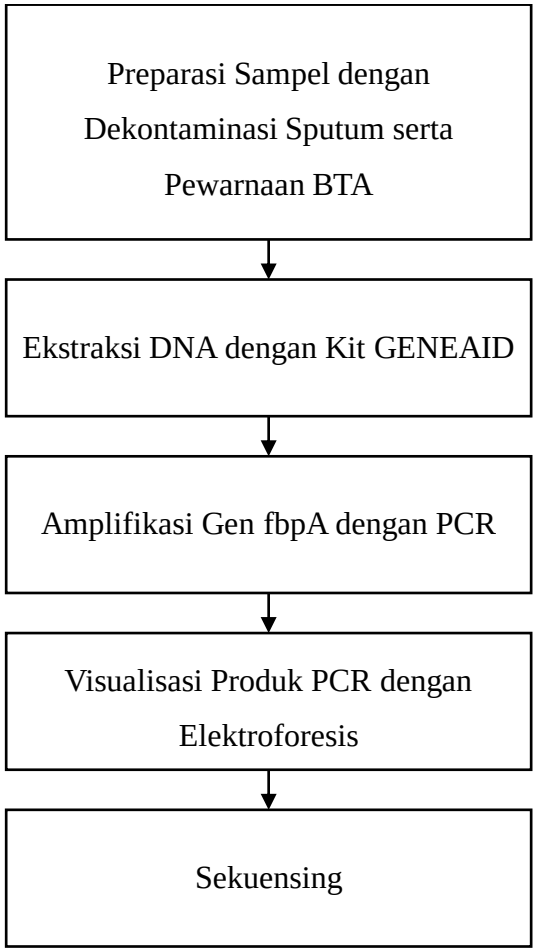
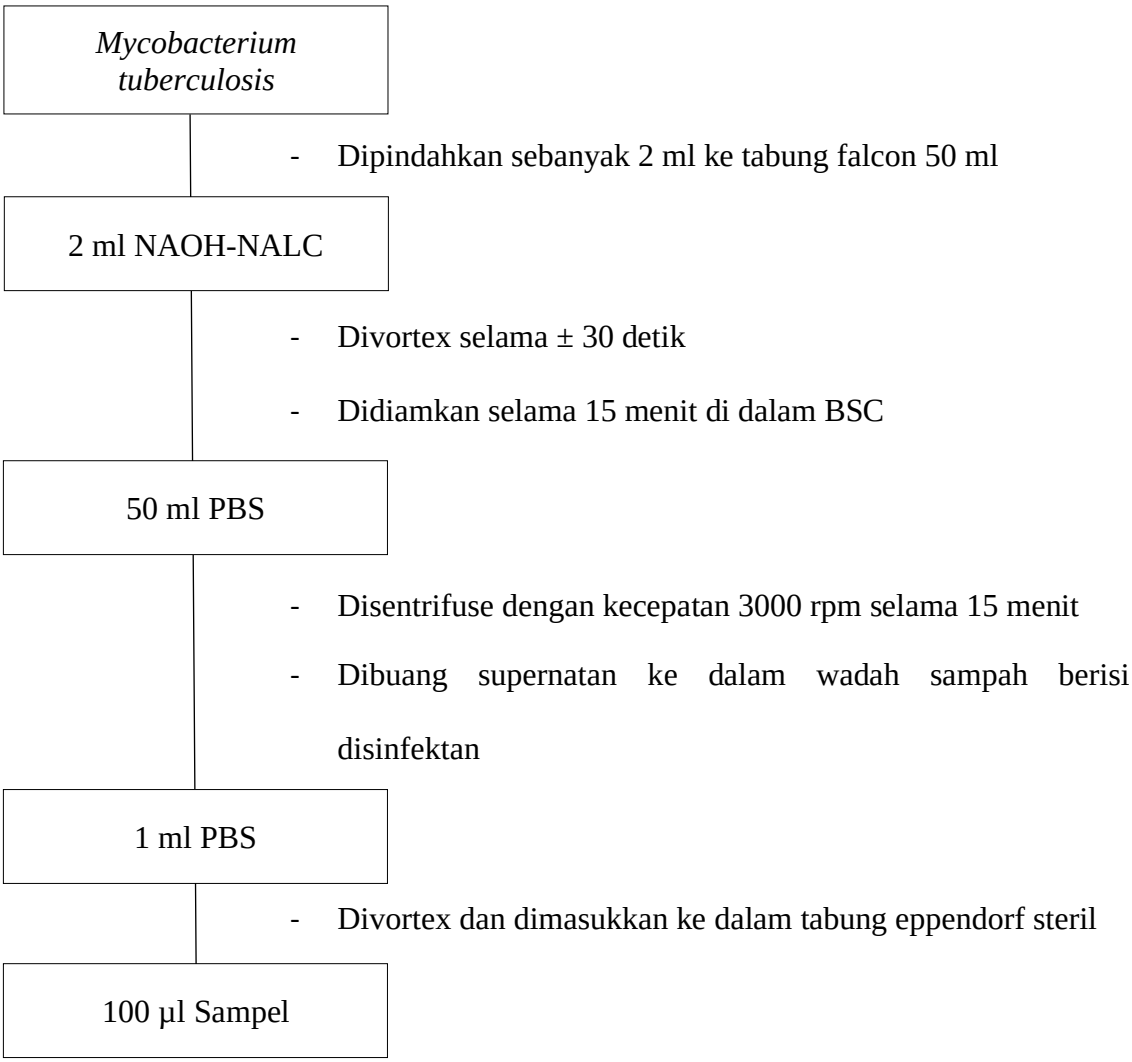
LAMPIRAN

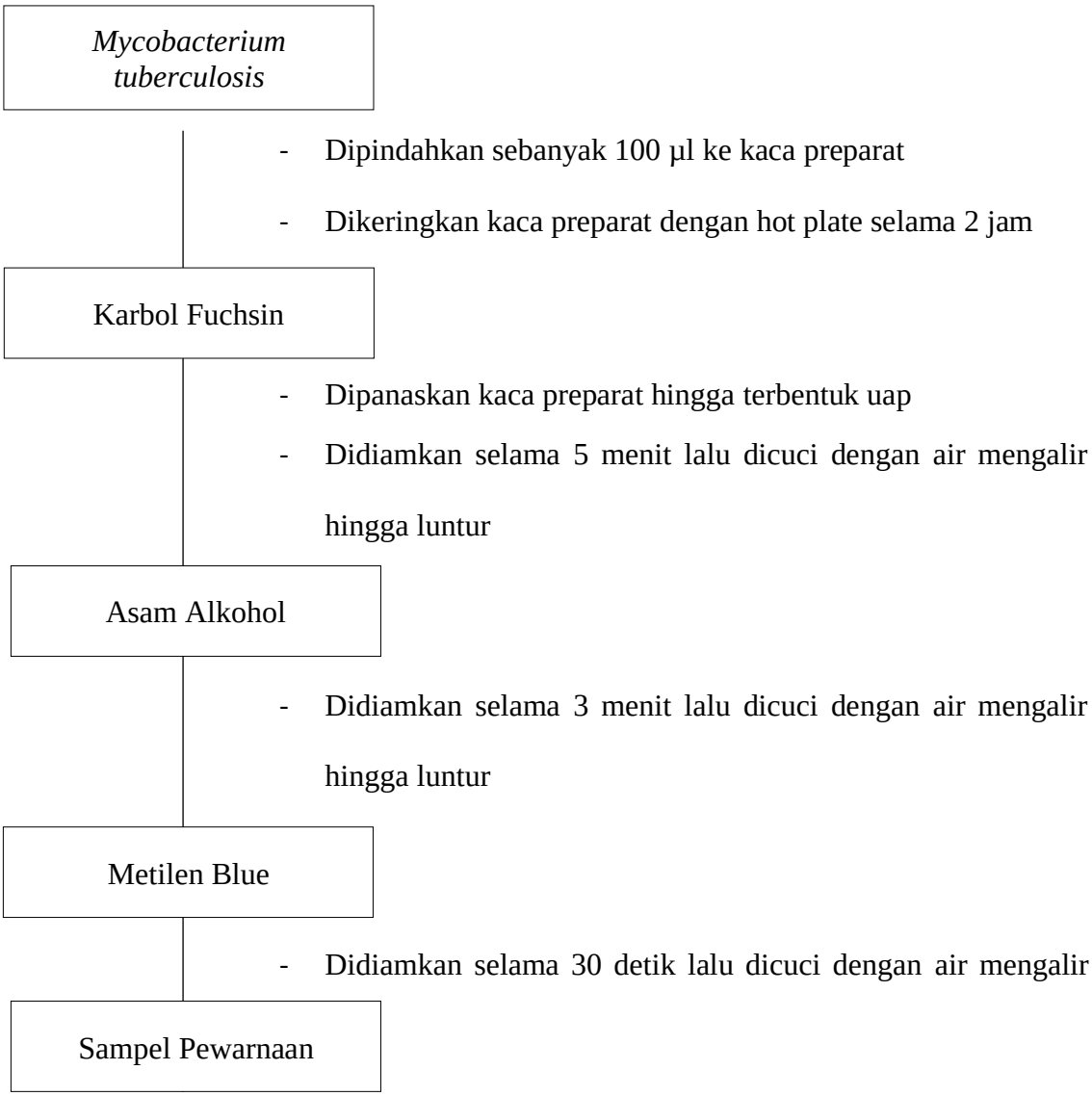
Lampiran 1. Skema Kerja



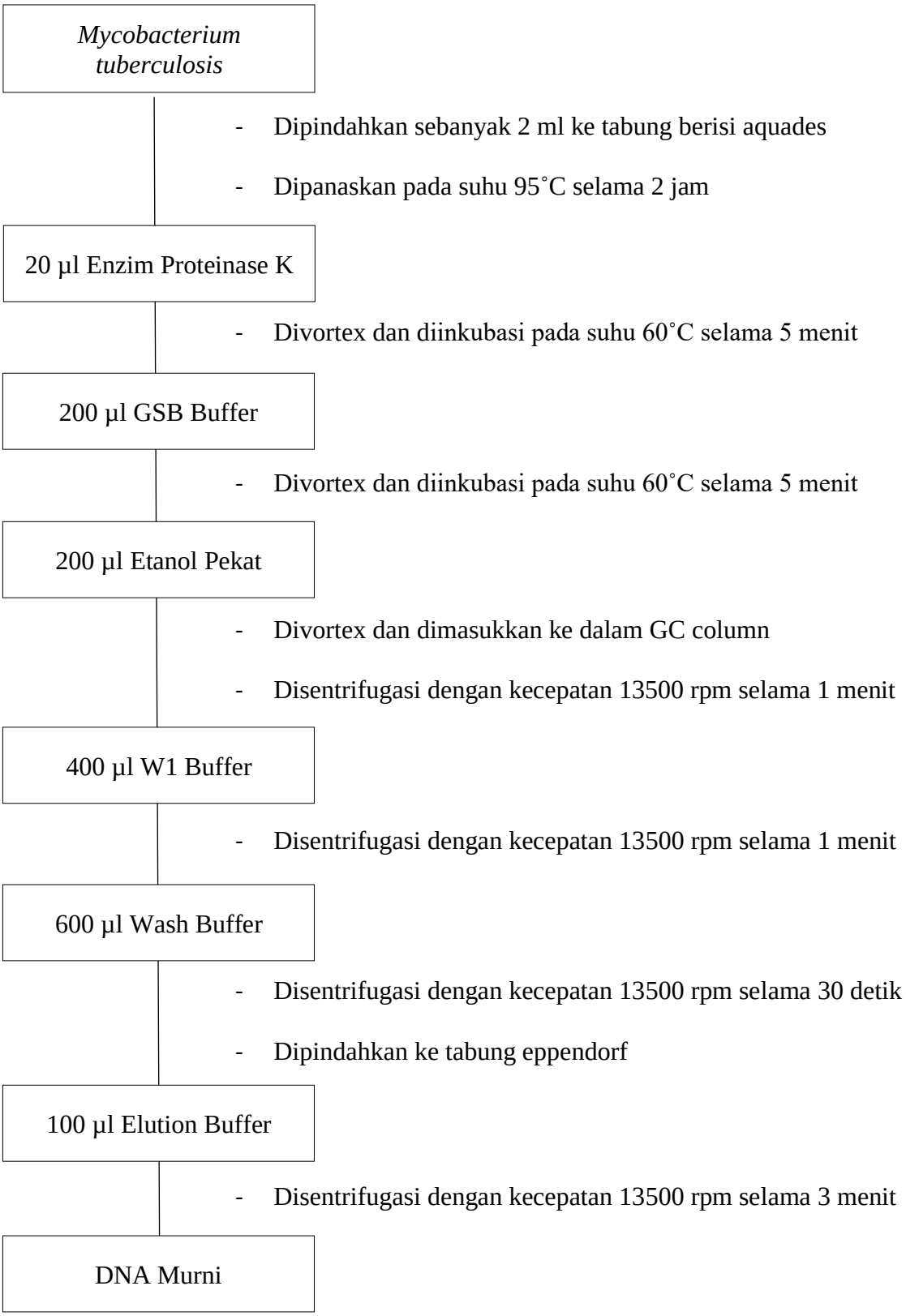
A. Dekontaminasi Sampel Sputum



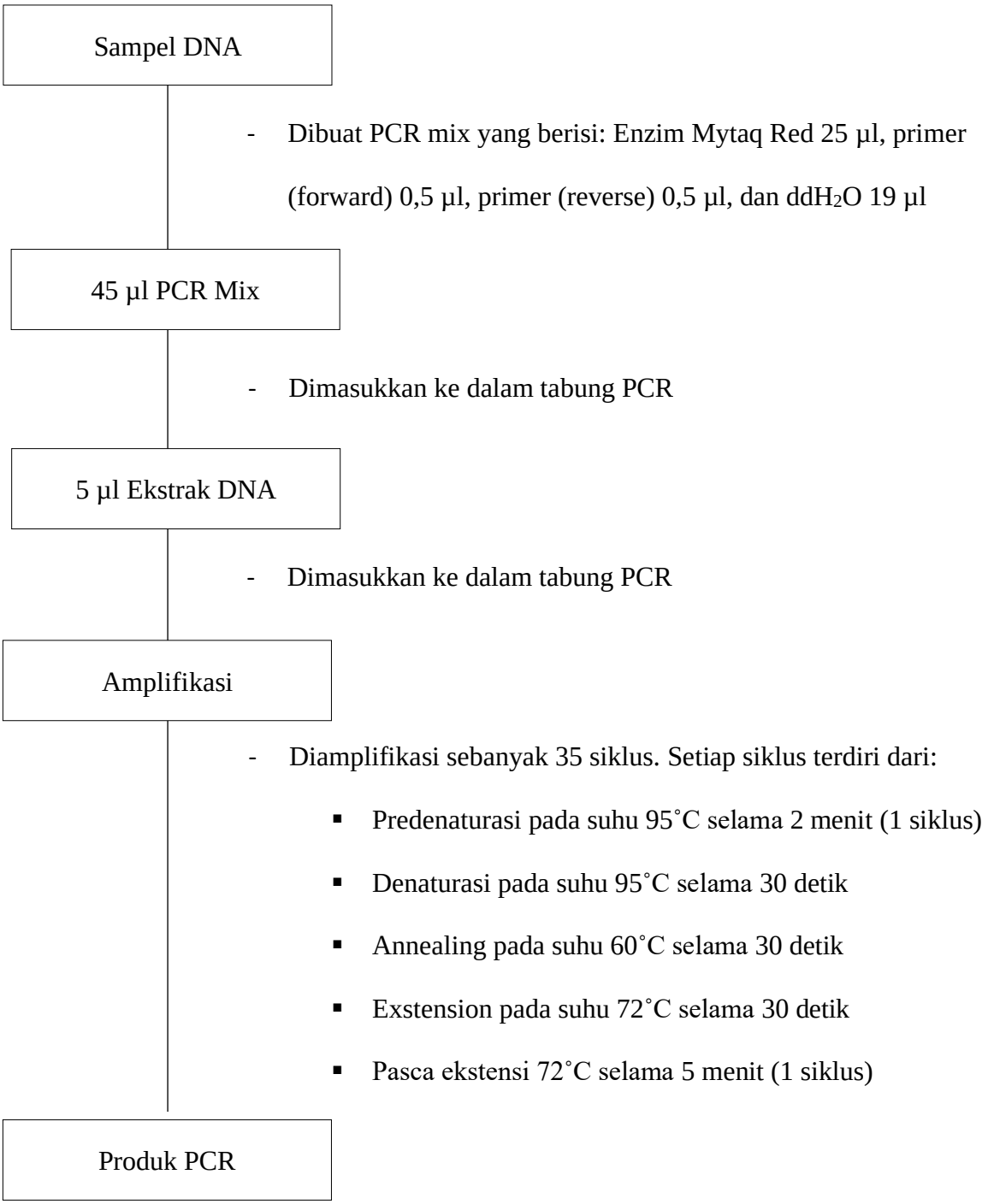
B. Pewarnaan Ziehl-Neelson



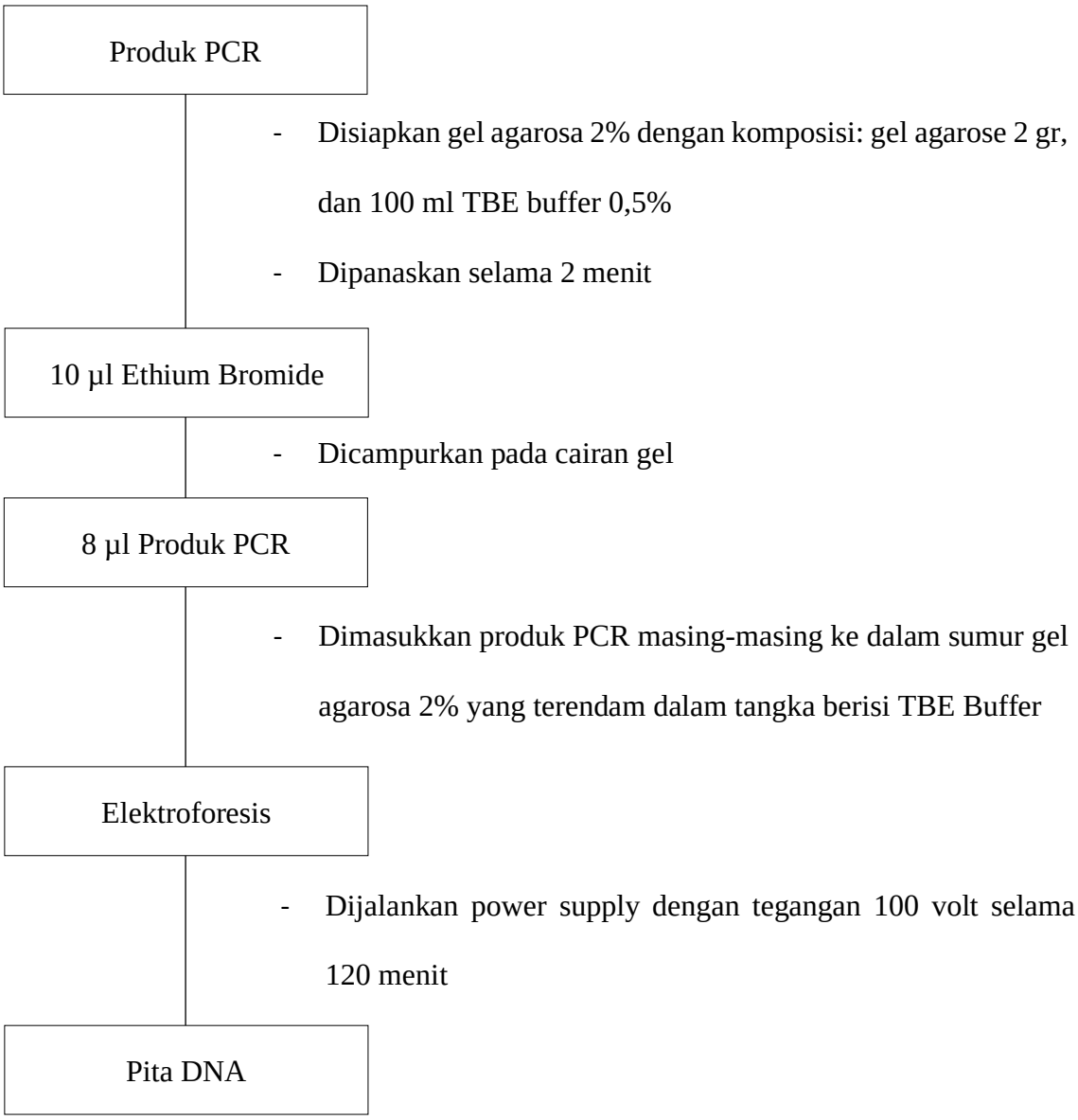
C. Ekstraksi DNA *Mycobacterium tuberculosis*



D. Amplifikasi DNA dengan PCR



E. Deteksi Produk PCR dengan Elektroforesis



Lampiran 2. Peta Origin Antara Primer dan Gen fbpA dari DataBank

A. Origin Gen fbpA dari DataBank

Mycobacterium tuberculosis H37Rv, complete genome

GenBank: CP003248.2

GenBank Graphics

>CP003248.2:4265809-4266707 Mycobacterium tuberculosis H37Rv, complete genome
TCTGTTCGGAGCTAGGCGCCCTGGGGCGCGGGCCCGGTGTTGGGCGTGGCACCCAGTGCCCGTTGCAGGT
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TCGAGGAACTTGGCCGGCAGGTTGTTGCCACCCAGATCCGACGGCTTGCCGTTGCCGCAGTACACCCAGA
CGCGGGTGTTGTTGGCGATCAGCTTCCCGACGTTCAACAGCGGGTCGTTGCGCTGCCACGCCGGGTCCTC
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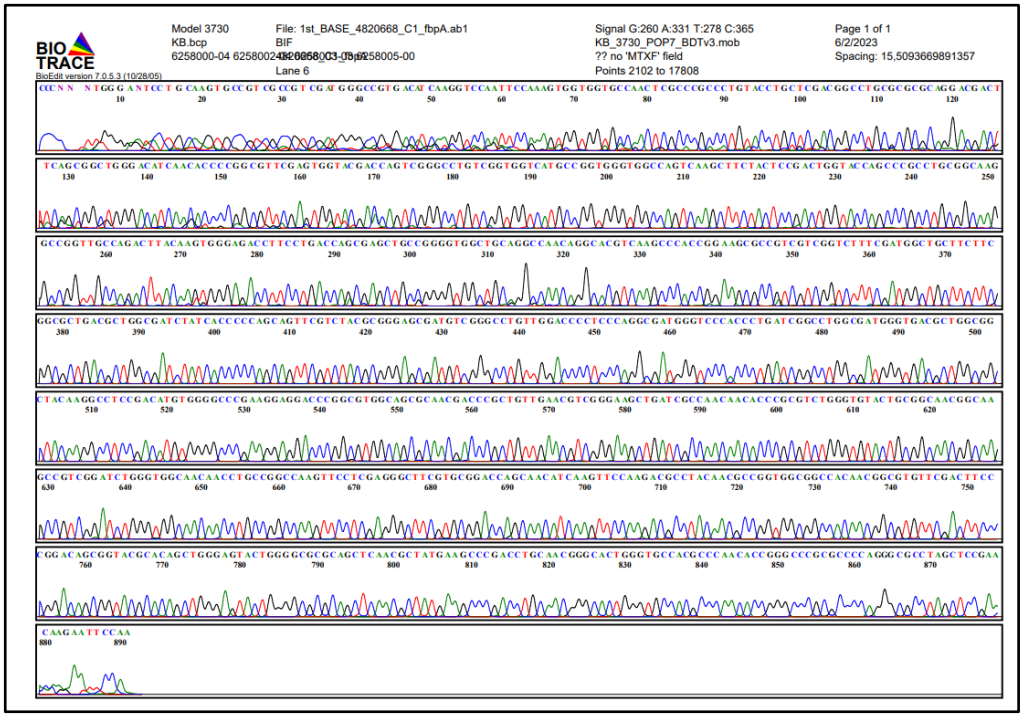
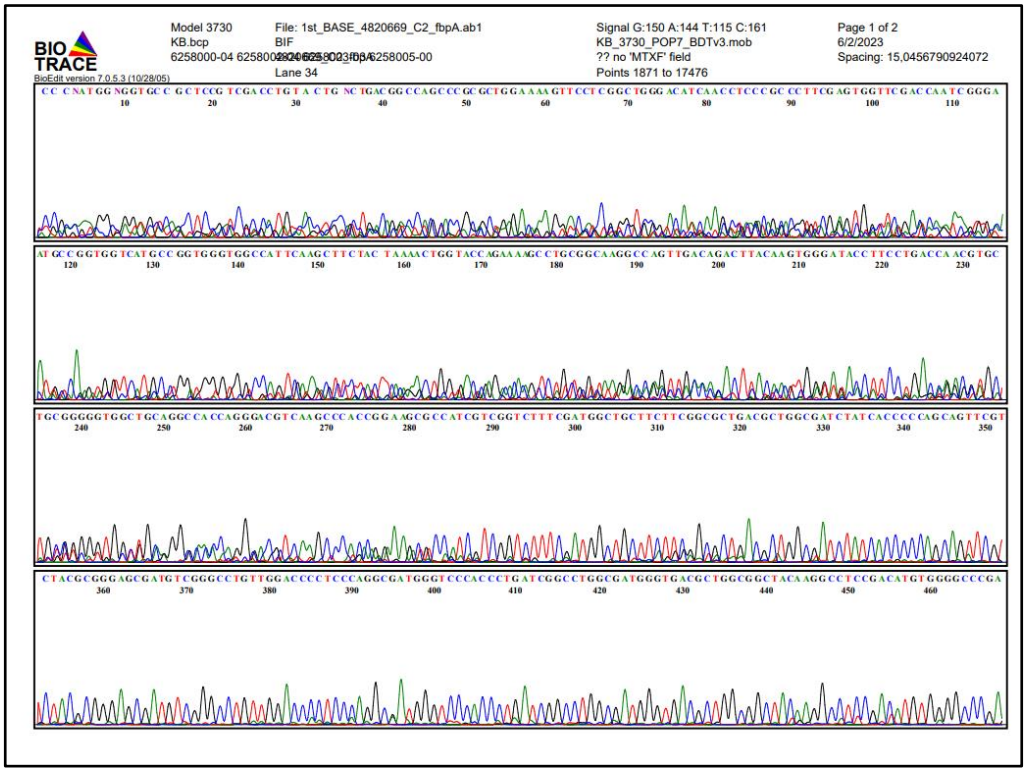
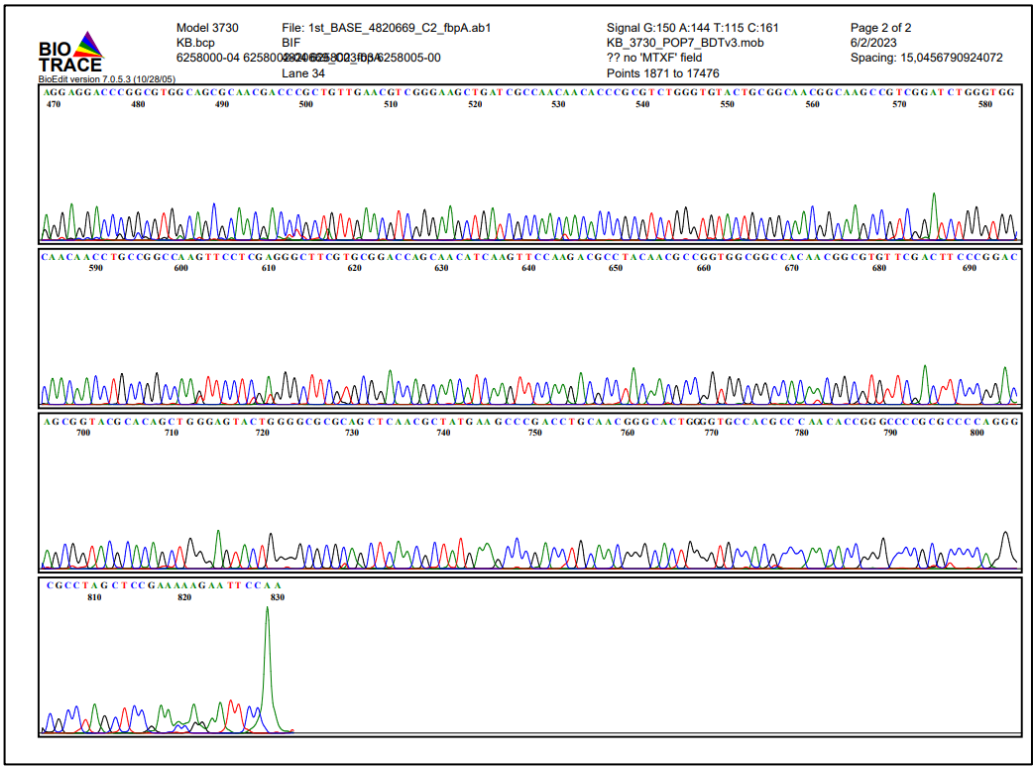
Lampiran 3. Hasil Sekuensing Sampel

A. Visualisasi Sekuens Sampel C1

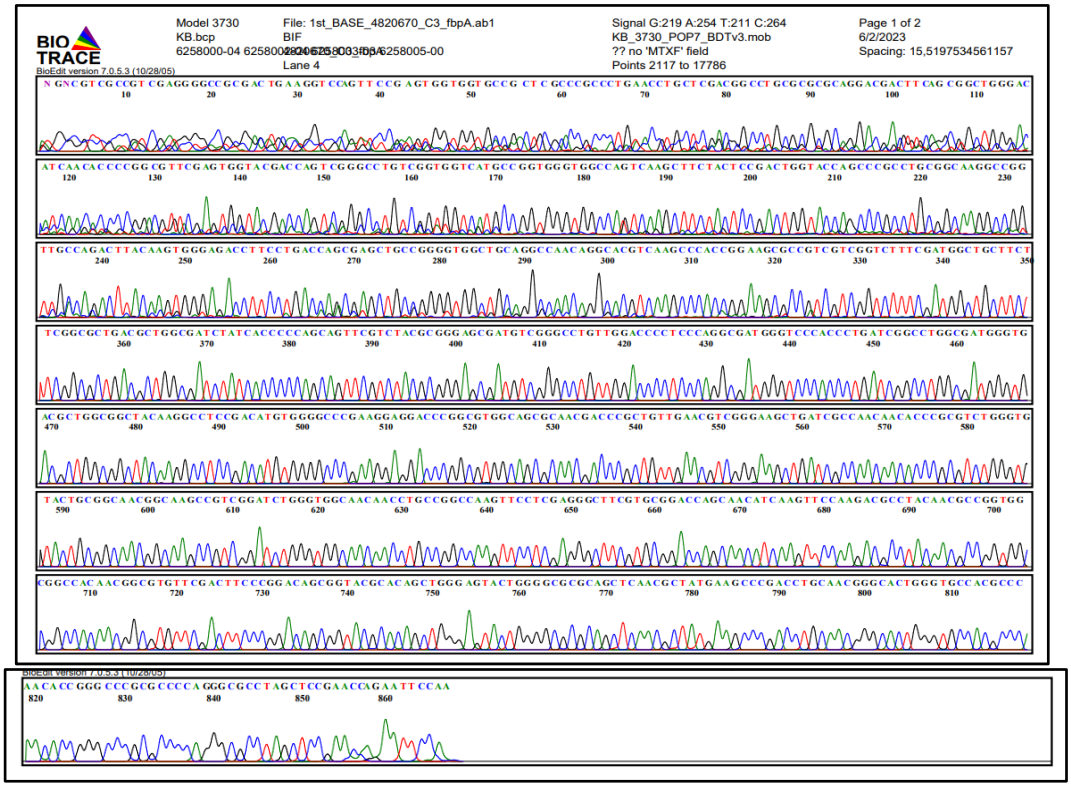


B. Visualisasi Sekuens Sampel C2

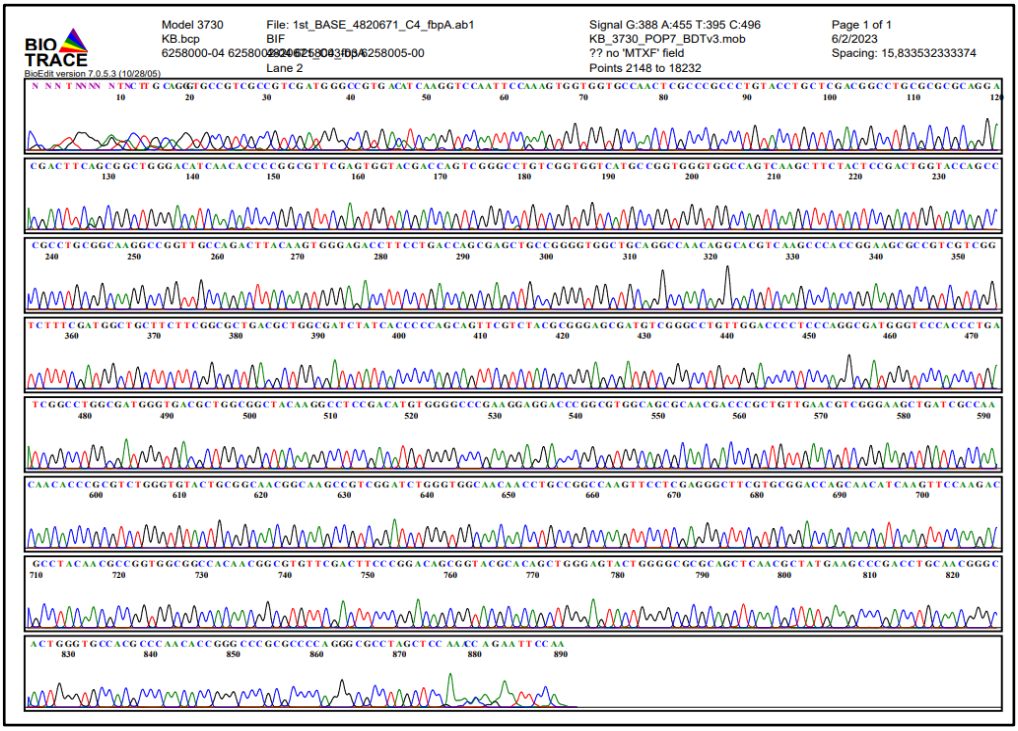




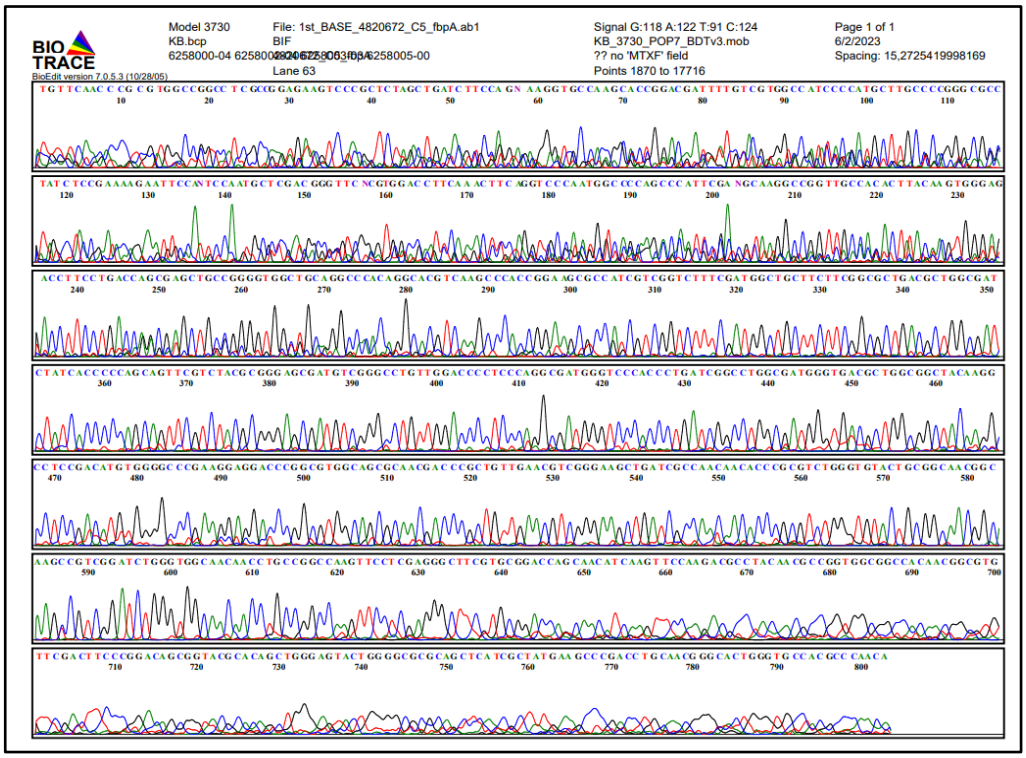
C. Visualisasi Sekuens Sampel C3



D. Visualisasi Sekuens Sampel C4



E. Visualisasi Sekuens Sampel C5



Lampiran 4. Hasil BLAST Sampel

A. Hasil BLAST Sampel C1

Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: CP003248.2 Length: 4411709 Number of Matches: 1

Range 1: 4265811 to 4266678 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1598 bits(865)	0.0	867/868(99%)	0/868(0%)	Plus/Minus

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Query  14       CCTGCAAGTGCCGTCGCCGTCGATGGGCCGTGACATCAAGGTCCAATTCCAAAGTGGTGG  73
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Query  494      CGCTGGCGGCTACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCG  553
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Sbjct  4265838  CGCGCCCCAGGGCGCCTAGCTCCGAACA  4265811
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B. Hasil BLAST Sampel C2

Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: CP003248.2 Length: 4411709 Number of Matches: 1

Range 1: 4265813 to 4266603 GenBank Graphics ▼ Next Match ▲ Previous M

Score	Expect	Identities	Gaps	Strand
1247 bits(675)	0.0	756/795(95%)	6/795(0%)	Plus/Minus

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Query  84       TCCCGCCCTTCGAGTGGTTCGACCAATCGGGAATGCCGGTGGTCATGCCGGTGGGTGGCC  143
                 ||||  |  ||||||||||  ||||||  |||||   ||  ||||||||||||||||||||||||
Sbjct  4266544  CCCCGGCGTTCGAGTGGTACGACCAGTCGGGCCTGTCGGTGGTCATGCCGGTGGGTGGCC  4266485

Query  144      ATTCAAGCTTCTACTAAAACTGGTACCAGAAAAGCCTGCGGCAAGGCCAGTTGACAGACT  203
                |  |||||||||||||    ||||||||||    ||||||||||||||| ||||  ||||||
Sbjct  4266484  AGTCAAGCTTCTACTCCGACTGGTACCAG-CCCGCCTGCGGCAAGGCCGGTTGCCAGACT  4266426

Query  204      TACAAGTGGGATACCTTCCTGACCAACGTGCTGCGGGGGTGGCTGCAGGCCACCAGGGAC  263
                ||||||||||| |||||||||||||  || |||||  ||||||||||||||||  ||||  ||
Sbjct  4266425  TACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGTGGCTGCAGGCCAACAGGCAC  4266366

Query  264      GTCAAGCCCACCGGAAGCGCCATCGTCGGTCTTTCGATGGCTGCTTCTTCGGCGCTGACG  323
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  4266365  GTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGGCTGCTTCTTCGGCGCTGACG  4266306

Query  324      CTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCGGGCCTGTTGGAC  383
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266305  CTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCGGGCCTGTTGGAC  4266246

Query  384      CCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCTAC  443
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266245  CCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCTAC  4266186

Query  444      AAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGCTG  503
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266185  AAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGCTG  4266126

Query  504      TTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTACTGCGGCAACGGC  563
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266125  TTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTACTGCGGCAACGGC  4266066

Query  564      AAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAGGGCTTCGTGCGG  623
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266065  AAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAGGGCTTCGTGCGG  4266006

Query  624      ACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCACAACGGCGTGTTC  683
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266005  ACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCACAACGGCGTGTTC  4265946

Query  684      GACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAGCTCAACGCTATG  743
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265945  GACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAGCTCAACGCTATG  4265886

Query  744      AAGCCCGACCTGCAACGGGCACTGGGGTGCCACGCCCAACACCGGGCCCCGCGCCCCAGG  803
                ||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Sbjct  4265885  AAGCCCGACCTGCAACGGGCACTGGG-TGCCACGCCCAACACCGGGCCC-GCGCCCCAGG  4265828

Query  804      GCGCCTAGCTCCGAA  818
                |||||||||||||||
Sbjct  4265827  GCGCCTAGCTCCGAA  4265813
```

C. Hasil BLAST Sampel C3

Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: CP003248.2 Length: 4411709 Number of Matches: 1

Range 1: 4265809 to 4266667 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1524 bits(825)	0.0	849/860(99%)	4/860(0%)	Plus/Minus

```
Query  4        CGTCGCCGTCGAGGGGCCGCGAC-TGAAGGTCCAGTTCC-GAGTGGTGGTGCC-GCTCGC  60
                ||||||||||||| |||||| ||| | |||||||| ||||  ||||||||||||  |||||
Sbjct  4266667  CGTCGCCGTCGATGGGCCGTGACATCAAGGTCCAATTCCAAAGTGGTGGTGCCAACTCGC  4266608

Query  61       CCGCCCTGAACCTGCTCGACGGCCTGCGCGCGCAGGACGACTTCAGCGGCTGGGACATCA  120
                |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266607  CCGCCCTGTACCTGCTCGACGGCCTGCGCGCGCAGGACGACTTCAGCGGCTGGGACATCA  4266548

Query  121      ACACCCCGGCGTTCGAGTGGTACGACCAGTCGGGCCTGTCGGTGGTCATGCCGGTGGGTG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266547  ACACCCCGGCGTTCGAGTGGTACGACCAGTCGGGCCTGTCGGTGGTCATGCCGGTGGGTG  4266488

Query  181      GCCAGTCAAGCTTCTACTCCGACTGGTACCAGCCCGCCTGCGGCAAGGCCGGTTGCCAGA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266487  GCCAGTCAAGCTTCTACTCCGACTGGTACCAGCCCGCCTGCGGCAAGGCCGGTTGCCAGA  4266428

Query  241      CTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGTGGCTGCAGGCCAACAGGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266427  CTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGTGGCTGCAGGCCAACAGGC  4266368

Query  301      ACGTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGGCTGCTTCTTCGGCGCTGA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266367  ACGTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGGCTGCTTCTTCGGCGCTGA  4266308

Query  361      CGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCGGGCCTGTTGG  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266307  CGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCGGGCCTGTTGG  4266248

Query  421      ACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCT  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266247  ACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCT  4266188

Query  481      ACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGC  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266187  ACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGC  4266128

Query  541      TGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTACTGCGGCAACG  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266127  TGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTACTGCGGCAACG  4266068

Query  601      GCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAGGGCTTCGTGC  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266067  GCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAGGGCTTCGTGC  4266008

Query  661      GGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCACAACGGCGTGT  720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266007  GGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCACAACGGCGTGT  4265948

Query  721      TCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAGCTCAACGCTA  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265947  TCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAGCTCAACGCTA  4265888

Query  781      TGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACACCGGGCCCGCGCCCCAGG  840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265887  TGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACACCGGGCCCGCGCCCCAGG  4265828

Query  841      GCGCCTAGCTCCGAACCAGA  860
                |||||||||||||||| |||
Sbjct  4265827  GCGCCTAGCTCCGAAC-AGA  4265809
```

D. Hasil BLAST Sampel C4

Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: CP003248.2 Length: 4411709 Number of Matches: 1

Range 1: 4265809 to 4266676 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1589 bits(860)	0.0	867/870(99%)	2/870(0%)	Plus/Minus

```
Query  14       TGCAGGGTGCCGTCGCCGTCGATGGGCCGTGACATCAAGGTCCAATTCCAAAGTGGTGGT  73
               ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266676  TGCA-GGTGCCGTCGCCGTCGATGGGCCGTGACATCAAGGTCCAATTCCAAAGTGGTGGT  4266618

Query  74       GCCAACTCGCCCGCCCTGTACCTGCTCGACGGCCTGCGCGCGCAGGACGACTTCAGCGGC  133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266617  GCCAACTCGCCCGCCCTGTACCTGCTCGACGGCCTGCGCGCGCAGGACGACTTCAGCGGC  4266558

Query  134      TGGGACATCAACACCCCGGCGTTCGAGTGGTACGACCAGTCGGGCCTGTCGGTGGTCATG  193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266557  TGGGACATCAACACCCCGGCGTTCGAGTGGTACGACCAGTCGGGCCTGTCGGTGGTCATG  4266498

Query  194      CCGGTGGGTGGCCAGTCAAGCTTCTACTCCGACTGGTACCAGCCCGCCTGCGGCAAGGCC  253
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266497  CCGGTGGGTGGCCAGTCAAGCTTCTACTCCGACTGGTACCAGCCCGCCTGCGGCAAGGCC  4266438

Query  254      GGTTGCCAGACTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGTGGCTGCAG  313
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266437  GGTTGCCAGACTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGTGGCTGCAG  4266378

Query  314      GCCAACAGGCACGTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGGCTGCTTCT  373
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266377  GCCAACAGGCACGTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGGCTGCTTCT  4266318

Query  374      TCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCG  433
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266317  TCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGTCG  4266258

Query  434      GGCCTGTTGGACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGAC  493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266257  GGCCTGTTGGACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGAC  4266198

Query  494      GCTGGCGGCTACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGC  553
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266197  GCTGGCGGCTACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGC  4266138

Query  554      AACGACCCGCTGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTAC  613
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266137  AACGACCCGCTGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCTGGGTGTAC  4266078

Query  614      TGCGGCAACGGCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAG  673
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266077  TGCGGCAACGGCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGTTCCTCGAG  4266018

Query  674      GGCTTCGTGCGGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCAC  733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266017  GGCTTCGTGCGGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTGGCGGCCAC  4265958

Query  734      AACGGCGTGTTCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAG  793
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265957  AACGGCGTGTTCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGGGCGCGCAG  4265898

Query  794      CTCAACGCTATGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACACCGGGCCC  853
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265897  CTCAACGCTATGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACACCGGGCCC  4265838

Query  854      GCGCCCCAGGGCGCCTAGCTCCAAACCAGA  883
               |||||||||||||||||||||| ||| |||
Sbjct  4265837  GCGCCCCAGGGCGCCTAGCTCCGAAC-AGA  4265809
```

E. Hasil BLAST Sampel C5

Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: CP003248.2 Length: 4411709 Number of Matches: 1

Range 1: 4265846 to 4266445 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1086 bits(588)	0.0	596/600(99%)	0/600(0%)	Plus/Minus

```
Query  204      GCAAGGCCGGTTGCCACACTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGT  263
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266445  GCAAGGCCGGTTGCCAGACTTACAAGTGGGAGACCTTCCTGACCAGCGAGCTGCCGGGGT  4266386

Query  264      GGCTGCAGGCCCACAGGCACGTCAAGCCCACCGGAAGCGCCATCGTCGGTCTTTCGATGG  323
               |||||||||| |||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  4266385  GGCTGCAGGCCAACAGGCACGTCAAGCCCACCGGAAGCGCCGTCGTCGGTCTTTCGATGG  4266326

Query  324      CTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAG  383
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266325  CTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAG  4266266

Query  384      CGATGTCGGGCCTGTTGGACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGA  443
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266265  CGATGTCGGGCCTGTTGGACCCCTCCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGA  4266206

Query  444      TGGGTGACGCTGGCGGCTACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGT  503
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266205  TGGGTGACGCTGGCGGCTACAAGGCCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGT  4266146

Query  504      GGCAGCGCAACGACCCGCTGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCT  563
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266145  GGCAGCGCAACGACCCGCTGTTGAACGTCGGGAAGCTGATCGCCAACAACACCCGCGTCT  4266086

Query  564      GGGTGTACTGCGGCAACGGCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGT  623
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266085  GGGTGTACTGCGGCAACGGCAAGCCGTCGGATCTGGGTGGCAACAACCTGCCGGCCAAGT  4266026

Query  624      TCCTCGAGGGCTTCGTGCGGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTG  683
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4266025  TCCTCGAGGGCTTCGTGCGGACCAGCAACATCAAGTTCCAAGACGCCTACAACGCCGGTG  4265966

Query  684      GCGGCCACAACGGCGTGTTCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGG  743
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265965  GCGGCCACAACGGCGTGTTCGACTTCCCGGACAGCGGTACGCACAGCTGGGAGTACTGGG  4265906

Query  744      GCGCGCAGCTCATCGCTATGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACA  803
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4265905  GCGCGCAGCTCAACGCTATGAAGCCCGACCTGCAACGGGCACTGGGTGCCACGCCCAACA  4265846
```

Lampiran 5. Komposisi Bahan

A. Komposisi Larutan Stok Dekontaminasi

Stok larutan NaOH-Sodium Sitrat:

NaOH 1 N : 20 gram, 500 ml akuades

Sodium Sitrat : 14,5 gram, 500 ml akuades

Stok larutan NaOH-NALC:

NaOH-Sodium sitrat : 100 ml

Massa NALC : 1 gram

Larutan stok PBS *buffer*:

Na_2HPO_4 : 300 ml (0,947%)

KH_2PO_4 : 200 ml (0,947%)

PBS *buffer* : 500 ml (0,067 M, pH 6,8)

B. Komposisi Reagen Ekstraksi DNA

Sampel sputum : 200µl

Enzim Proteinase K : 20µl

GSB *buffer* : 200µl

Etanol absolut : 200µl

W1 *buffer* : 400µl

Wash buffer : 600µl

Elusion buffer : 100µl

C. Komposisi Larutan Stok Primer

Massa primer kering : 0,23 mg (26,1 nmol)

Volume ddH_2O : 261 µl

Konsentrasi stok : 100 µl (261 µl)

Pengenceran larutan stok:

$V_1N_1 = V_1N_1$

$V_1 \cdot 100 = 100\ \mu l \cdot 20$

$V_1 = 20\ \mu l \rightarrow$ **Volume ddH_2O = 80 µl**

D. Komposisi PCR *Mix*

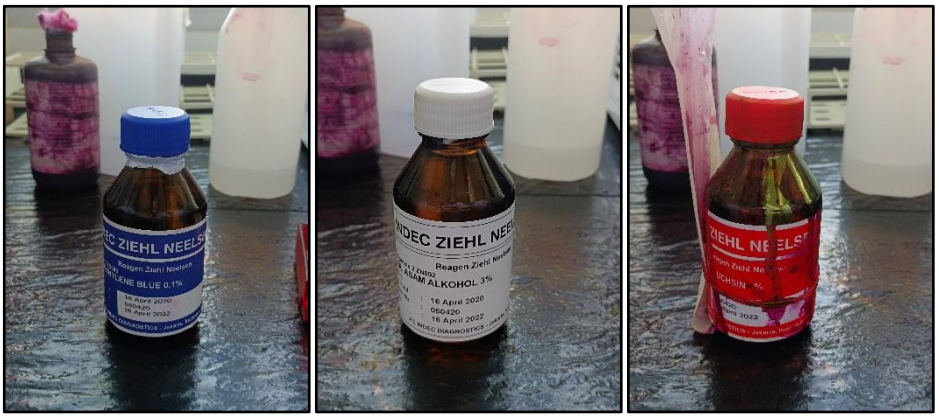
Enzim *mytaq red*	: 25 µl
Primer *forward*	: 0,5 µl
Primer *reverse*	: 0,5 µl
ddH_2O	: 19 µl
Sampel DNA	: 5 µl
Volume Total	**: 25** µl

E. Komposisi Gel Agarosa

Berat agarosa	: 2 gram
Volume TBE *buffer*	: 100 ml

Lampiran 6. Bahan yang Digunakan

A. Pewarnaan Ziehl-Neelson



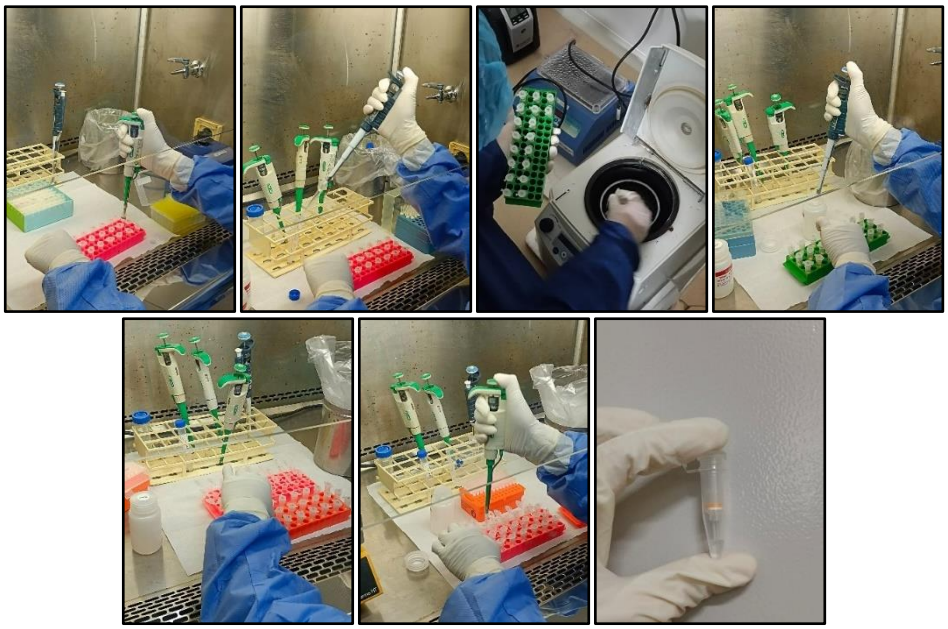
B. Ekstraksi DNA

Lampiran 7. Dokumentasi Penelitian

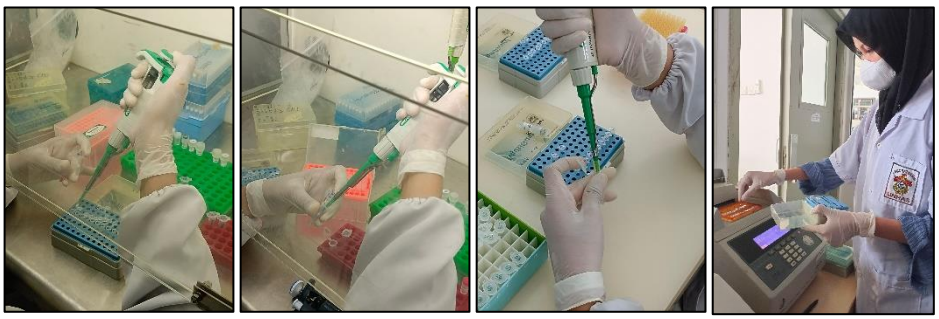
A. Dekontaminasi Sputum

B. Pewarnaan Ziehl-Neelsens

C. Ekstraksi DNA



D. Amplifikasi Gen fbpA dengan PCR



E. Elektroforesis