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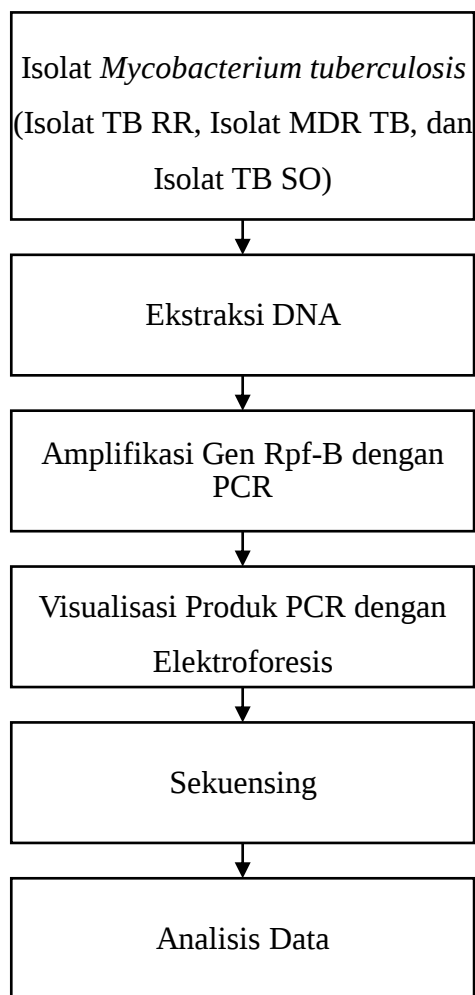
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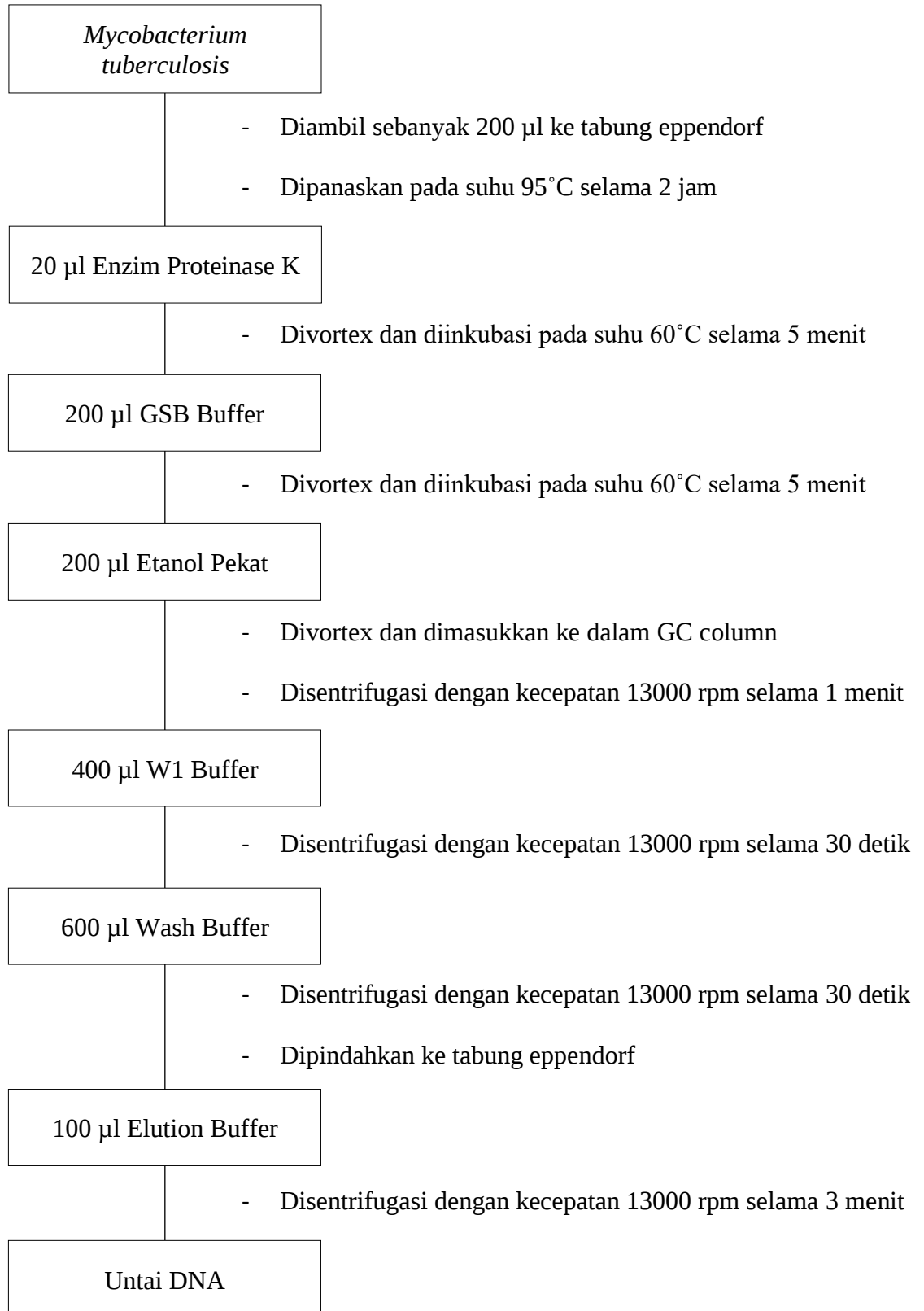
LAMPIRAN

Lampiran 1. Skema Kerja

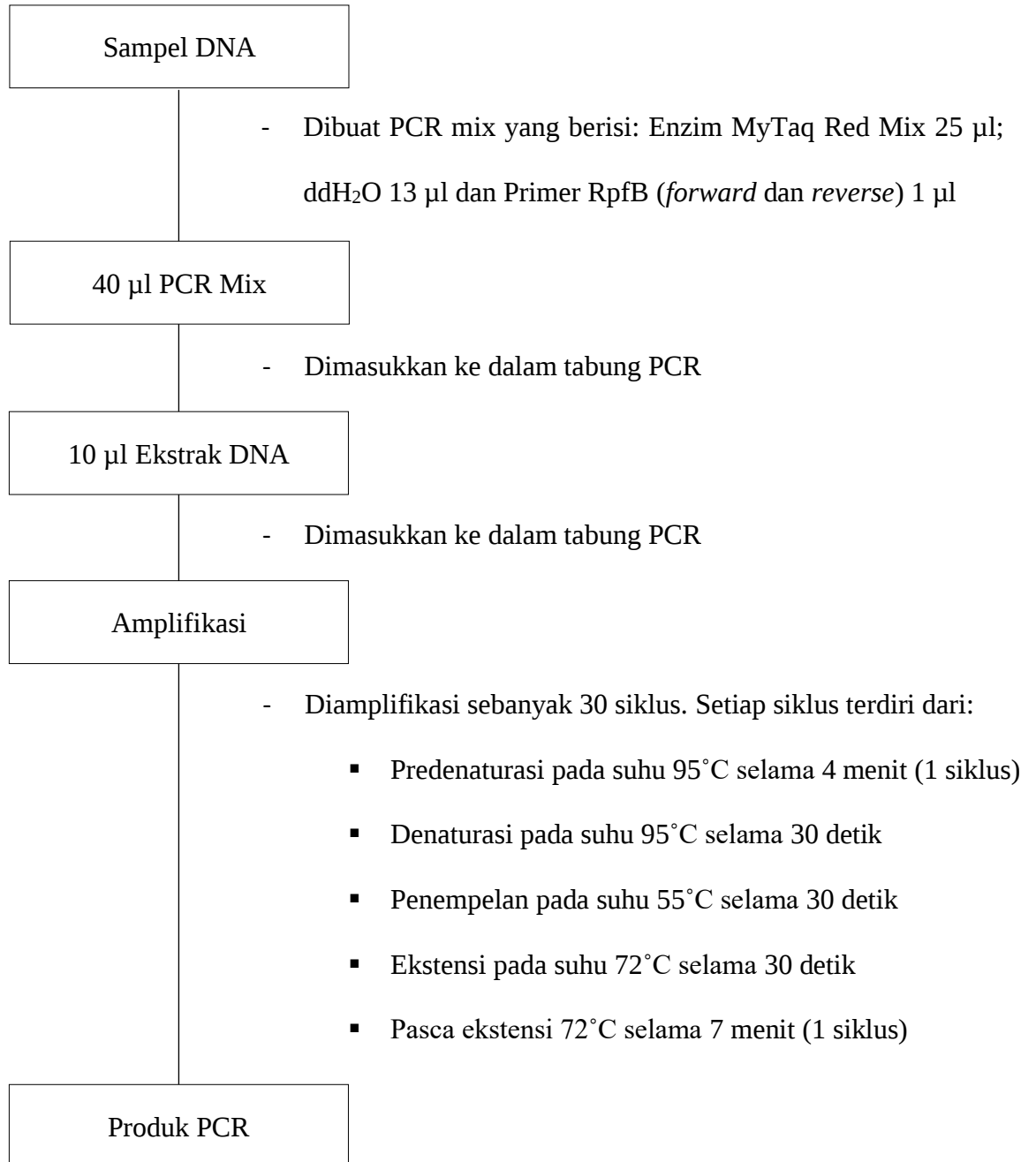
A. Skema Kerja Penelitian



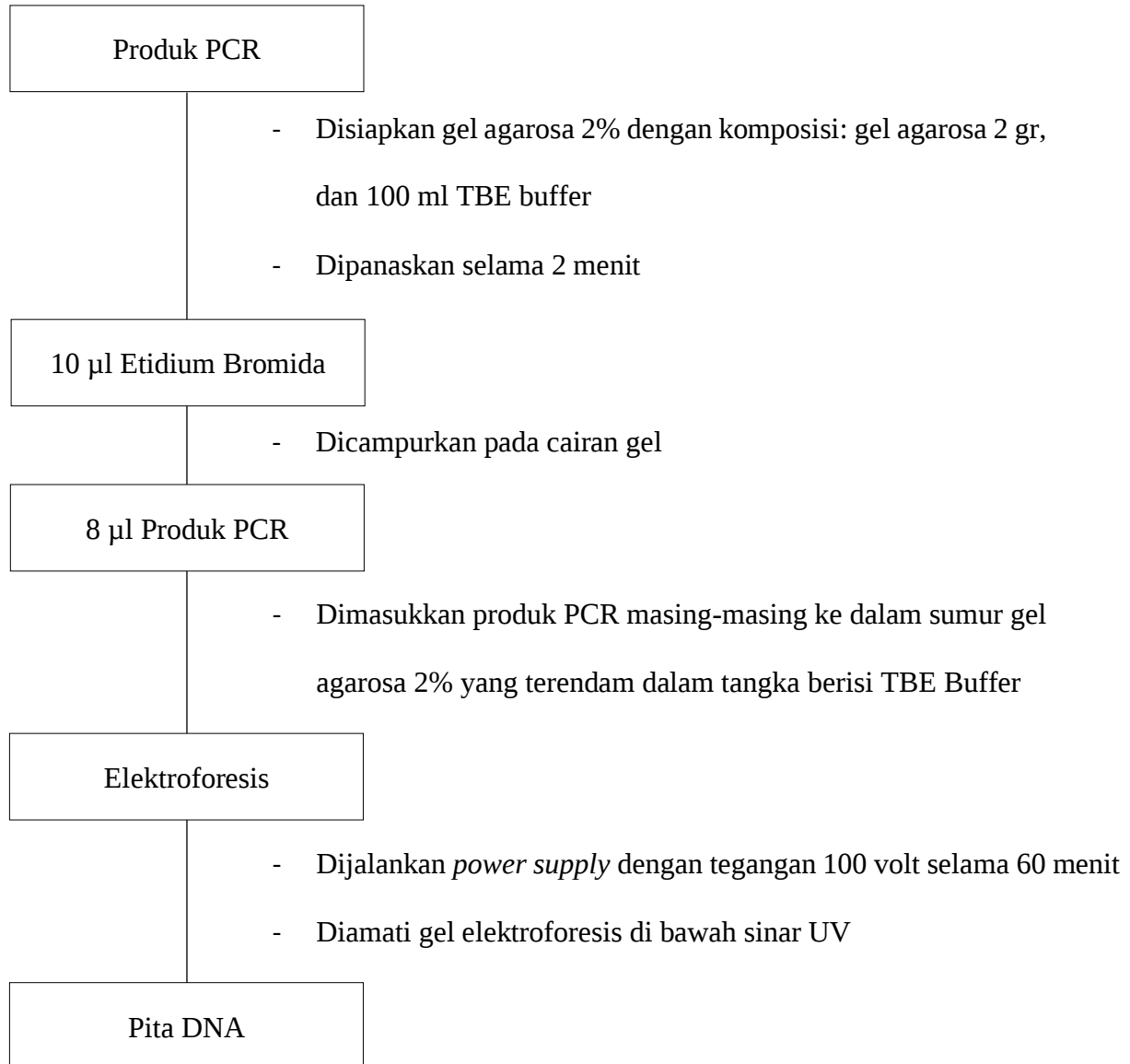
B. Skema Kerja Ekstraksi DNA *Mycobacterium tuberculosis*



C. Skema Kerja Amplifikasi Gen Rpf-B dengan PCR



D. Skema Kerja Deteksi Produk PCR dengan Elektroforesis



Lampiran 2. Gen Pengkode Rpf-B pada Genom *Mycobacterium tuberculosis* H37Rv

NIH National Library of Medicine
National Center for Biotechnology Information

Nucleotide Nucleotide Search Advanced Help

FASTA Send to: Change region shown

Mycobacterium tuberculosis H37Rv, complete genome

NCBI Reference Sequence: NC_000962.3

GenBank Graphics

>NC_000962.3:1128091-1129179 Mycobacterium tuberculosis H37Rv, complete genome

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Analyze this sequence

Run BLAST

Pick Primers

Related information

Assembly

BioProject

Protein

Lampiran 3. Hasil Analisis BLAST

A. Hasil BLAST Sampel C1

Mycobacterium tuberculosis H37Rv, complete genome					
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B. Hasil BLAST Sampel C2

Mycobacterium tuberculosis H37Rv, complete genome					
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C. Hasil BLAST Sampel C3

Mycobacterium tuberculosis H37Rv, complete genome					
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Query 421		GTGACGCTCAACGACGCGCGGTTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			480
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Sbjct 1128871		GCCACGAAGCCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC			1128930
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D. Hasil BLAST Sampel C4

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC 000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				Next Match	Previous Match
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2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			60
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			1128150
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			120
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			1128210
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			180
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			1128270
Query 181		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGCTGCGGGCT			240
Sbjct 1128271		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGCTGCGGGCT			1128330
Query 241		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			300
Sbjct 1128331		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			1128390
Query 301		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT			360
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT			1128450
Query 361		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			420
Sbjct 1128451		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			1128510
Query 421		GTGACGCTCAACGACGCGGGTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			480
Sbjct 1128511		GTGACGCTCAACGACGCGGGTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			1128570
Query 481		GGGCTGCTGAGTGCGGCCGGCGTGCCTGTGTGCAAGCGACACCGTGGTGCCCGCCGCG			540
Sbjct 1128571		GGGCTGCTGAGTGCGGCCGGCGTGCCTGTGTGCAAGCGACACCGTGGTGCCCGCCGCG			1128630
Query 541		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			600
Sbjct 1128631		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			1128690
Query 601		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTGTGAGGACCCGGAGATGAACATG			660
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTGTGAGGACCCGGAGATGAACATG			1128750
Query 661		AGCCGGGAGGTCTGTGAAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			720
Sbjct 1128751		AGCCGGGAGGTCTGTGAAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			1128810
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			780
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			1128870
Query 781		GCCCAAGAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			840
Sbjct 1128871		GCCCAAGAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			1128930
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			900
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			1128990
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			960
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			1129050
Query 961		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC			1020
Sbjct 1129051		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC			1129110
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1080
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1129170
Query 1081		GCGCGCTGA			1089
Sbjct 1129171		GCGCGCTGA			1129179

E. Hasil BLAST Sampel C5

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			60
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			1128150
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			120
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			1128210
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			180
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			1128270
Query 181		GACCTGTATCCCGCGGCGGCGTGCAGGTCATGACGCCGACACCATCGTGCTGCGGCGT			240
Sbjct 1128271		GACCTGTATCCCGCGGCGGCGTGCAGGTCATGACGCCGACACCATCGTGCTGCGGCGT			1128330
Query 241		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			300
Sbjct 1128331		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			1128390
Query 301		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCGGCGCGGCT			360
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCGGCGCGGCT			1128450
Query 361		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			420
Sbjct 1128451		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			1128510
Query 421		GTGACGCTCAACGACGCGGGTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTCGCG			480
Sbjct 1128511		GTGACGCTCAACGACGCGGGTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTCGCG			1128570
Query 481		GGGCTGCTGAGTGCGGCGGCGTGCCTGTTGCAAAAGCGACACGTTGGTGCCTGCGCG			540
Sbjct 1128571		GGGCTGCTGAGTGCGGCGGCGTGCCTGTTGCAAAAGCGACACGTTGGTGCCTGCGCG			1128630
Query 541		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			600
Sbjct 1128631		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			1128690
Query 601		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			660
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			1128750
Query 661		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			720
Sbjct 1128751		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			1128810
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			780
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			1128870
Query 781		GCCACGAAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			840
Sbjct 1128871		GCCACGAAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			1128930
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			900
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			1128990
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			960
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			1129050
Query 961		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1020
Sbjct 1129051		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1129110
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1080
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1129170
Query 1081		GCGCGCTGA			1089
Sbjct 1129171		GCGCGCTGA			1129179

F. Hasil BLAST Sampel C6

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			60
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			1128150
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			120
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			1128210
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			180
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			1128270
Query 181		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGTGCGGGCT			240
Sbjct 1128271		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGTGCGGGCT			1128330
Query 241		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			300
Sbjct 1128331		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			1128390
Query 301		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT			360
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT			1128450
Query 361		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCGCCAGACG			420
Sbjct 1128451		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCGCCAGACG			1128510
Query 421		GTGACGCTCAACGACGCGCGGTTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			480
Sbjct 1128511		GTGACGCTCAACGACGCGCGGTTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			1128570
Query 481		GGGCTGCTGAGTGCAGCGCGGCTGCCGCTGTGCAAGACGACACCGTGGTGCCCGCCGCG			540
Sbjct 1128571		GGGCTGCTGAGTGCAGCGCGGCTGCCGCTGTGCAAGACGACACCGTGGTGCCCGCCGCG			1128630
Query 541		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			600
Sbjct 1128631		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			1128690
Query 601		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			660
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			1128750
Query 661		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			720
Sbjct 1128751		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			1128810
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			780
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG			1128870
Query 781		GCCCCAAGCCGTTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC			840
Sbjct 1128871		GCCCCAAGCCGTTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC			1128930
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			900
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			1128990
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			960
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			1129050
Query 961		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1020
Sbjct 1129051		GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1129110
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1080
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1129170
Query 1081		GCGCGCTGA			1089
Sbjct 1129171		GCGCGCTGA			1129179

G. Hasil BLAST Sampel C7

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				▼ Next Match	▲ Previous Match
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCGGTGGCTATGCG	60			
Sbjct 1128091	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCGGTGGCTATGCG	1128150			
Query 61	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACACG	120			
Sbjct 1128151	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACACG	1128210			
Query 121	ATGAAATCGCGGTGATCGACATCGTCGAAGAGAAGCGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGTGATCGACATCGTCGAAGAGAAGCGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCGCGGCGCGGTGACAGTCCATGACGCCGACACCATCGTGTGCGGCGT	240			
Sbjct 1128271	GACCTGTATCCCGCGGCGCGGTGACAGTCCATGACGCCGACACCATCGTGTGCGGCGT	1128330			
Query 241	AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCGCGCGCGCT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCGCGCGCGCT	1128450			
Query 361	TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCGCCAAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCGCCAAAGACG	1128510			
Query 421	GTGACGCTCAACGACGCGCGGTTGGTGCACGCGTGCACCTTGCCGGCCCCAATGTCGCG	480			
Sbjct 1128511	GTGACGCTCAACGACGCGCGGTTGGTGCACGCGTGCACCTTGCCGGCCCCAATGTCGCG	1128570			
Query 481	GGGCTGCTGAGTGCGGCCGGCGTGGCGCTGTTGCAAGCGACACGTTGGTGCCTCCGCGCG	540			
Sbjct 1128571	GGGCTGCTGAGTGCGGCCGGCGTGGCGCTGTTGCAAGCGACACGTTGGTGCCTCCGCGCG	1128630			
Query 541	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGCTGTCGAGGACCCGGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGCTGTCGAGGACCCGGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGCTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTTCGCGGTA	720			
Sbjct 1128751	AGCCGGGAGGTGCTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTTCGCGGTA	1128810			
Query 721	GCTAAGGTCAACGGCGTCGAGACCGGCGTTTGCCTGTCGCAACGTCGTGGTGACCCCG	780			
Sbjct 1128811	GCTAAGGTCAACGGCGTCGAGACCGGCGTTTGCCTGTCGCAACGTCGTGGTGACCCCG	1128870			
Query 781	GCCCCAGAACCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC	840			
Sbjct 1128871	GCCCCAGAACCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACAGGGCACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACAGGGCACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

H. Hasil BLAST Sampel C8

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			60
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG			1128150
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			120
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG			1128210
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			180
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			1128270
Query 181		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGTGCGGGCT			240
Sbjct 1128271		GACCTGTATCCCGCGGCCGGCTGCAGGTCATGACGCCGACACCATCGTGTGCGGGCT			1128330
Query 241		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			300
Sbjct 1128331		AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			1128390
Query 301		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT			360
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT			1128450
Query 361		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			420
Sbjct 1128451		TCTCGCGCCAGCCGCTCCCGCTGTCCGGGATGGCGCTACCGGTCTGACGCCCAAGACG			1128510
Query 421		GTGACGCTCAACGACGCGCGGTTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			480
Sbjct 1128511		GTGACGCTCAACGACGCGCGGTTGGTGCGCACGGTGCACTTGCCGGCCCCAATGTGCGG			1128570
Query 481		GGGCTGCTGAGTGCGGCGCGGCTGCCGCTGTGCAAAAGCGACACCGTGGTGCCCGCCGCG			540
Sbjct 1128571		GGGCTGCTGAGTGCGGCGCGGCTGCCGCTGTGCAAAAGCGACACCGTGGTGCCCGCCGCG			1128630
Query 541		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			600
Sbjct 1128631		ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			1128690
Query 601		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			660
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTGTCGAGGACCCGGAGATGAACATG			1128750
Query 661		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			720
Sbjct 1128751		AGCCGGGAGGTCTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA			1128810
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG			780
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG			1128870
Query 781		GCCCAAGAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			840
Sbjct 1128871		GCCCAAGAGCGTGGTGCGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC			1128930
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			900
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC			1128990
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			960
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC			1129050
Query 961		GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1020
Sbjct 1129051		GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC			1129110
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1080
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1129170
Query 1081		GCGCGCTGA			1089
Sbjct 1129171		GCGCGCTGA			1129179

I. Hasil BLAST Sampel C9

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				▼ Next Match	▲ Previous Match
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	60			
Sbjct 1128091	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	1128150			
Query 61	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCCGGTGACACG	120			
Sbjct 1128151	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCCGGTGACACG	1128210			
Query 121	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCGCGCGCGGTGCAGGTCCATGACCGCGACCATCGTGTGCGGCGT	240			
Sbjct 1128271	GACCTGTATCCCGCGCGCGGTGCAGGTCCATGACCGCGACCATCGTGTGCGGCGT	1128330			
Query 241	AGCCGTCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT	1128450			
Query 361	TCTCGCGCCAGCCGCGTCCGCTGTCCGGGATGGCGTACCGGTCGTGAGCGCCAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCGTCCGCTGTCCGGGATGGCGTACCGGTCGTGAGCGCCAAGACG	1128510			
Query 421	GTGCAGCTCAACGACGGCGGGTTGGTGCACGCGTGCATTTGCCGGCCCCAATGTCGCG	480			
Sbjct 1128511	GTGCAGCTCAACGACGGCGGGTTGGTGCACGCGTGCATTTGCCGGCCCCAATGTCGCG	1128570			
Query 481	GGGCTGTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACACGTGGTGCCTGCCGCG	540			
Sbjct 1128571	GGGCTGTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACACGTGGTGCCTGCCGCG	1128630			
Query 541	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGTA	720			
Sbjct 1128751	AGCCGGGAGGTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGTA	1128810			
Query 721	GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	780			
Sbjct 1128811	GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	1128870			
Query 781	GCCACGAAGCCGTGGTGGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC	840			
Sbjct 1128871	GCCACGAAGCCGTGGTGGGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAAGGACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAAGGACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGGAAGAGCAGATCGCCGTTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGGAAGAGCAGATCGCCGTTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGTCGACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGTCGACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

J. Hasil BLAST Sampel C10

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics Next Match Previous Match					
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	60			
Sbjct 1128091	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	1128150			
Query 61	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCAACG	120			
Sbjct 1128151	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCAACG	1128210			
Query 121	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCGCGCCGGCGTGACAGTCCATGACGCCGACACCATCGTGCTGCGGGCT	240			
Sbjct 1128271	GACCTGTATCCCGCGCCGGCGTGACAGTCCATGACGCCGACACCATCGTGCTGCGGGCT	1128330			
Query 241	AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT	1128450			
Query 361	TCTCGCGCCAGCCGCGTCCCGCTGTCCGGATGGCGCTACCGGTCGTACGCGCAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCGTCCCGCTGTCCGGATGGCGCTACCGGTCGTACGCGCAAGACG	1128510			
Query 421	GTGCAAGTCAACGACGGCGGGTTGGTGCACGCGTCACTTGCCGGCCCCCAATGTCGCG	480			
Sbjct 1128511	GTGCAAGTCAACGACGGCGGGTTGGTGCACGCGTCACTTGCCGGCCCCCAATGTCGCG	1128570			
Query 481	GGGCTGCTGAGTGCAGCGCGGTGCGCGCTGTTGCAAGGACACGAGTGGTGCCCGCCGCG	540			
Sbjct 1128571	GGGCTGCTGAGTGCAGCGCGGTGCGCGCTGTTGCAAGGACACGAGTGGTGCCCGCCGCG	1128630			
Query 541	ACGGCCCCGATCGTCGAAGGCATGACATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCGAAGGCATGACATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGTGCGCGTGCAGCGGACGCGCTCGTGTGAGGACCCGGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGTGCGCGTGCAGCGGACGCGCTCGTGTGAGGACCCGGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGCTGCAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGTA	720			
Sbjct 1128751	AGCCGGGAGGTGCTGCAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGTA	1128810			
Query 721	GCTAAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	780			
Sbjct 1128811	GCTAAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	1128870			
Query 781	GCCACGAAGCCGTGGTGCAGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC	840			
Sbjct 1128871	GCCACGAAGCCGTGGTGCAGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCAAGGACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGACACCCCGCTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGACACCCCGCTGACCTCGCCACCCGCAAGAGCAGATCGCCGTTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

K. Hasil BLAST Sampel C11

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3		Length: 4411532		Number of Matches: 1	
Range 1: 1128091 to 1129179		GenBank	Graphics	Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCCGCCGGTGGCTATGCG			60
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCCGCCGGTGGCTATGCG			1128150
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCACG			120
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCACG			1128210
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			180
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC			1128270
Query 181		GACCTGTATCCCGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGTGCGGCGT			240
Sbjct 1128271		GACCTGTATCCCGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGTGCGGCGT			1128330
Query 241		AGCCGTCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			300
Sbjct 1128331		AGCCGTCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG			1128390
Query 301		TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT			360
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT			1128450
Query 361		TCTCGGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTGTCAGCGCCAAGACG			420
Sbjct 1128451		TCTCGGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTGTCAGCGCCAAGACG			1128510
Query 421		GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG			480
Sbjct 1128511		GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG			1128570
Query 481		GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACACGTGGTGCCCGCCGCG			540
Sbjct 1128571		GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACACGTGGTGCCCGCCGCG			1128630
Query 541		ACGGCCCCGATCGTCGAAGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			600
Sbjct 1128631		ACGGCCCCGATCGTCGAAGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC			1128690
Query 601		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG			660
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG			1128750
Query 661		AGCCGGGAGGTGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGGTA			720
Sbjct 1128751		AGCCGGGAGGTGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCCGCGGTA			1128810
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG			780
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG			1128870
Query 781		GCCACGAAGCCGTGGTGCGGGTGGGACCAAGCCGGTACCGAGGTGCCCGCGGTGATC			840
Sbjct 1128871		GCCACGAAGCCGTGGTGCGGGTGGGACCAAGCCGGTACCGAGGTGCCCGCGGTGATC			1128930
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGTTGGCAACTGGGCGATCAAC			900
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGTTGGCAACTGGGCGATCAAC			1128990
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACGAGGGACCTGGGAGGCCAACGGC			960
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACGAGGGACCTGGGAGGCCAACGGC			1129050
Query 961		GGGCTGCGGTATGACACCCGCGCTGACCGCGCCACCCGCGAAGAGCAGATCGCCGTTGCC			1020
Sbjct 1129051		GGGCTGCGGTATGACACCCGCGCTGACCGCGCCACCCGCGAAGAGCAGATCGCCGTTGCC			1129110
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1080
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT			1129170
Query 1081		GCGCGCTGA			1089
Sbjct 1129171		GCGCGCTGA			1129179

L. Hasil BLAST Sampel C12

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				▼ Next Match	▲ Previous Match
Score	Expect	Identities	Gaps	Strand	
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTTCGCCGGTGGCTATGCG		60	
Sbjct 1128091		ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTTCGCCGGTGGCTATGCG		1128150	
Query 61		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG		120	
Sbjct 1128151		GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACACG		1128210	
Query 121		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC		180	
Sbjct 1128211		ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC		1128270	
Query 181		GACCTGTATCCCGCGGCGGGCTGCAGGTCCATGACGCCGACACCATCGTGTGCGGGCT		240	
Sbjct 1128271		GACCTGTATCCCGCGGCGGGCTGCAGGTCCATGACGCCGACACCATCGTGTGCGGGCT		1128330	
Query 241		AGCCGTCGCTGCAGATCTCGCTGGATGGTACGACGCTAAGCAGGTGTGGACGACCGG		300	
Sbjct 1128331		AGCCGTCGCTGCAGATCTCGCTGGATGGTACGACGCTAAGCAGGTGTGGACGACCGG		1128390	
Query 301		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT		360	
Sbjct 1128391		TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT		1128450	
Query 361		TCTCGCGCCAGCCGCTCCCGCTGTCGGGATGGCGCTACCGGTCGTAGCGCCAAGACG		420	
Sbjct 1128451		TCTCGCGCCAGCCGCTCCCGCTGTCGGGATGGCGCTACCGGTCGTAGCGCCAAGACG		1128510	
Query 421		GTGACGCTAACGACGGCGGGTGGTGGCAGCGGTGCACTTGCCGGCCCCCAATGTCGCG		480	
Sbjct 1128511		GTGACGCTAACGACGGCGGGTGGTGGCAGCGGTGCACTTGCCGGCCCCCAATGTCGCG		1128570	
Query 481		GGGCTGCTGAGTGCGGCGGGCTGCCGCTGTTGCAAGCGACACAGTGGTGCCCGCGCG		540	
Sbjct 1128571		GGGCTGCTGAGTGCGGCGGGCTGCCGCTGTTGCAAGCGACACAGTGGTGCCCGCGCG		1128630	
Query 541		ACGGCCCCGATCGTCAAGGATGCAATCCAGGTGACCCGCAATCGGATCAAGAAGGTC		600	
Sbjct 1128631		ACGGCCCCGATCGTCAAGGATGCAATCCAGGTGACCCGCAATCGGATCAAGAAGGTC		1128690	
Query 601		ACCGAGCGGCTGCCGCTGCCGCGAACGCGCGTGTGTCGAGGACCCGAGATGAACATG		660	
Sbjct 1128691		ACCGAGCGGCTGCCGCTGCCGCGAACGCGCGTGTGTCGAGGACCCGAGATGAACATG		1128750	
Query 661		AGCCGGGAGGTGCTCAAGACCCGGGGTTCGGGGACCCAGGATGTGACGTTTCGCGGTA		720	
Sbjct 1128751		AGCCGGGAGGTGCTCAAGACCCGGGGTTCGGGGACCCAGGATGTGACGTTTCGCGGTA		1128810	
Query 721		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG		780	
Sbjct 1128811		GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCG		1128870	
Query 781		GCCCACGAAGCCGTGGTGGGTCGCGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC		840	
Sbjct 1128871		GCCCACGAAGCCGTGGTGGGTCGCGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC		1128930	
Query 841		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC		900	
Sbjct 1128931		GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC		1128990	
Query 901		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACAGGGCACCTGGGAGGCCAACGGC		960	
Sbjct 1128991		ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACAGGGCACCTGGGAGGCCAACGGC		1129050	
Query 961		GGGCTGCGGTATGACCCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC		1020	
Sbjct 1129051		GGGCTGCGGTATGACCCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC		1129110	
Query 1021		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT		1080	
Sbjct 1129111		GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT		1129170	
Query 1081		GCGCGCTGA	1089		
Sbjct 1129171		GCGCGCTGA	1129179		

M. Hasil BLAST Sampel C13

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	60			
Sbjct 1128091	ATGTTGCGCCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	1128150			
Query 61	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCACG	120			
Sbjct 1128151	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACCACG	1128210			
Query 121	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCAGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGCTGCGGCGT	240			
Sbjct 1128271	GACCTGTATCCCAGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGCTGCGGCGT	1128330			
Query 241	AGCCGTCGCTGAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCGCTGAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGT	1128450			
Query 361	TCTCGCGCCAGCCGCTCCCGCTGTCCGGATGGCGCTACCGGTCGTGAGCGCAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCTCCCGCTGTCCGGATGGCGCTACCGGTCGTGAGCGCAAGACG	1128510			
Query 421	GTGCAAGCTCAACGACGGCGGGTTGGTGCACGCGTGCATTTGCCGGCCCCCAATGTCGCG	480			
Sbjct 1128511	GTGCAAGCTCAACGACGGCGGGTTGGTGCACGCGTGCATTTGCCGGCCCCCAATGTCGCG	1128570			
Query 481	GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAGCGACACGTTGGTGGCCGCGCG	540			
Sbjct 1128571	GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAGCGACACGTTGGTGGCCGCGCG	1128630			
Query 541	ACGGCCCCGATCGTCGAAGGATGACGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCGAAGGATGACGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTGTGTCGAGGACCCGGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGCTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA	720			
Sbjct 1128751	AGCCGGGAGGTGCTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGGGTA	1128810			
Query 721	GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	780			
Sbjct 1128811	GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	1128870			
Query 781	GCCACGAAGCGTGGTGCCTGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC	840			
Sbjct 1128871	GCCACGAAGCGTGGTGCCTGGTGGGACCAAGCCCGGTACCGAGGTGCCCGCGGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGCAAGTTGACCAAGGACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGCAAGTTGACCAAGGACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGCACCCCGCGTGACCGCGCCACCCGGAAGAGCAGATCGCCGTTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGCACCCCGCGTGACCTCGCCACCCGGAAGAGCAGATCGCCGTTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

N. Hasil BLAST Sampel C14

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics			Next Match Previous Match		
Score	Expect	Identities	Gaps	Strand	
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	60			
Sbjct 1128091	ATGTTGCGCTGGTAGTCGGTGCCTGCTGCTGGTGTGGCGTTCGCCGGTGGCTATGCG	1128150			
Query 61	GTGCGCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACACG	120			
Sbjct 1128151	GTGCGCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCATGCGGGTGACACG	1128210			
Query 121	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGTGCGGCGT	240			
Sbjct 1128271	GACCTGTATCCCGCGCCGGCGTGACGGTCCATGACGCCGACACCATCGTGTGCGGCGT	1128330			
Query 241	AGCCGTCGCTGCAGATCTCGCTGGATGGTCAACGAGTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCGCTGCAGATCTCGCTGGATGGTCAACGAGTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGCTGGCCAACTCGCGATGACCGACACGGCGCCGGCCGCGCT	1128450			
Query 361	TCTCGCGCCAGCCGCTCCCGCTGTCCGGATGGCGCTACCGGTGTCAGCGCCAAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCTCCCGCTGTCCGGATGGCGCTACCGGTGTCAGCGCCAAAGACG	1128510			
Query 421	GTGCAGTCAACGACGCGGGTTGGTGCACACGGTGACTTGCCGGCCCCAATGTGCGG	480			
Sbjct 1128511	GTGCAGTCAACGACGCGGGTTGGTGCACACGGTGACTTGCCGGCCCCAATGTGCGG	1128570			
Query 481	GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAGCGACACGTTGGTGCCCGCCGCG	540			
Sbjct 1128571	GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAGCGACACGTTGGTGCCCGCCGCG	1128630			
Query 541	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTCGTGTGAGGACCCGGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCTCGTGTGAGGACCCGGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGCGTA	720			
Sbjct 1128751	AGCCGGGAGGTGTCGAAGACCCGGGGTTCCGGGGACCCAGGATGTGACGTTGCGCGTA	1128810			
Query 721	GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCTCGCCAACTGCTGGTGACCCCG	780			
Sbjct 1128811	GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCTCGCCAACTGCTGGTGACCCCG	1128870			
Query 781	GCCCACGAAGCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCGCGTGATC	840			
Sbjct 1128871	GCCCACGAAGCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCGCGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCGGTTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCGGTTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCGAGGACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGAGTTTGACCGAGGACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGACCCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGACCCCCGCGTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

O. Hasil BLAST Sampel C15

Mycobacterium tuberculosis H37Rv, complete genome					
Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1					
Range 1: 1128091 to 1129179 GenBank Graphics				▼ Next Match	▲ Previous Match
Score	Expect	Identities	Gaps	Strand	
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus	
Query 1	ATGTTGCGCCTGGTAGTCGGTGC	60			
Sbjct 1128091	ATGTTGCGCCTGGTAGTCGGTGC	1128150			
Query 61	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCAAG	120			
Sbjct 1128151	GTCGCCGATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCAAG	1128210			
Query 121	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	180			
Sbjct 1128211	ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC	1128270			
Query 181	GACCTGTATCCCGCGGCGGGCGTGACGGTCCATGACCGCGACACCATCGTGTGCGGGCT	240			
Sbjct 1128271	GACCTGTATCCCGCGGCGGGCGTGACGGTCCATGACCGCGACACCATCGTGTGCGGGCT	1128330			
Query 241	AGCCGTCGCTGCAGATCTCGCTGGATGGTACGACGCTAAGCAGGTGTGGACGACCGCG	300			
Sbjct 1128331	AGCCGTCGCTGCAGATCTCGCTGGATGGTACGACGCTAAGCAGGTGTGGACGACCGCG	1128390			
Query 301	TCGACGGTGGACGAGGCGTGCGCCAACTCGCGATGACCGACACGGCGCGCGCGCGGCT	360			
Sbjct 1128391	TCGACGGTGGACGAGGCGTGCGCCAACTCGCGATGACCGACACGGCGCGCGCGCGGCT	1128450			
Query 361	TCTCGCGCCAGCCGCTCCCGCTGTCGGGATGGCGCTACCGGTCGTAGCGCCAAGACG	420			
Sbjct 1128451	TCTCGCGCCAGCCGCTCCCGCTGTCGGGATGGCGCTACCGGTCGTAGCGCCAAGACG	1128510			
Query 421	GTGACGCTAACGACGGCGGGTGGTGGCGACGGTGCACCTTGCCGGCCCCAATGTCGCG	480			
Sbjct 1128511	GTGACGCTAACGACGGCGGGTGGTGGCGACGGTGCACCTTGCCGGCCCCAATGTCGCG	1128570			
Query 481	GGGCTGCTGAGTGCGGCGGGCTGCGCTGTTGCAAGCGACACAGTGGTGCCCGCGCG	540			
Sbjct 1128571	GGGCTGCTGAGTGCGGCGGGCTGCGCTGTTGCAAGCGACACAGTGGTGCCCGCGCG	1128630			
Query 541	ACGGCCCCGATCGTCAAGGCAATGACATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	600			
Sbjct 1128631	ACGGCCCCGATCGTCAAGGCAATGACATCCAGGTGACCCGCAATCGGATCAAGAAGGTC	1128690			
Query 601	ACCGAGCGGCTGCCGCTGCCGCGAACGCGCGTGTGTCGAGGACCCGAGATGAACATG	660			
Sbjct 1128691	ACCGAGCGGCTGCCGCTGCCGCGAACGCGCGTGTGTCGAGGACCCGAGATGAACATG	1128750			
Query 661	AGCCGGGAGGTGCTCAAGACCCGGGGTTCGGGGACCCAGGATGTGACGTTTCGCGGTA	720			
Sbjct 1128751	AGCCGGGAGGTGCTCAAGACCCGGGGTTCGGGGACCCAGGATGTGACGTTTCGCGGTA	1128810			
Query 721	GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	780			
Sbjct 1128811	GCTGAGGTCAACGGCGTCGAGACCGGCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG	1128870			
Query 781	GCCACGAAAGCGTGGTGGCGGTGGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC	840			
Sbjct 1128871	GCCACGAAAGCGTGGTGGCGGTGGGACCAAGCCCGGTACCGAGGTGCCCCGGTGATC	1128930			
Query 841	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	900			
Sbjct 1128931	GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC	1128990			
Query 901	ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACAGGGCACCTGGGAGGCCAACGGC	960			
Sbjct 1128991	ACCGGCAACGGGTATTACGGTGGTGTGACGTTTGACAGGGCACCTGGGAGGCCAACGGC	1129050			
Query 961	GGGCTGCGGTATGACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC	1020			
Sbjct 1129051	GGGCTGCGGTATGACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC	1129110			
Query 1021	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1080			
Sbjct 1129111	GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCTGGCCGGTATGTGCTGCACGAGCGGGT	1129170			
Query 1081	GCGCGCTGA	1089			
Sbjct 1129171	GCGCGCTGA	1129179			

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 ddH₂O : 184 µl

Konsentrasi stok : 100 µl (184 µl)

Pengenceran larutan stok:

$$V_1N_1 = V_2N_2$$

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

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

b. Primer *Reverse*

Massa primer kering : 20,6 nmol

Volume ddH₂O : 206 µl

Konsentrasi stok : 100 µl (206 µl)

Pengenceran larutan stok:

$$V_1N_1 = V_2N_2$$

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

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

D. Komposisi PCR Mix

Enzim <i>mytaq red</i>	: 25 μl
Primer <i>forward</i>	: 1 μl
Primer <i>reverse</i>	: 1 μl
ddH ₂ O	: 13 μl
Sampel DNA	: 10 μl
Volume Total	: 50 μl

E. Komposisi Gel Agarosa

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

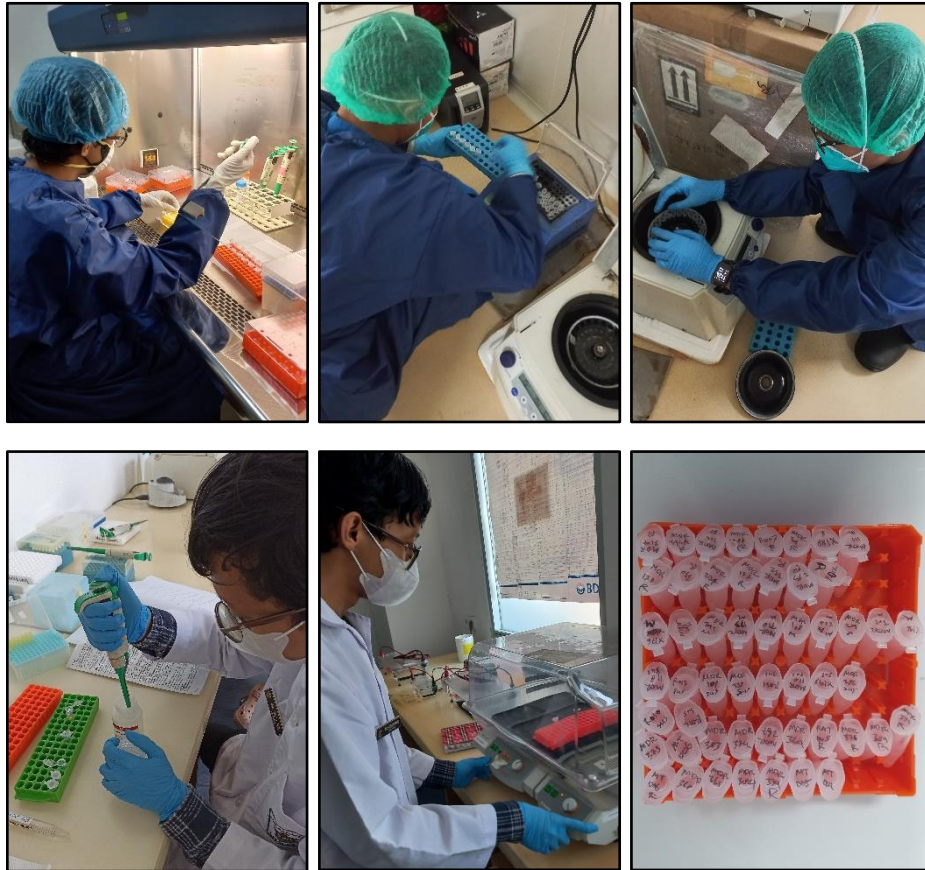
Genome map of Ag85B showing gene locations and coordinates. The map is a circle with a scale from 0 to 4,000,000. Genes are labeled around the circle with their coordinates. Some genes are highlighted in yellow in the original image.

Genes and coordinates (clockwise from top):

- Ag85BRev-Rv3875-Davila (4,352,399 .. 4,353,020)
- ESAT-6Fwd-SbyEdit (4,352,913 .. 4,352,927)
- ESAT-6Rev-SbyEdit (4,352,609 .. 4,352,629)
- esxA-F-Rv3875-Davila (4,352,076 .. 4,352,096)
- Ag85ARev-Rv3804c (4,266,758 .. 4,266,777)
- Ag85AFwd-Rv3804c (4,265,611 .. 4,265,630)
- pepA-F (151,045 .. 151,066)
- pepA-C1 (151,403 .. 151,424)
- pepA-C2 (151,698 .. 151,708)
- pepA-R (152,288 .. 152,309)
- Ag85CRev-Rv0129c-edit (156,339 .. 156,355)
- Ag85CRev-SbyEdit (156,425 .. 156,446)
- Ag85CFwd-SbyEdit (157,578 .. 157,600)
- Ag85CFwd-Rv0129c (157,815 .. 157,834)
- Rv0287F-Okkals (349,614 .. 349,633)
- EscGH-F-Sukkuu (351,293 .. 351,309)
- EsxH-F-Davila (351,437 .. 351,460)
- Rv0288R-Okkals (352,145 .. 352,164)
- EsxH-R-Davila (352,203 .. 352,224)
- EscGH-R-Sukkuu (352,226 .. 352,242)
- pepA-C1 (1,102,971 .. 1,102,985)
- RpIB_all_fw (1,128,006 .. 1,128,025)
- RpIB_all_rv (1,129,250 .. 1,129,269)
- PPE18-F (1,338,764 .. 1,338,785)
- Rv1196FPref (1,339,126 .. 1,339,144)
- PPE18-C1 (1,339,529 .. 1,339,550)
- PPE18-C2 (1,339,956 .. 1,339,977)
- Rv1196RPref (1,340,553 .. 1,340,571)
- PPE18-R (1,340,621 .. 1,340,644)
- PPE18-C1 (1,533,432 .. 1,533,453)
- Ag85BFwd-Rv0129c (2,134,749 .. 2,134,767)
- RpB-F-Davila (2,134,749 .. 2,134,769)
- Ag85BRev-SbyEdit (2,134,862 .. 2,134,885)
- Ag85BFwd-SbyEdit (2,135,840 .. 2,135,867)
- Ag85BRev-Rv0129c (2,135,961 .. 2,135,980)
- fbpB-R-Davila (2,136,009 .. 2,136,032)
- RpIE_rv (2,752,230 .. 2,752,249)
- RpIE-Fw (2,751,568 .. 2,751,587)
- RpID_rv (2,683,743 .. 2,683,763)
- RpID-Fw (2,683,164 .. 2,683,182)
- Rv1196RPref (2,626,607 .. 2,626,625)
- PPE18-R (2,626,534 .. 2,626,557)
- Rv2660C-R4-Perez-Martinez (2,981,466 .. 2,981,485)
- Rv2660C-R6-Perez-Martinez (2,981,286 .. 2,981,304)
- Rv2660C-F4-Perez-Martinez (2,980,694 .. 2,980,713)

Lampiran 6. Dokumentasi Penelitian

A. Ekstraksi DNA



B. Amplifikasi Gen Rpf-B



C. Elektroforesis

