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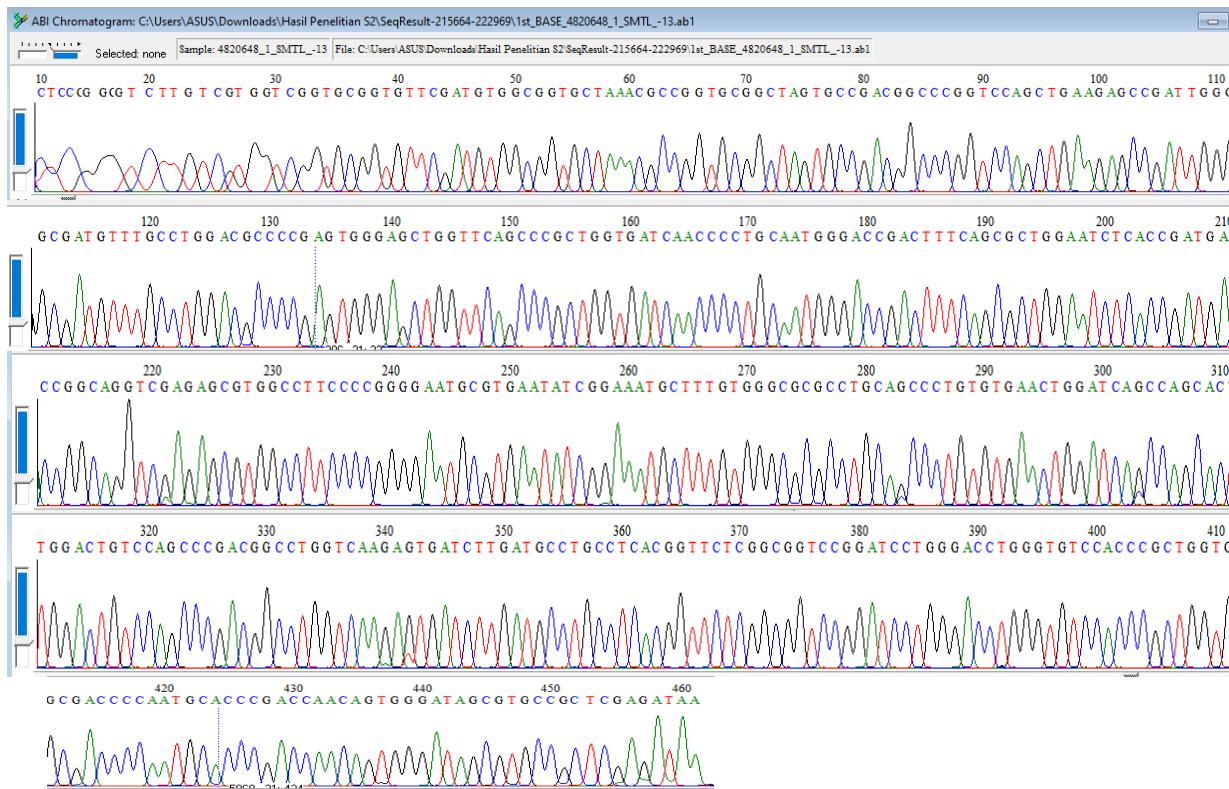
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LAMPIRAN-LAMPIRAN

Lampiran 1 Elektroferogram Sampel 1



Lampiran 2 Elektroferogram Sampel 6



Lampiran 3 Elektroferogram Sampel 7



Lampiran 4 Elektroferogram Sampel 8



Lampiran 5 Elektroferogram Sampel 12



Lampiran 6 Elektroferogram Sampel 13



Lampiran 7 Elektroferogram sampel 15



Lampiran 8 Elektroferogram Sampel 16



Lampiran 9 Elektroferogram sampel 18



Lampiran 10 Elektroferogram Sampel 20



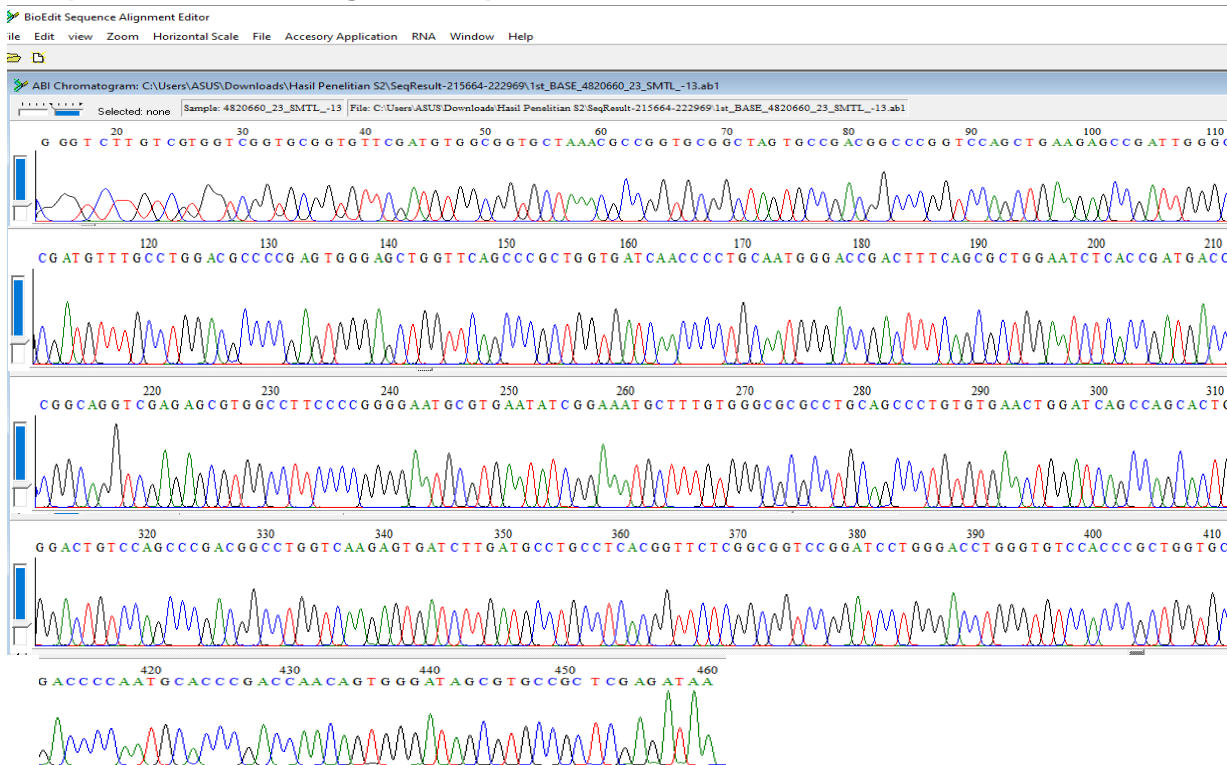
Lampiran 11 Elektroferogram Sampel 21



Lampiran 12 Elektroferogram Sampel 22



Lampiran 13 Elektroferogram Sampel 23



Lampiran 14 Elektroferogram Sampel 26



Lampiran 15 Elektroferogram Sampel 30



Lampiran 16

Hasil BLAST Alignment Sampel 1

Query: None Query ID: lcl|Query_3013425 Length: 461

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593539 to 1593975

Score:800 bits(433), Expect:0.0,

Identities:436/437(99%), Gaps:1/437(0%), Strand: Plus/Plus

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Query 16      GGGT-CTTGTCTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGCAGGCTA 74
          ||| |
Sbjct 1593539 GGGTCTTGTCTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGCAGGCTA 1593598

Query 75      GTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCGA 134
          ||| |
Sbjct 1593599 GTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCGA 1593658

Query 135     GTGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGCT 194
          ||| |
Sbjct 1593659 GTGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGCT 1593718

Query 195     GGAATCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATA 254
          ||| |
Sbjct 1593719 GGAATCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATA 1593778

Query 255     TCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGA 314
          ||| |
Sbjct 1593779 TCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGA 1593838

Query 315     CTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCG 374
          ||| |
Sbjct 1593839 CTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCG 1593898

Query 375     GTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAAC 434
          ||| |
Sbjct 1593899 GTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAAC 1593958

Query 435     AGTGGGATAGCGTGCCG 451
          ||| |
Sbjct 1593959 AGTGGGATAGCGTGCCG 1593975

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Lampiran 17

Hasil BLAST Alignment Sampel 6

Query: None Query ID: lc1|Query_7310273 Length: 463

>Mycobacterium tuberculosis H37Rv complete genome
Sequence ID: AL123456.3 Length: 4411532
Range 1: 1593533 to 1593975

Score:806 bits(436), Expect:0.0,
Identities:441/443(99%), Gaps:2/443(0%), Strand: Plus/Plus

Query	13	TGCT-CGGGT-CTTGTCTGGTCCGGTGC	70
Sbjct	1593533	TGCTCCGGGTCCTGTCTGGTCCGGTGC	1593592
Query	71	CGGCTAGTGCCGACGGCCCGGTCCAGCT	130
Sbjct	1593593	CGGCTAGTGCCGACGGCCCGGTCCAGCT	1593652
Query	131	CCCCGAGTGGGAGCTGGTTTCAGCCCGCT	190
Sbjct	1593653	CCCCGAGTGGGAGCTGGTTTCAGCCCGCT	1593712
Query	191	AGCGCTGGAATCTCACCGATGACCGGCAG	250
Sbjct	1593713	AGCGCTGGAATCTCACCGATGACCGGCAG	1593772
Query	251	TGAATATCGGAAATGCTTTGTGGGCGCCT	310
Sbjct	1593773	TGAATATCGGAAATGCTTTGTGGGCGCCT	1593832
Query	311	ACTGGACTGTCCAGCCCGACGGCCTGGTCA	370
Sbjct	1593833	ACTGGACTGTCCAGCCCGACGGCCTGGTCA	1593892
Query	371	TCGGCGGTCCGGATCCTGGGACCTGGGTGT	430
Sbjct	1593893	TCGGCGGTCCGGATCCTGGGACCTGGGTGT	1593952
Query	431	ACCAACAGTGGGATAGCGTGCCG	453
Sbjct	1593953	ACCAACAGTGGGATAGCGTGCCG	1593975

Lampiran 18

Hasil BLAST Alignment Sampel 7

 Query: None Query ID: lcl|Query_7458495 Length: 460

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593533 to 1593975

Score:806 bits(436), Expect:0.0,

Identities:441/443(99%), Gaps:1/443(0%), Strand: Plus/Plus

Query	9	TGCTTCGGGT-CTTGTCGTGGTCCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTG	67
Sbjct	1593533	TGCTCCGGGTCTTGTCGTGGTCCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTG	1593592
Query	68	CGGCTAGTGCCGACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACG	127
Sbjct	1593593	CGGCTAGTGCCGACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACG	1593652
Query	128	CCCCGAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTC	187
Sbjct	1593653	CCCCGAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTC	1593712
Query	188	AGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCG	247
Sbjct	1593713	AGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCG	1593772
Query	248	TGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGC	307
Sbjct	1593773	TGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGC	1593832
Query	308	ACTGGACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTC	367
Sbjct	1593833	ACTGGACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTC	1593892
Query	368	TCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCG	427
Sbjct	1593893	TCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCG	1593952
Query	428	ACCAACAGTGGGATAGCGTGCCG	450
Sbjct	1593953	ACCAACAGTGGGATAGCGTGCCG	1593975

Lampiran 19

Hasil BLAST Alignment Sampel 8

Query: None Query ID: lcl|Query_7626941 Length: 459

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593538 to 1593975

Score:804 bits(435), Expect:0.0,

Identities:437/438(99%), Gaps:0/438(0%), Strand: Plus/Plus

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Query 12      CGGGTCCTTGTCTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGCAGCT 71
          |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593538 CGGGTCCTTGTCTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGCAGCT 1593597

Query 72      AGTGCCGACGGCCCGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCG 131
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593598 AGTGCCGACGGCCCGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCG 1593657

Query 132     AGTGGGAGCTGGTTCAGCCCCTGGTATCAACCCCTGCAATGGGACCGACTTTCAGCGC 191
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593658 AGTGGGAGCTGGTTCAGCCCCTGGTATCAACCCCTGCAATGGGACCGACTTTCAGCGC 1593717

Query 192     TGGAACTCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAAT 251
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593718 TGGAACTCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAAT 1593777

Query 252     ATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGG 311
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Sbjct 1593778 ATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGG 1593837

Query 312     ACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC 371
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593838 ACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC 1593897

Query 372     GGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAA 431
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Sbjct 1593898 GGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAA 1593957

Query 432     CAGTGGGATAGCGTGCCG 449
          |||||
Sbjct 1593958 CAGTGGGATAGCGTGCCG 1593975

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Lampiran 20

Hasil BLAST Alignment Sampel 12

 Query: None Query ID: lcl|Query_729303 Length: 459

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593533 to 1593975

Score:806 bits(436), Expect:0.0,

Identities:441/443(99%), Gaps:2/443(0%), Strand: Plus/Plus

```

Query  9      TGCT-CGGGT-CTTGTCTGGTTCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTG  66
          ||||  ||||  ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593533 TGCTCCGGGTCCTTGTCTGGTTCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTG  1593592

Query  67      CGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACG  126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593593 CGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACG  1593652

Query  127     CCCCAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTC  186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593653 CCCCAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTC  1593712

Query  187     AGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCG  246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593713 AGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCG  1593772

Query  247     TGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGC  306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593773 TGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGC  1593832

Query  307     ACTGGACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTC  366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593833 ACTGGACTGTCCAGCCCAGCGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTC  1593892

Query  367     TCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCGACCCCAATGCACCCG  426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593893 TCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCGACCCCAATGCACCCG  1593952

Query  427     ACCAACAGTGGGATAGCGTGCCG  449
          ||||||||||||||||
Sbjct 1593953 ACCAACAGTGGGATAGCGTGCCG  1593975
  
```

Lampiran 21

Hasil BLAST Alignment Sampel 13

 Query: None Query ID: lcl|Query_2805009 Length: 461

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593529 to 1593975

Score:808 bits(437), Expect:0.0,

Identities:444/447(99%), Gaps:1/447(0%), Strand: Plus/Plus

Query	6	GGTG-GCTCCGGGGTCTTGTCTGGTGGTGGTGGTTCGATGTGGCGGTGCTAAACGCC	64
Sbjct	1593529	GGTGTGCTCCGGGTCTTGTCTGGTGGTGGTTCGATGTGGCGGTGCTAAACGCC	1593588
Query	65	GGTGCGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTG	124
Sbjct	1593589	GGTGCGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTG	1593648
Query	125	GACGCCCCGAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGAC	184
Sbjct	1593649	GACGCCCCGAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGAC	1593708
Query	185	TTTCAGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAA	244
Sbjct	1593709	TTTCAGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAA	1593768
Query	245	TGCGTGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAAGTGGATCAGC	304
Sbjct	1593769	TGCGTGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAAGTGGATCAGC	1593828
Query	305	CAGCACTGGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACG	364
Sbjct	1593829	CAGCACTGGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACG	1593888
Query	365	GTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGACCCCAATGCA	424
Sbjct	1593889	GTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGACCCCAATGCA	1593948
Query	425	CCCGACCAACAGTGGGATAGCGTGCCG	451
Sbjct	1593949	CCCGACCAACAGTGGGATAGCGTGCCG	1593975

Lampiran 22

Hasil BLAST Alignment Sampel 15

 Query: None Query ID: lc1|Query_993451 Length: 461

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593536 to 1593975

Score:800 bits(433), Expect:0.0,

Identities:438/440(99%), Gaps:1/440(0%), Strand: Plus/Plus

```

Query 13      TCGGGG-CTTGTCGTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGC GG 71
           || |||| |
Sbjct 1593536 TCCGGGTCTTGTCTGTGGTCCGGTGCAGTTCGATGTGGCGGTGCTAAACGCCGGTGC GG 1593595

Query 72      CTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCC 131
           |||
Sbjct 1593596 CTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCC 1593655

Query 132     CGAGTGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGC 191
           |||
Sbjct 1593656 CGAGTGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGC 1593715

Query 192     GCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGA 251
           |||
Sbjct 1593716 GCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGA 1593775

Query 252     ATATCGGAAATGCTTTGTGGGCGCCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACT 311
           |||
Sbjct 1593776 ATATCGGAAATGCTTTGTGGGCGCCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACT 1593835

Query 312     GGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGTTCTCG 371
           |||
Sbjct 1593836 GGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGTTCTCG 1593895

Query 372     GCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGACCCCAATGCACCCGACC 431
           |||
Sbjct 1593896 GCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGACCCCAATGCACCCGACC 1593955

Query 432     AACAGTGGGATAGCGTGCCG 451
           |||
Sbjct 1593956 AACAGTGGGATAGCGTGCCG 1593975

```

Lampiran 23

Hasil BLAST Alignment Sampel 16

Query: None Query ID: lcl|Query_3007797 Length: 459

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593538 to 1593975

Score:802 bits(434), Expect:0.0,

Identities:437/438(99%), Gaps:1/438(0%), Strand: Plus/Plus

```

Query  13      CGGGT-CTTGTCTGTGGTCCGGTCCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCT  71
          |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593538  CGGGTCTTGTCTGTGGTCCGGTCCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCT 1593597

Query  72      AGTGCCGACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCG  131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593598  AGTGCCGACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCG 1593657

Query  132     AGTGGGAGCTGGTTCAGCCCGCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGC  191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593658  AGTGGGAGCTGGTTCAGCCCGCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGC 1593717

Query  192     TGGAACTCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAAT  251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593718  TGGAACTCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAAT 1593777

Query  252     ATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGG  311
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593778  ATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGG 1593837

Query  312     ACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC  371
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593838  ACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC 1593897

Query  372     GGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGCACCCTAATGCACCCGACCAA  431
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593898  GGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGGCACCCTAATGCACCCGACCAA 1593957

Query  432     CAGTGGGATAGCGTGCCG  449
          ||||||||||||||||
Sbjct 1593958  CAGTGGGATAGCGTGCCG  1593975

```

Lampiran 24

Hasil BLAST Alignment Sampel 18

Query: None Query ID: lc1|Query_3133171 Length: 455

>Mycobacterium tuberculosis H37Rv complete genome
 Sequence ID: AL123456.3 Length: 4411532
 Range 1: 1593545 to 1593975

Score:797 bits(431), Expect:0.0,
 Identities:431/431(100%), Gaps:0/431(0%), Strand: Plus/Plus

Query	15	TTGTCGTGGTTCGGTGC	GGTGTTCGATGTGGCGGTGCTAAACGCCGGTGC	GGCTAGTGCCG	74
Sbjct	1593545	TTGTCGTGGTTCGGTGC	GGTGTTCGATGTGGCGGTGCTAAACGCCGGTGC	GGCTAGTGCCG	1593604
Query	75	ACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCGAGTGGGA	134		
Sbjct	1593605	ACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCGAGTGGGA	1593664		
Query	135	GCTGGTTCAGCCCCTGGTGTATCAACCCCTGCAATGGGACCGACTTTCAGCGCTGGAATC	194		
Sbjct	1593665	GCTGGTTCAGCCCCTGGTGTATCAACCCCTGCAATGGGACCGACTTTCAGCGCTGGAATC	1593724		
Query	195	TCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATATCGGAA	254		
Sbjct	1593725	TCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATATCGGAA	1593784		
Query	255	ATGCTTTGTGGGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGACTGTCC	314		
Sbjct	1593785	ATGCTTTGTGGGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGACTGTCC	1593844		
Query	315	AGCCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGGTCCGG	374		
Sbjct	1593845	AGCCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGGTCCGG	1593904		
Query	375	ATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAACAGTGGG	434		
Sbjct	1593905	ATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAACAGTGGG	1593964		
Query	435	ATAGCGTGCCG	445		
Sbjct	1593965	ATAGCGTGCCG	1593975		

Lampiran 25

Hasil BLAST Alignment Sampel 20

Query: None Query ID: lcl|Query_3207967 Length: 460

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593527 to 1593975

Score:691 bits(374), Expect:0.0,

Identities:424/449(94%), Gaps:0/449(0%), Strand: Plus/Plus

```

Query 2      GCCGTGTTCCCGGGGTCTTGTCTGGTCCGGTGCGGTGTTCATGTGGCGGTGCTAAACG 61
           || ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593527 GCGGTGTGCTCCGGGTCTTGTCTGGTCCGGTGCGGTGTTCGATGTGGCGGTGCTAAACG 1593586

Query 62     CCGGTGCGGCTAGTGCCAACGGCCCGTCCAGCTGAAAACCAATTGGGCAATGTTTGCC 121
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593587 CCGGTGCGGCTAGTGCCGACGGCCCGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCC 1593646

Query 122    TGGACCCCCGAGTGGGAGCTGGTTCACCCCGCTGGTGATCAACCCCTGCAATGGGACCG 181
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593647 TGGACGCCCCGAGTGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCG 1593706

Query 182    ACTTTCACCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGG 241
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593707 ACTTTCAGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGG 1593766

Query 242    AATGCGTGAATATCGAAAATGCTTTGTGGGCCCCCTGCACCCCTGTGTGAACTGGATCA 301
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593767 AATGCGTGAATATCGAAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCA 1593826

Query 302    CCCACCACTGGACTGTCCACCCCAACGGCCTGGTCAAAAGTGATCTTGATGCCTGCCTCA 361
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593827 GCCAGCACTGGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCA 1593886

Query 362    CGGTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCAACCCCAATG 421
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593887 CGGTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCGACCCCAATG 1593946

Query 422    CACCCAACCAACAGTGGGATAGCGTGCCG 450
           ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 1593947 CACCCGACCAACAGTGGGATAGCGTGCCG 1593975

```


Lampiran 26

Hasil BLAST Alignment Sampel 21

Query: None Query ID: lcl|Query_298345 Length: 458

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593529 to 1593975

Score:813 bits(440), Expect:0.0,

Identities:445/447(99%), Gaps:2/447(0%), Strand: Plus/Plus

```

Query 4      GGT-TGCTCCGGGT-CTTGTCTGGTCCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCC 61
          ||| ||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593529 GGTGTGCTCCGGGTCCTTGTCTGGTCCGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCC 1593588

Query 62     GGTGCGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTG 121
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593589 GGTGCGGCTAGTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTG 1593648

Query 122    GACGCCCCGAGTGGGAGCTGGTTCAGCCCCTGGTATCAACCCCTGCAATGGGACCGAC 181
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593649 GACGCCCCGAGTGGGAGCTGGTTCAGCCCCTGGTATCAACCCCTGCAATGGGACCGAC 1593708

Query 182    TTTCAGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAA 241
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593709 TTTCAGCGCTGGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAA 1593768

Query 242    TGCGTGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGC 301
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593769 TGCGTGAATATCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGC 1593828

Query 302    CAGCACTGGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACG 361
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593829 CAGCACTGGACTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACG 1593888

Query 362    GTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCA 421
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 1593889 GTTCTCGGCGGTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCA 1593948

Query 422    CCCGACCAACAGTGGGATAGCGTGCCG 448
          |||||||||||||||
Sbjct 1593949 CCCGACCAACAGTGGGATAGCGTGCCG 1593975

```

Lampiran 27

Hasil BLAST Alignment Sampel 22

Query: None Query ID: lc1|Query_3678983 Length: 458

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593540 to 1593975

Score:798 bits(432), Expect:0.0,

Identities:435/436(99%), Gaps:1/436(0%), Strand: Plus/Plus

```

Query  14      GGT-CTTGTCTGGTCCGGTGC GGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAG 72
          ||| |
Sbjct 1593540  GGTCTTGTCTGGTCCGGTGC GGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAG 1593599

Query  73      TGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCGAG 132
          ||| |
Sbjct 1593600  TGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTGCCTGGACGCCCCGAG 1593659

Query  133     TGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTCAGCGCTG 192
          ||| |
Sbjct 1593660  TGGGAGCTGGTTCAGCCCGCTGGTGATCAACCCCTGCAATGGGACCGACTTTCAGCGCTG 1593719

Query  193     GAATCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATAT 252
          ||| |
Sbjct 1593720  GAATCTACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATAT 1593779

Query  253     CGGAAATGCTTTGTGGGCGGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGAC 312
          ||| |
Sbjct 1593780  CGGAAATGCTTTGTGGGCGGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGAC 1593839

Query  313     TGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGG 372
          ||| |
Sbjct 1593840  TGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGG 1593899

Query  373     TCCGGATCCTGGGACCTGGGTGTCACCCGCTGGTGCGACCCCAATGCACCCGACCAACA 432
          ||| |
Sbjct 1593900  TCCGGATCCTGGGACCTGGGTGTCACCCGCTGGTGCGACCCCAATGCACCCGACCAACA 1593959

Query  433     GTGGGATAGCGTGCCG 448
          ||| |
Sbjct 1593960  GTGGGATAGCGTGCCG 1593975

```

Lampiran 28

Hasil BLAST Alignment Sampel 23

Query: None Query ID: lcl|Query_3788053 Length: 460

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593539 to 1593975

Score:800 bits(433), Expect:0.0,

Identities:436/437(99%), Gaps:1/437(0%), Strand: Plus/Plus

```

Query  15      GGGT-CTTGTCGTGGTCGGTGCGGTGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTA  73
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593539  GGGTCCTTGTCGTGGTCGGTGCGGTGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTA 1593598

Query  74      GTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCGA  133
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593599  GTGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCCGA 1593658

Query  134     GTGGGAGCTGGTTCAGCCCCTGGTGATCAACCCCTGCAATGGGACCGACTTTCAGCGCT  193
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593659  GTGGGAGCTGGTTCAGCCCCTGGTGATCAACCCCTGCAATGGGACCGACTTTCAGCGCT 1593718

Query  194     GGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATA  253
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593719  GGAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATA 1593778

Query  254     TCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGA  313
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593779  TCGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGA 1593838

Query  314     CTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCG  373
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593839  CTGTCCAGCCCGACGGCCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCG 1593898

Query  374     GTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCGACCCCAATGCACCCGACCAAC  433
      |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593899  GTCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCGACCCCAATGCACCCGACCAAC 1593958

Query  434     AGTGGGATAGCGTGCCG  450
      |||  |||||||||||||||
Sbjct 1593959  AGTGGGATAGCGTGCCG  1593975

```

Lampiran 29

Hasil BLAST Alignment Sampel 26

Query: None Query ID: lcl|Query_1926507 Length: 458

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593544 to 1593975

Score:798 bits(432), Expect:0.0,

Identities:432/432(100%), Gaps:0/432(0%), Strand: Plus/Plus

```

Query 16      CTTGTCGTGGTCCGGTGCAGGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAGTGCC 75
                |||
Sbjct 1593544 CTTGTCGTGGTCCGGTGCAGGTTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAGTGCC 1593603

Query 76      GACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCGAGTGGG 135
                |||
Sbjct 1593604 GACGGCCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCGAGTGGG 1593663

Query 136     AGCTGGTTCAGCCCCTGGTGTATCAACCCCTGCAATGGGACCGACTTTCAGCGCTGGAAT 195
                |||
Sbjct 1593664 AGCTGGTTCAGCCCCTGGTGTATCAACCCCTGCAATGGGACCGACTTTCAGCGCTGGAAT 1593723

Query 196     CTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATATCGGA 255
                |||
Sbjct 1593724 CTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATATCGGA 1593783

Query 256     AATGCTTTGTGGGCGCCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGACTGTC 315
                |||
Sbjct 1593784 AATGCTTTGTGGGCGCCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGACTGTC 1593843

Query 316     CAGCCCAGCGGCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGGTCCG 375
                |||
Sbjct 1593844 CAGCCCAGCGGCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGCGGTCCG 1593903

Query 376     GATCCTGGGACCTGGGTGTCCACCCGCTGGTGGCAGCCCAATGCACCCGACCAACAGTGG 435
                |||
Sbjct 1593904 GATCCTGGGACCTGGGTGTCCACCCGCTGGTGGCAGCCCAATGCACCCGACCAACAGTGG 1593963

Query 436     GATAGCGTGCCG 447
                |||
Sbjct 1593964 GATAGCGTGCCG 1593975

```

Lampiran 30

Hasil BLAST Alignment Sampel 30

Query: None Query ID: lc1|Query_3968779 Length: 456

>Mycobacterium tuberculosis H37Rv complete genome

Sequence ID: AL123456.3 Length: 4411532

Range 1: 1593540 to 1593975

Score:798 bits(432), Expect:0.0,

Identities:435/436(99%), Gaps:1/436(0%), Strand: Plus/Plus

```

Query  12      GGT-CTTGTCTGGTGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAG  70
      ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593540  GGTCTTGTCTGGTGGTGCGGTGTTCGATGTGGCGGTGCTAAACGCCGGTGCGGCTAG  1593599

Query  71      TGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCGAG  130
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593600  TGCCGACGGCCCGGTCCAGCTGAAGAGCCGATTGGGCGATGTTTGCCTGGACGCCCGAG  1593659

Query  131     TGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGCTG  190
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593660  TGGGAGCTGGTTCAGCCCCTGGTGTCAACCCCTGCAATGGGACCGACTTTCAGCGCTG  1593719

Query  191     GAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATAT  250
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593720  GAATCTCACCGATGACCGGCAGGTCGAGAGCGTGGCCTTCCCCGGGGAATGCGTGAATAT  1593779

Query  251     CGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGAC  310
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593780  CGGAAATGCTTTGTGGGCGCGCCTGCAGCCCTGTGTGAACTGGATCAGCCAGCACTGGAC  1593839

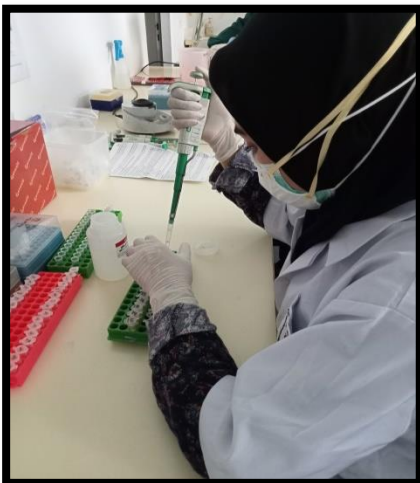
Query  311     TGTCCAGCCCAGCGGCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC GG  370
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593840  TGTCCAGCCCAGCGGCTGGTCAAGAGTGATCTTGATGCCTGCCTCACGGTTCTCGGC GG  1593899

Query  371     TCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAACA  430
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1593900  TCCGGATCCTGGGACCTGGGTGTCCACCCGCTGGTGCACCCCAATGCACCCGACCAACA  1593959

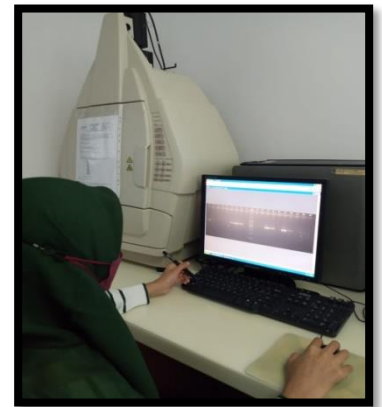
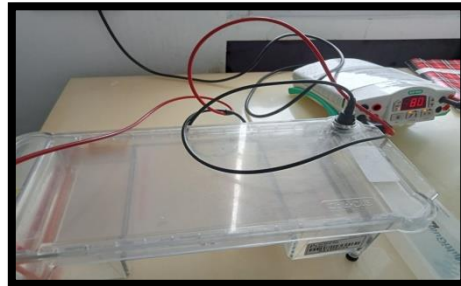
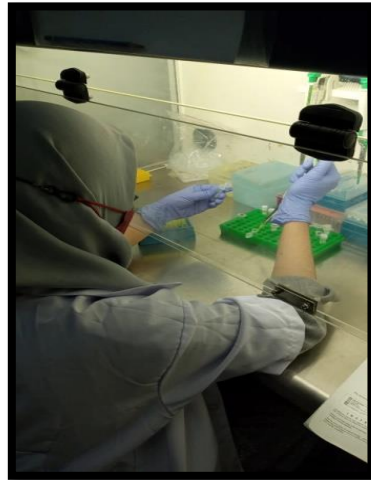
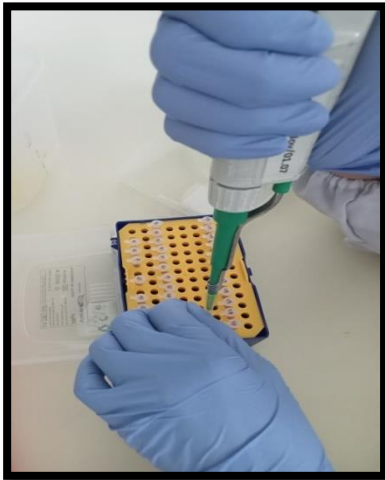
Query  431     GTGGGATAGCGTGCCG  446
      ||||||||||||
Sbjct 1593960  GTGGGATAGCGTGCCG  1593975

```

Lampiran 31. Proses Ekstraksi DNA



Lampiran 32. Proses PCR



Lampiran 33. Hasil BLAST Primer

Sequence ID: Query_92011 Length: 474 Number of Matches: 1				
Range 1: 1 to 18 Graphics			▼ Next Match ▲ Previous Match	
Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	1e-07	18/18(100%)	0/18(0%)	Plus/Plus
Query 11	ATGGGTGAATTACGGTTG	28		
Sbjct 1	ATGGGTGAATTACGGTTG	18		

Primer Forward

Sequence ID: Query_41539 Length: 474 Number of Matches: 1				
Range 1: 457 to 471 Graphics			▼ Next Match ▲ Previous Match	
Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	7e-06	15/15(100%)	0/15(0%)	Plus/Minus
Query 10	CGGCACGCTATCCCA	24		
Sbjct 471	CGGCACGCTATCCCA	457		

Primer Reverse

Lampiran 34. Reverensi Strain

Protein Rv1419 H37RV

```

atg ggt gaa tta cgg ttg gtg ggc ggt gtg ctc cgg gtc ctt gtc gtg gtc ggt gcg gtg
M G E L R L V G G V L R V L V V V G A V
ttc gat gtg gcg gtg cta aac gcc ggt gcg gct agt gcc gac ggc ccg gtc cag ctg aag
F D V A V L N A G A A S A D G P V Q L K
agc cga ttg ggc gat gtt tgc ctg gac gcc ccg agt ggg agc tgg ttc agc ccg ctg gtg
S R L G D V C L D A P S G S W F S P L V
atc aac ccc tgc aat ggg acc gac ttt cag cgc tgg aat ctc acc gat gac cgg cag gtc
I N P C N G T D F Q R W N L T D D R Q V
gag agc gtg gcc ttc ccc ggg gaa tgc gtg aat atc gga aat gct ttg tgg gcg cgc ctg
E S V A F P G E C V N I G N A L W A R L
cag ccc tgt gtg aac tgg atc agc cag cac tgg act gtc cag ccc gac ggc ctg gtc aag
Q P C V N W I S Q H W T V Q P D G L V K
agt gat ctt gat gcc tgc ctc acg gtt ctc ggc ggt ccg gat cct ggg acc tgg gtg tcc
S D L D A C L T V L G G P D P G T W V S
acc cgc tgg tgc gac ccc aat gca ccc gac caa cag tgg gat agc gtg ccg taa
T R W C D P N A P D Q Q W D S V p -

```

```

1 mgelrlvggv lrvlvvvgav fdvavlnaga asadgpvqlk srlgdvclda psgswfslpv
61 inpcngtdfq rwnltddrqv esvafpgecv nignalwarl qpcvnwisqh wtvqpdglvk
121 slddacltvl ggpdpgtwvs trwcdpnapd qqwdsvp

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