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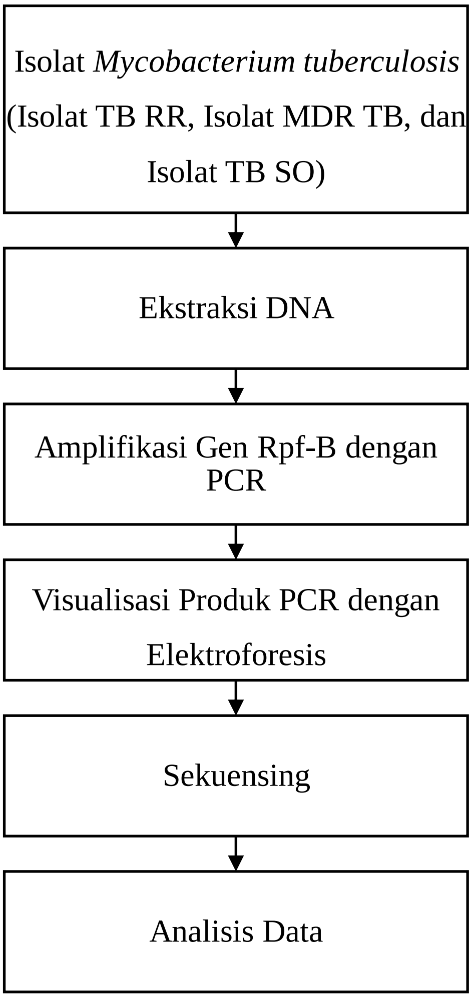
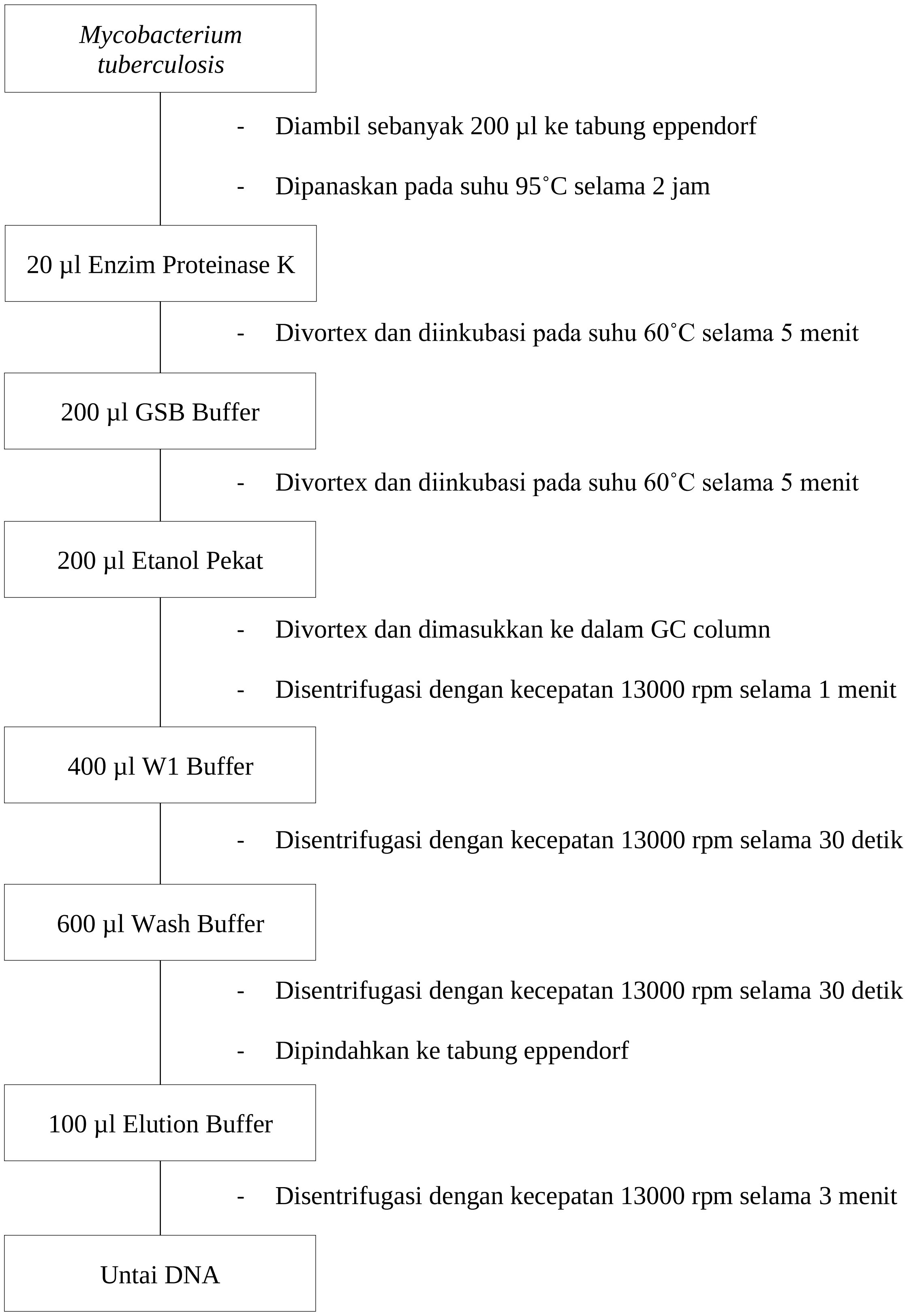
LAMPIRAN

Lampiran 1. Skema Kerja

A. Skema Kerja Penelitian



B. Skema Kerja Ekstraksi DNA *Mycobacterium tuberculosis*



Mycobacterium tuberculosis

- Diambil sebanyak 200 µl ke tabung eppendorf
- Dipanaskan pada suhu 95˚C selama 2 jam

20 µl Enzim Proteinase K

- Divortex dan diinkubasi pada suhu 60˚C selama 5 menit

200 µl GSB Buffer

- Divortex dan diinkubasi pada suhu 60˚C selama 5 menit

200 µl Etanol Pekat

- Divortex dan dimasukkan ke dalam GC column
- Disentrifugasi dengan kecepatan 13000 rpm selama 1 menit

400 µl W1 Buffer

- Disentrifugasi dengan kecepatan 13000 rpm selama 30 detik

600 µl Wash Buffer

- Disentrifugasi dengan kecepatan 13000 rpm selama 30 detik
- Dipindahkan ke tabung eppendorf

100 µl Elution Buffer

- Disentrifugasi dengan kecepatan 13000 rpm selama 3 menit

Untai DNA

C. Skema Kerja Amplifikasi Gen Rpf-B dengan PCR

Sampel DNA

- Dibuat PCR mix yang berisi: Enzim MyTaq Red Mix 25 µl; ddH_2O 13 µl dan Primer RpfB (*forward* dan *reverse*) 1 µl

40 µl PCR Mix

- Dimasukkan ke dalam tabung PCR

10 µl Ekstrak DNA

- Dimasukkan ke dalam tabung PCR

Amplifikasi

- Diamplifikasi sebanyak 30 siklus. Setiap siklus terdiri dari:
    - Predenaturasi pada suhu 95˚C selama 4 menit (1 siklus)
    - Denaturasi pada suhu 95˚C selama 30 detik
    - Penempelan pada suhu 55˚C selama 30 detik
    - Ekstensi pada suhu 72˚C selama 30 detik
    - Pasca ekstensi 72˚C selama 7 menit (1 siklus)

Produk PCR

D. Skema Kerja Deteksi Produk PCR dengan Elektroforesis

Produk PCR

- Disiapkan gel agarosa 2% dengan komposisi: gel agarosa 2 gr, dan 100 ml TBE buffer
- Dipanaskan selama 2 menit

10 µl Etidium Bromida

- Dicampurkan pada cairan gel

8 µl Produk PCR

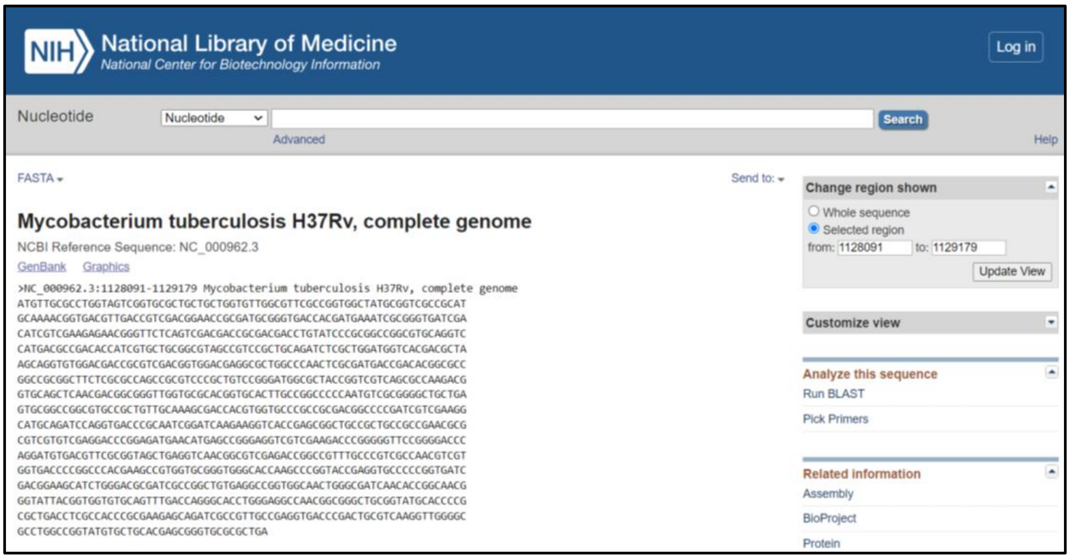
- Dimasukkan produk PCR masing-masing ke dalam sumur gel agarosa 2% yang terendam dalam tangka berisi TBE Buffer

Elektroforesis

- Dijalankan *power supply* dengan tegangan 100 volt selama 60 menit
- Diamati gel elektroforesis di bawah sinar UV

Pita DNA

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



Mycobacterium tuberculosis H37Rv, complete genome

NCBI Reference Sequence: NC_000962.3

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>NC_000962.3:1128091-1129179 Mycobacterium tuberculosis H37Rv, complete genome
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CGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCCGAGGTGACCCGACTGCGTCAAGGTTGGGGC
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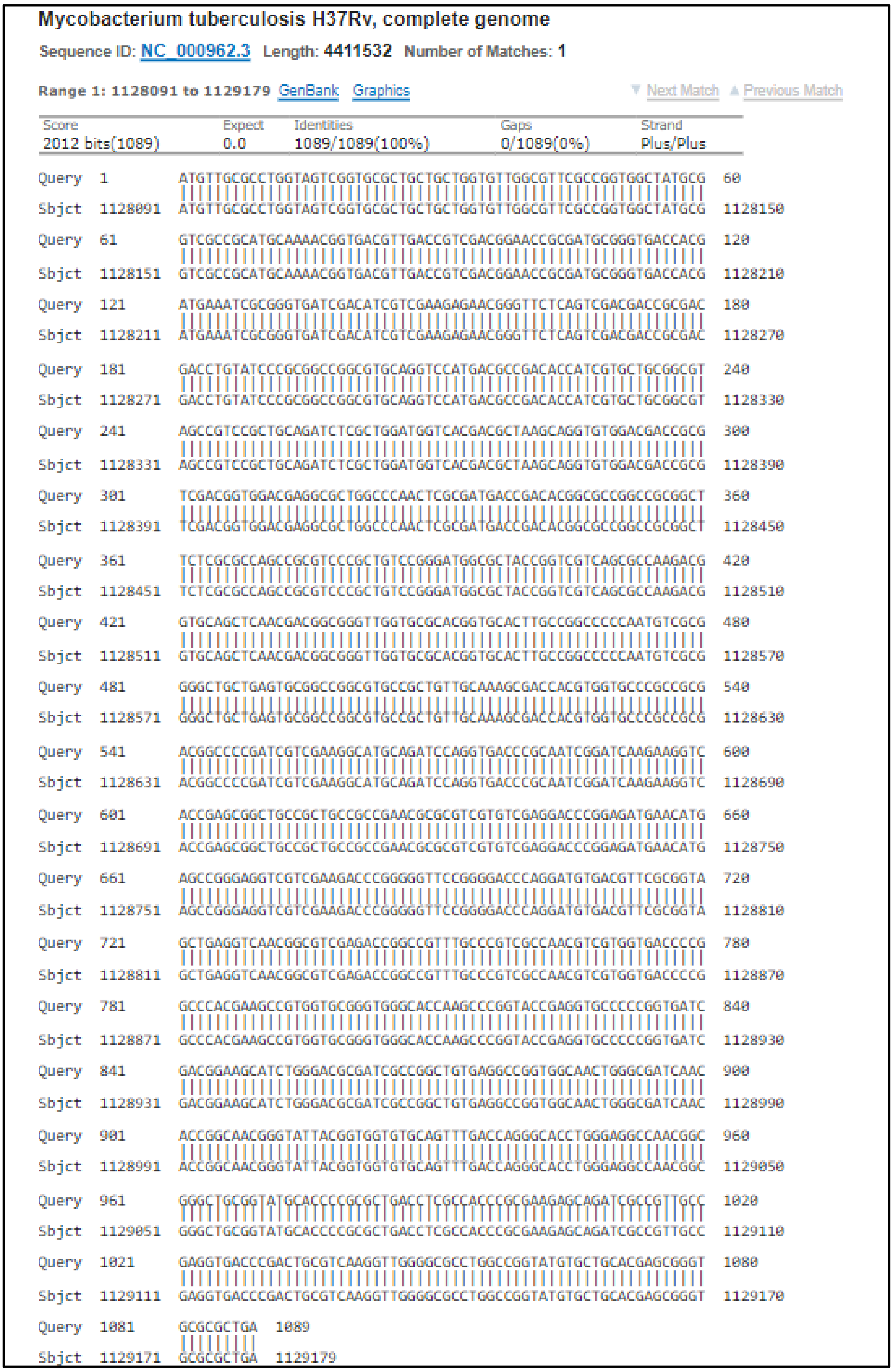
Lampiran 3. Hasil Analisis BLAST

A. Hasil BLAST Sampel C1



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

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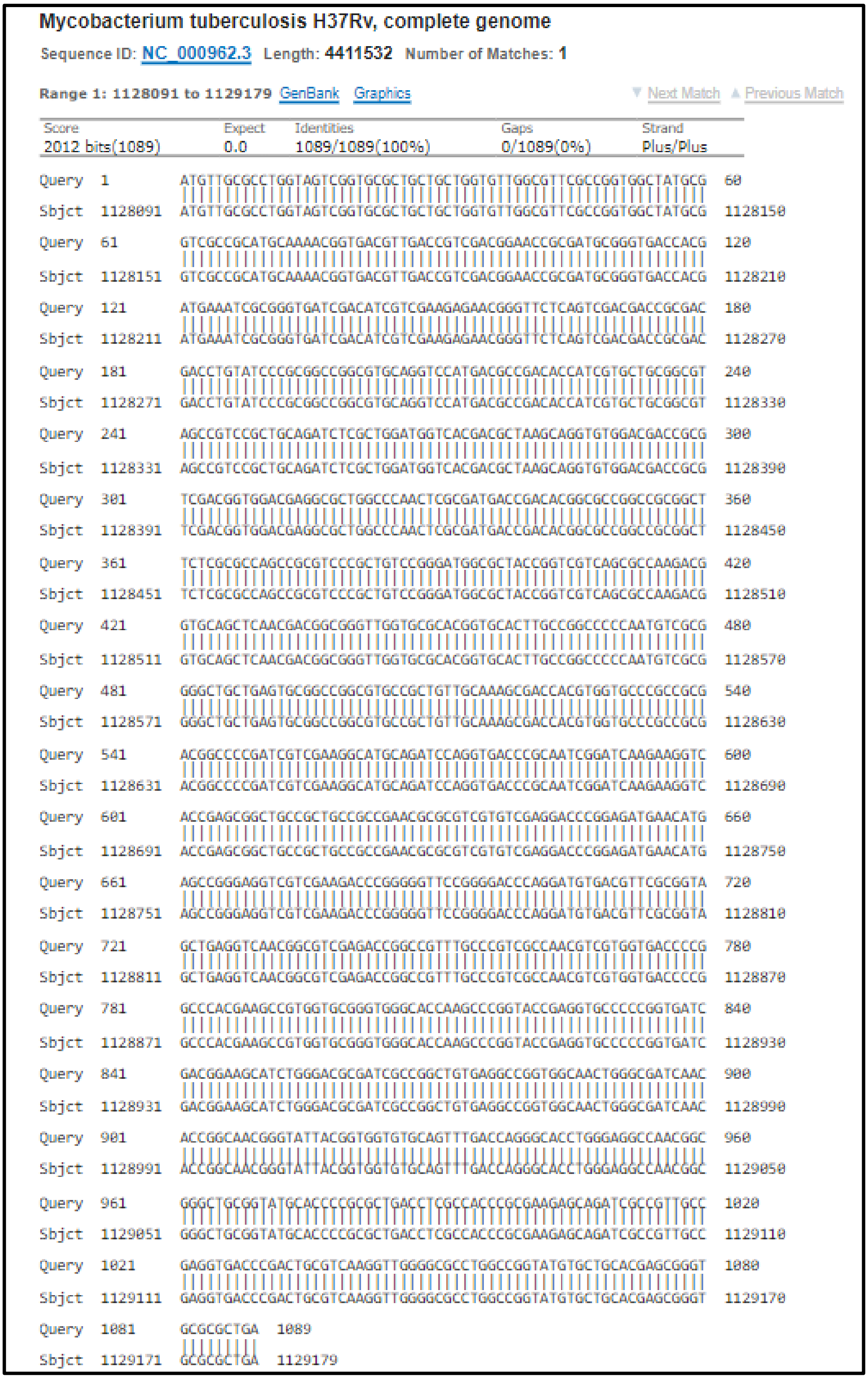
B. Hasil BLAST Sampel C2



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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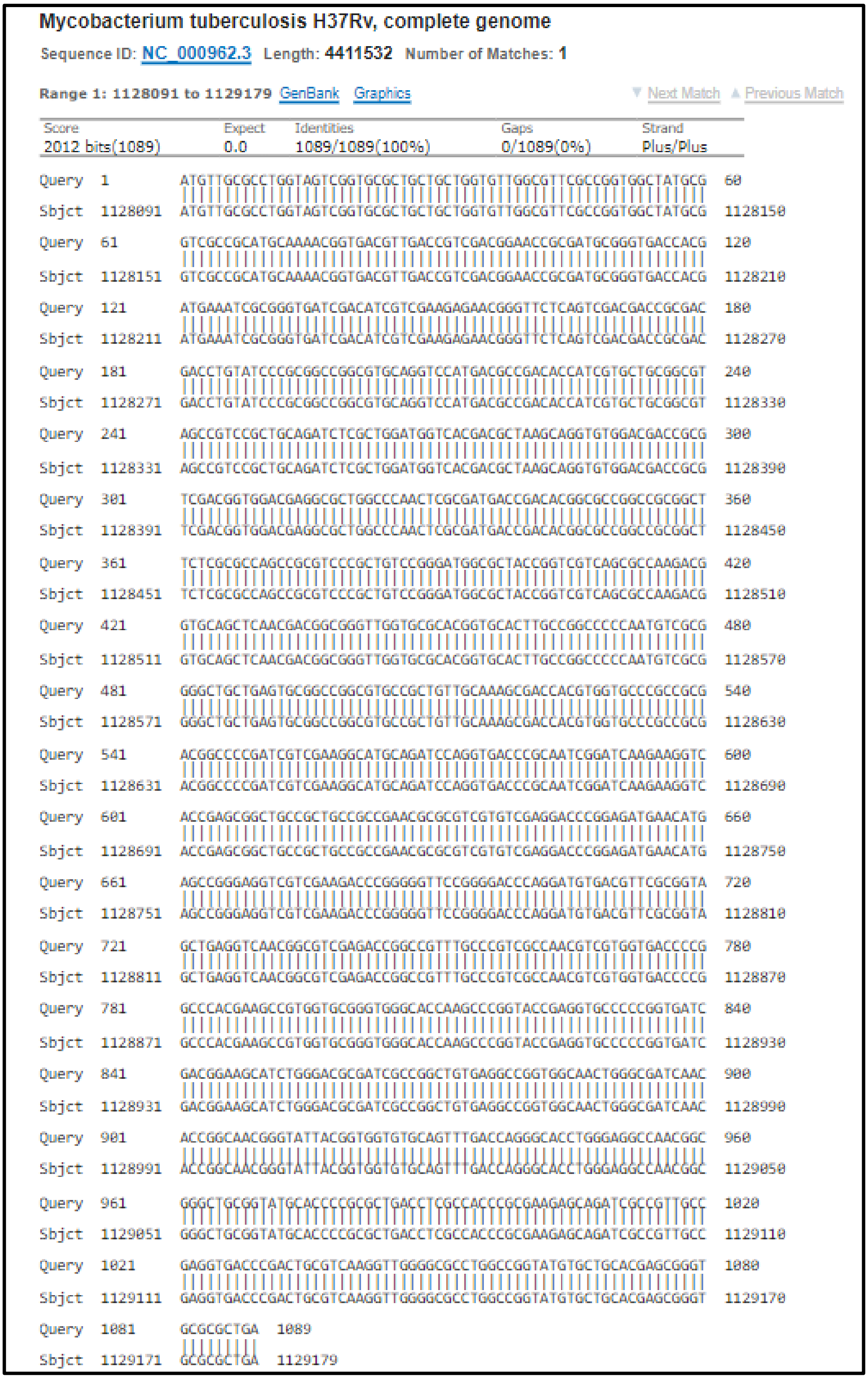
C. Hasil BLAST Sampel C3



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: **4411532** Number of Matches: **1**

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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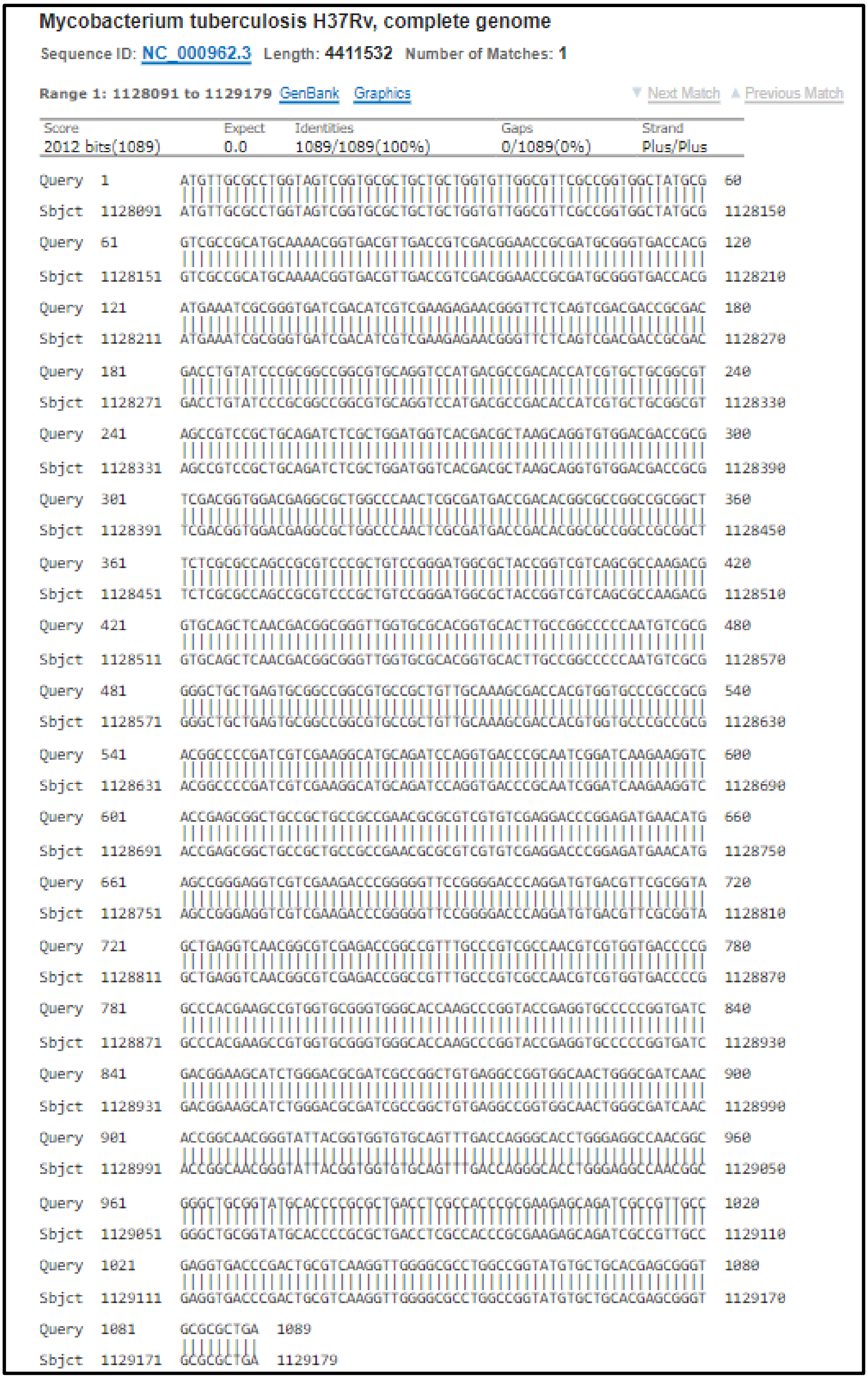
D. Hasil BLAST Sampel C4



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
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Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

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Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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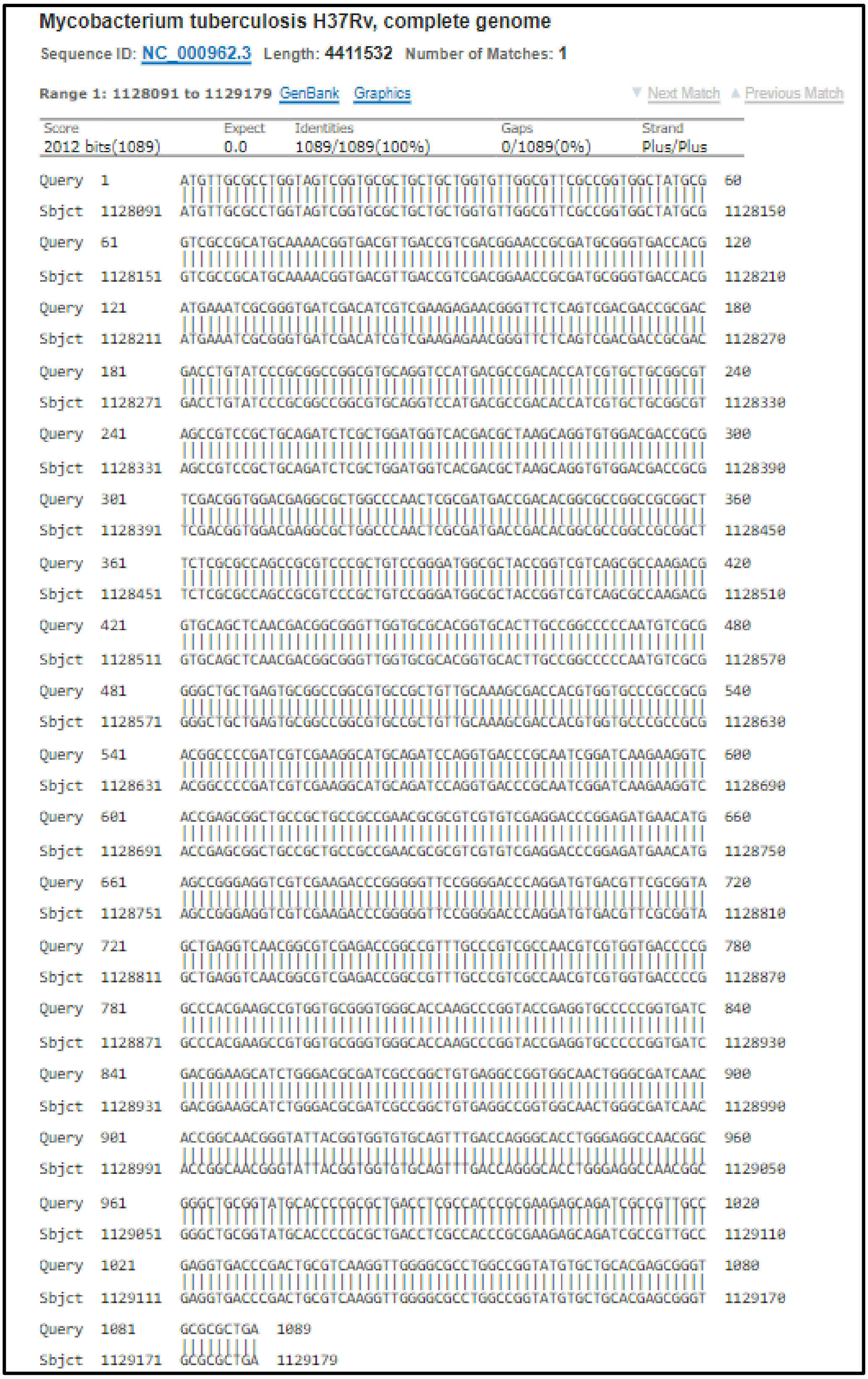
E. Hasil BLAST Sampel C5



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: **4411532** Number of Matches: **1**

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
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Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

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Sbjct  1129171  GCGCGCTGA  1129179
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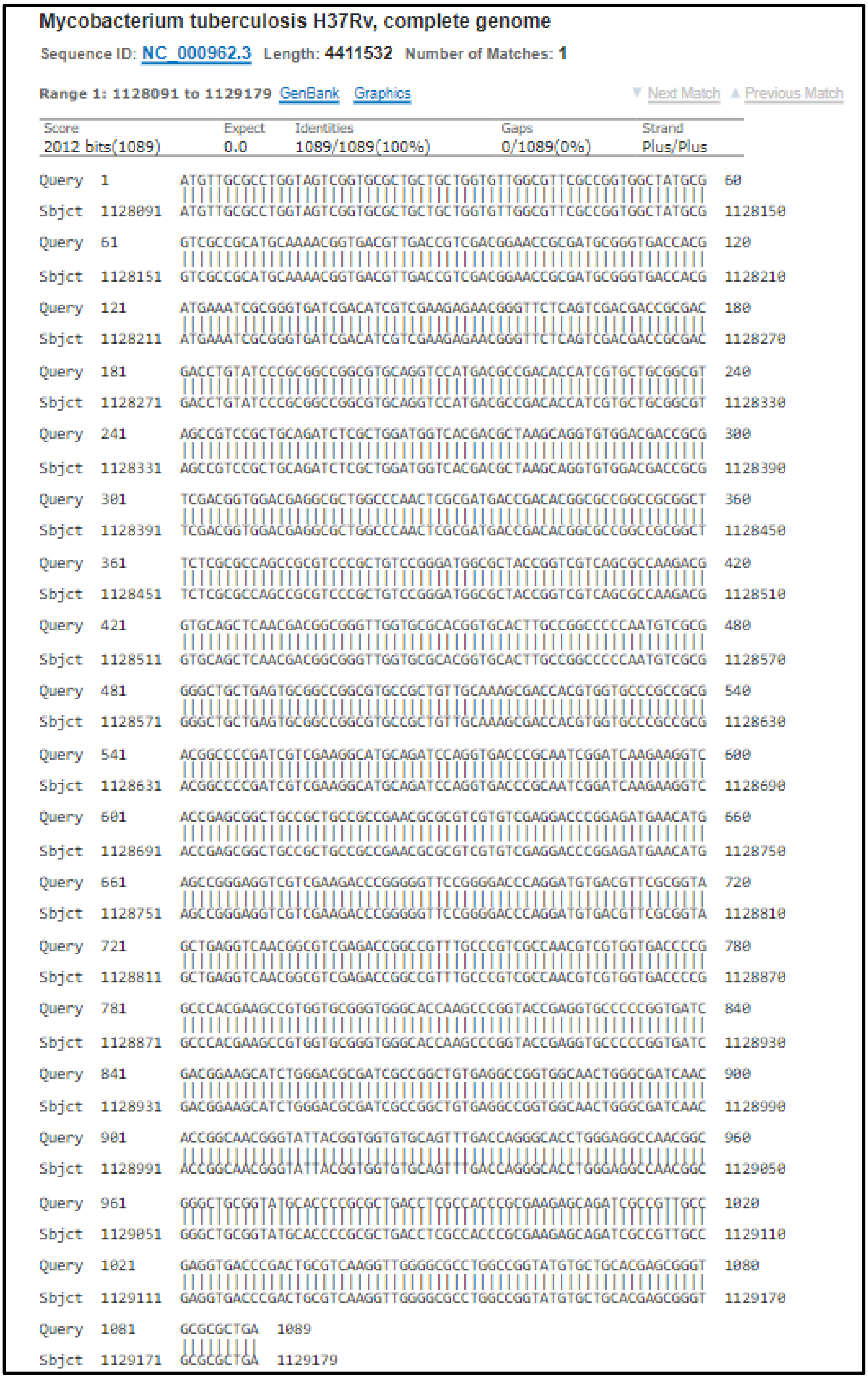
F. Hasil BLAST Sampel C6



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: **4411532** Number of Matches: **1**

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
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Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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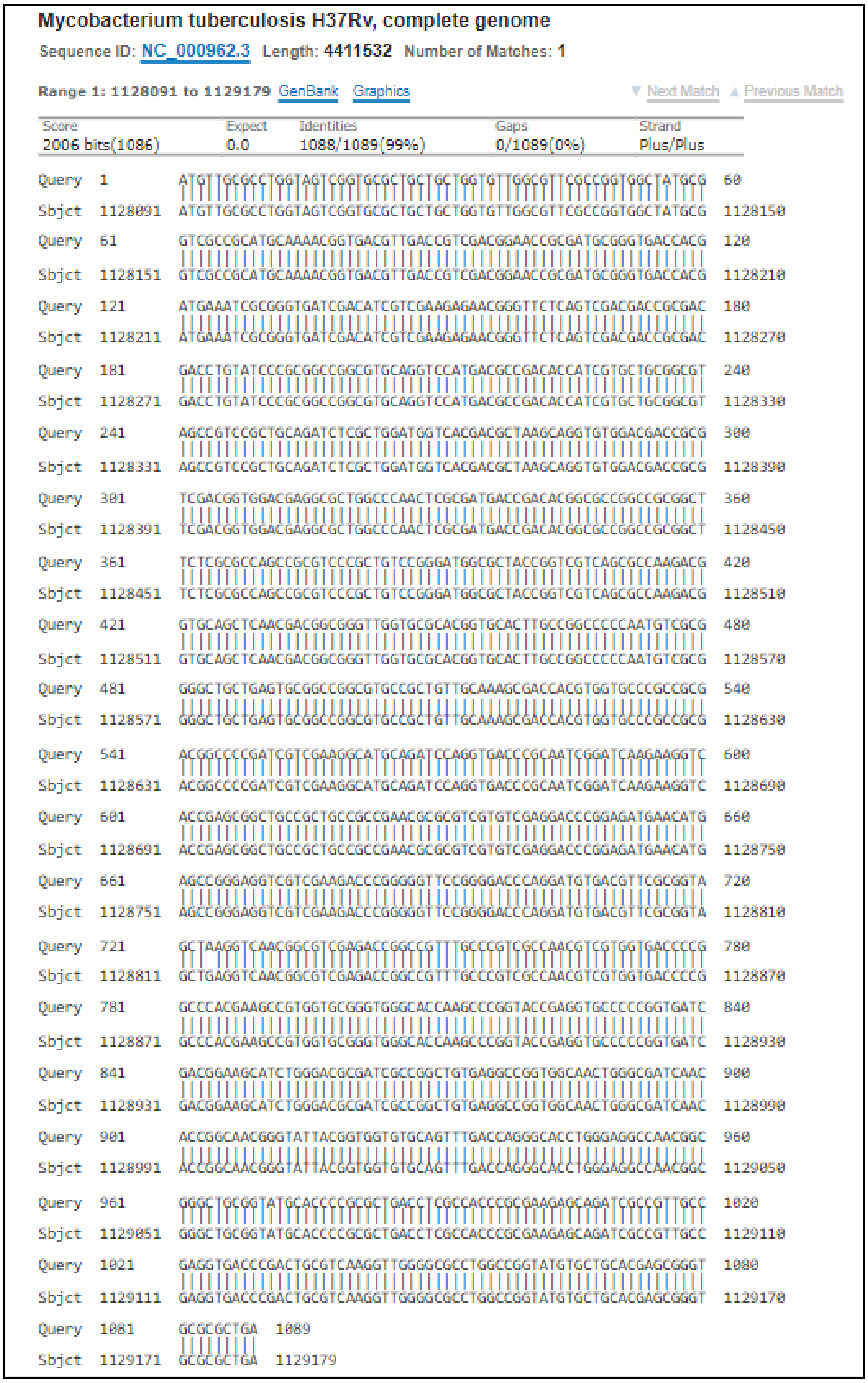
G. Hasil BLAST Sampel C7



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
                ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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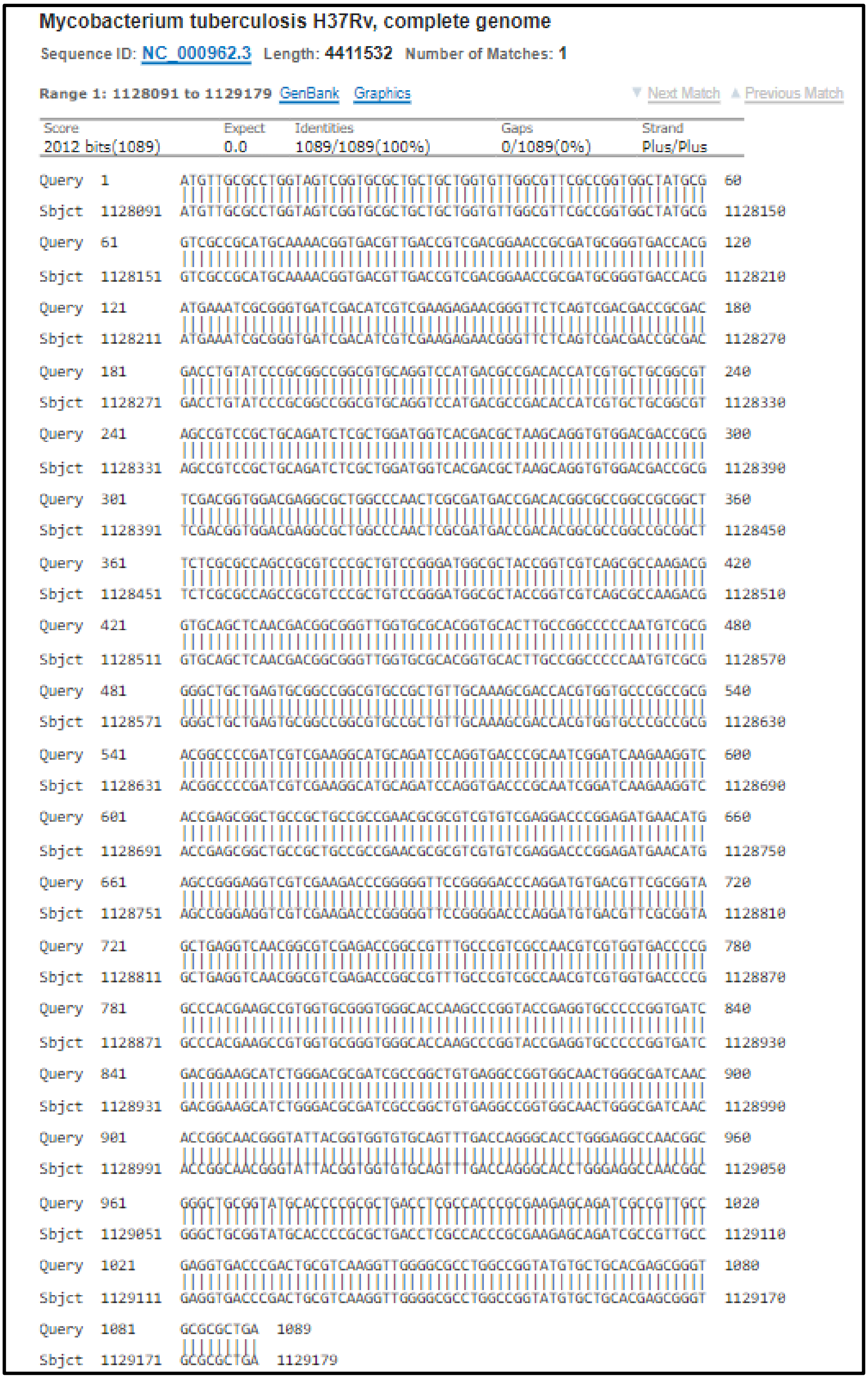
H. Hasil BLAST Sampel C8



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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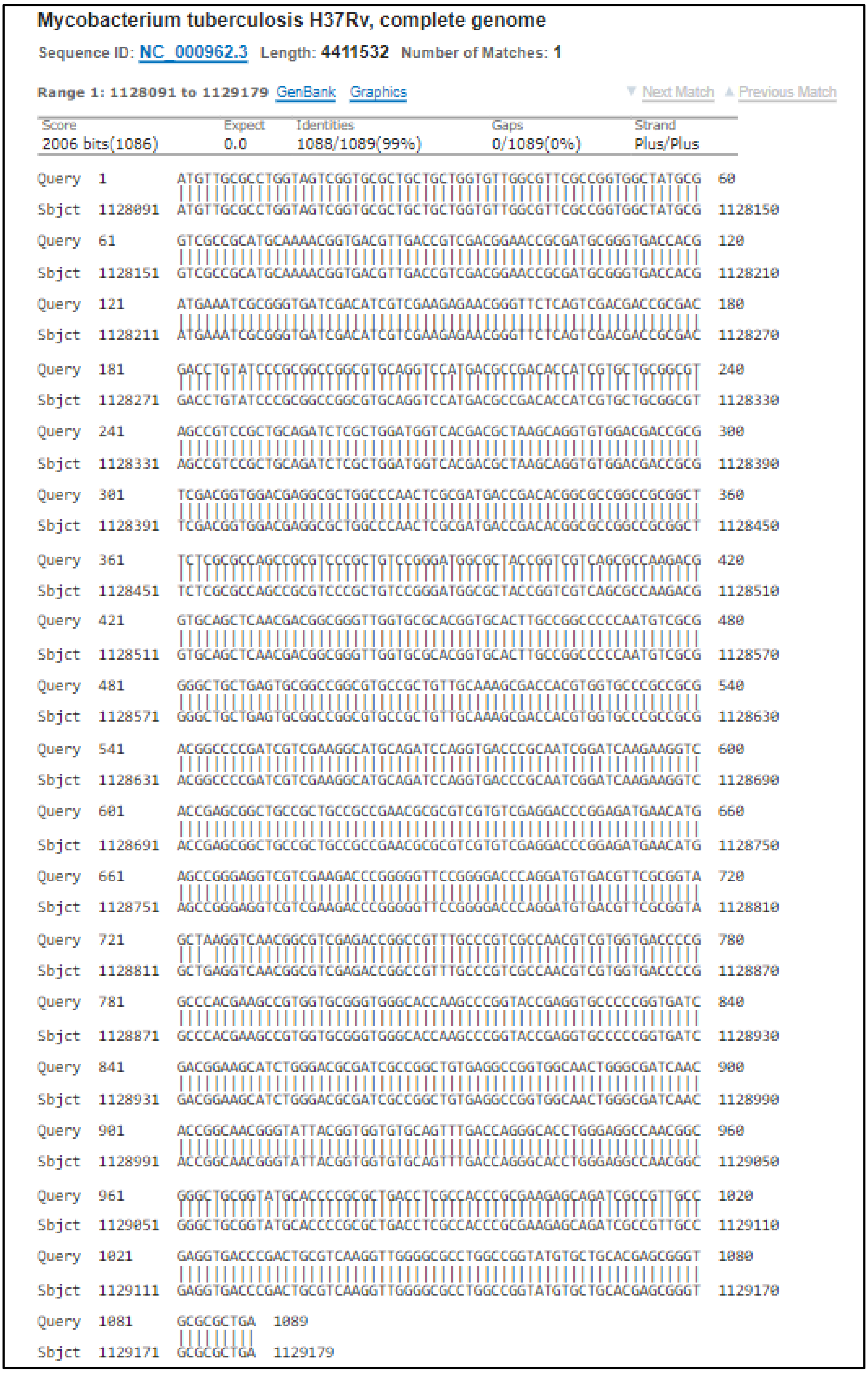
I. Hasil BLAST Sampel C9



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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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

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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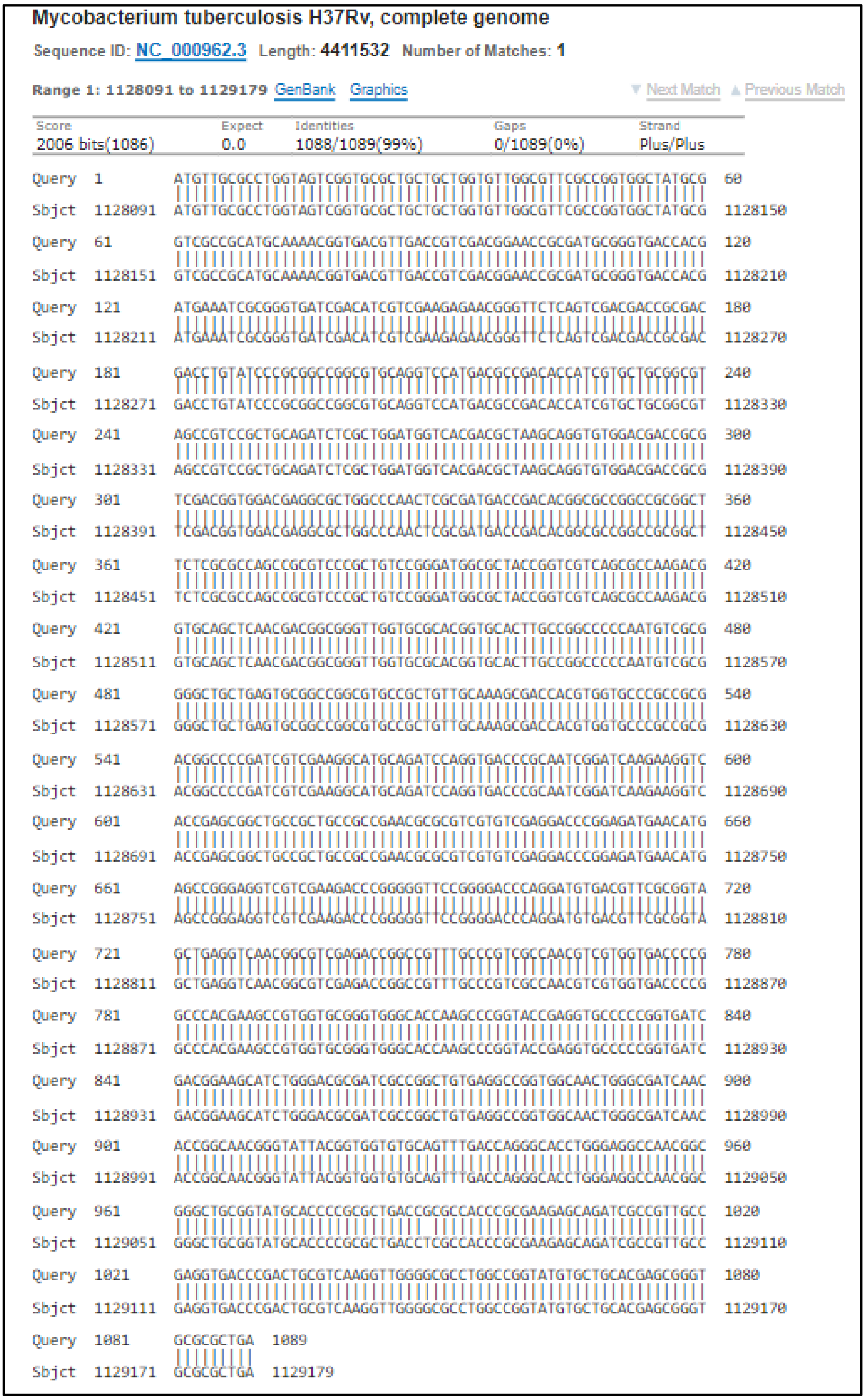
K. Hasil BLAST Sampel C11



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCGCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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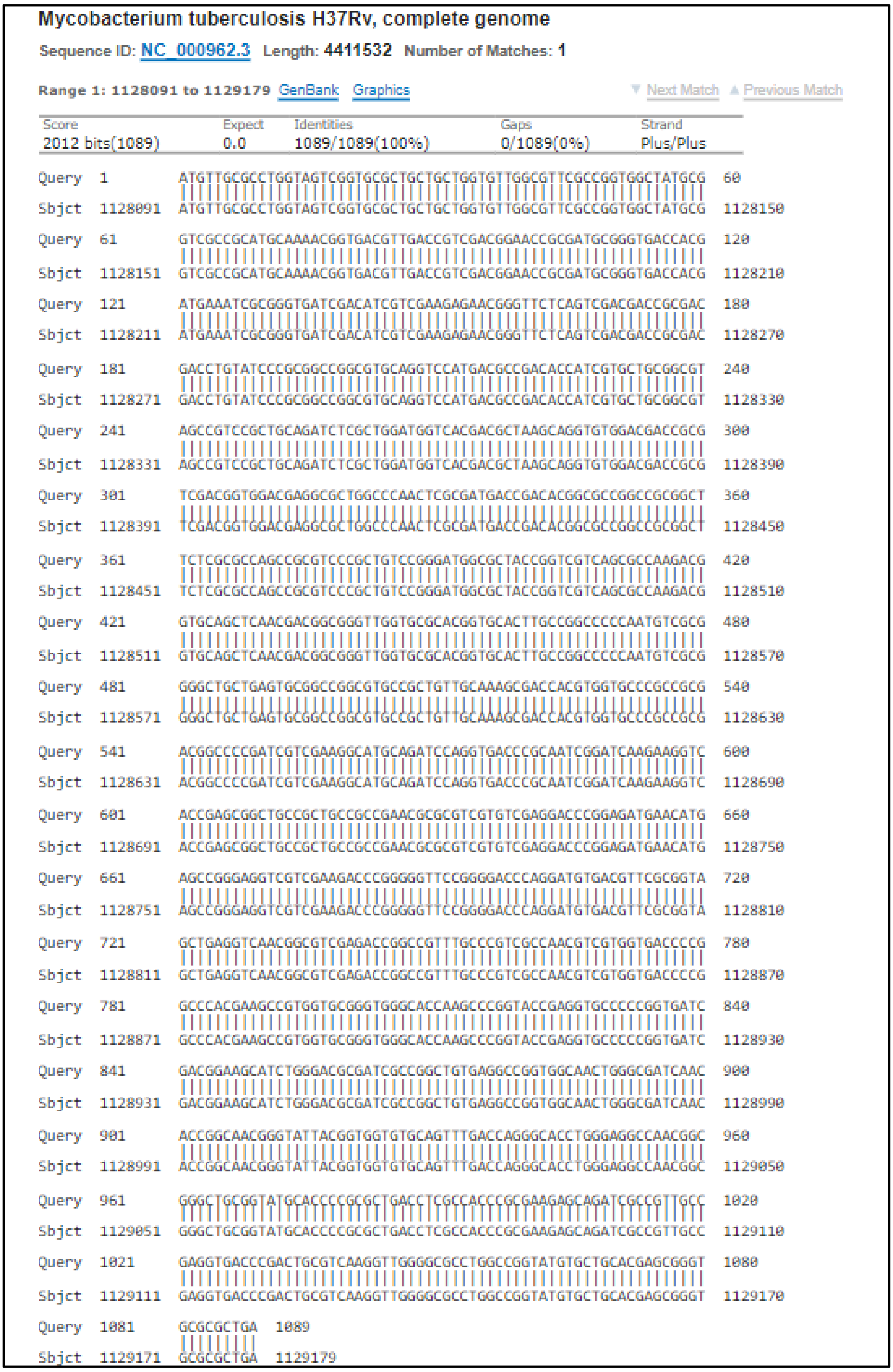
L. Hasil BLAST Sampel C12



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: **4411532** Number of Matches: **1**

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2012 bits(1089)	0.0	1089/1089(100%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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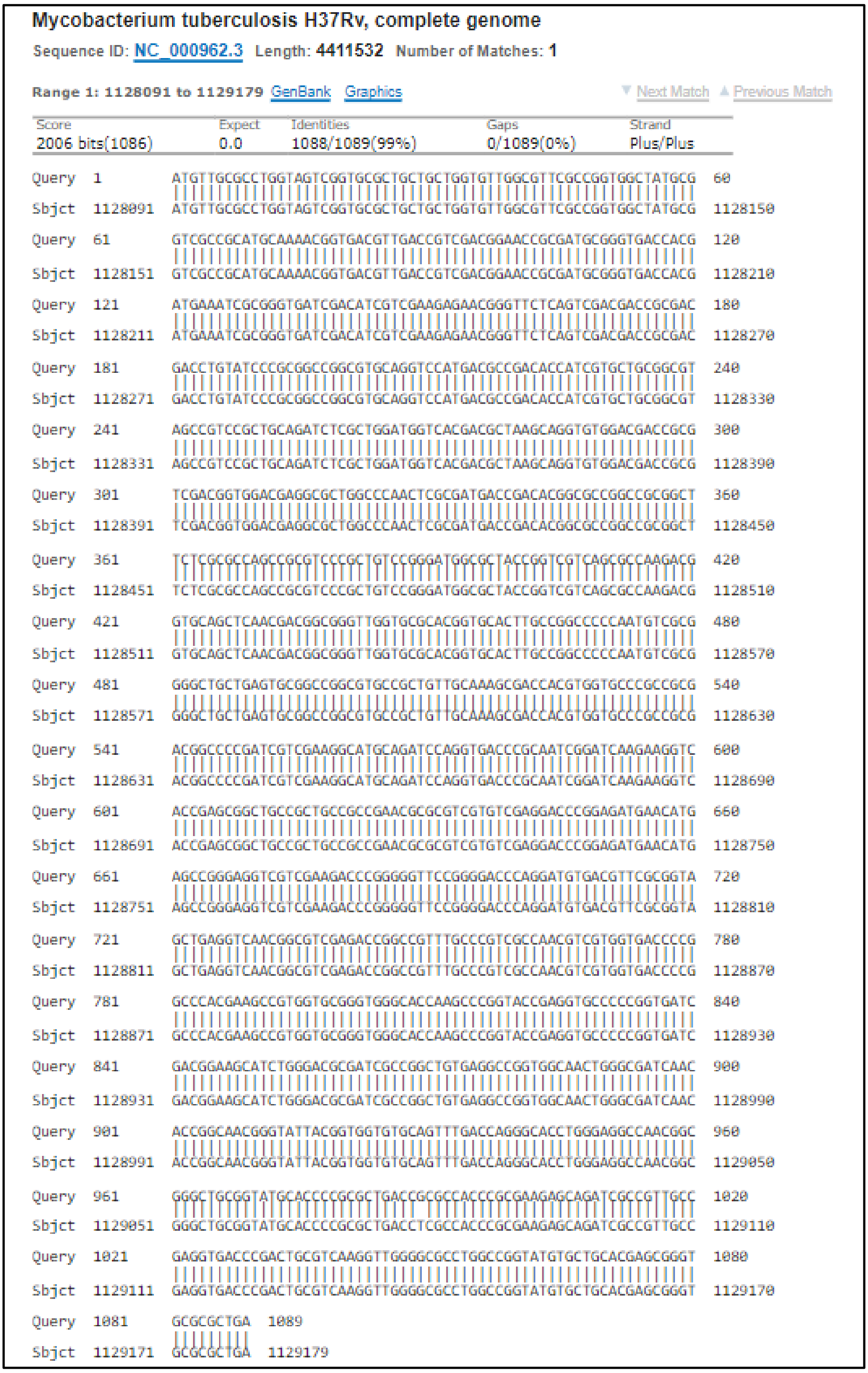
M. Hasil BLAST Sampel C13



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: **4411532** Number of Matches: **1**

Range 1: 1128091 to 1129179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCGCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
                |||||||||
Sbjct  1129171  GCGCGCTGA  1129179
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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

Score	Expect	Identities	Gaps	Strand
2006 bits(1086)	0.0	1088/1089(99%)	0/1089(0%)	Plus/Plus

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Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
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Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
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Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTAAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128811  GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  1128870

Query  781      GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  840
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Sbjct  1128871  GCCCACGAAGCCGTGGTGCGGGTGGGCACCAAGCCCGGTACCGAGGTGCCCCCGGTGATC  1128930

Query  841      GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  900
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1129170

Query  1081     GCGCGCTGA  1089
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Sbjct  1129171  GCGCGCTGA  1129179
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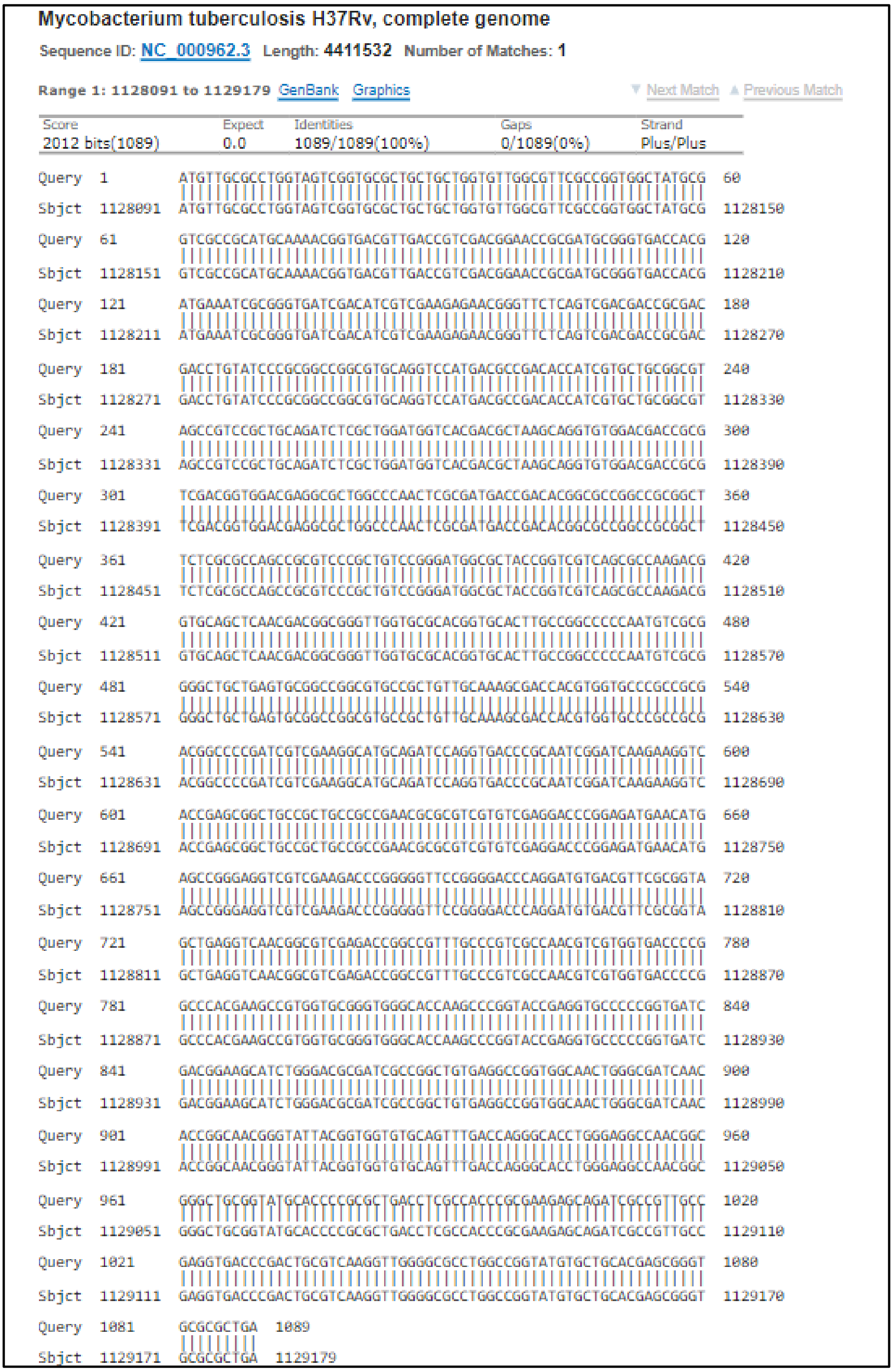
O. Hasil BLAST Sampel C15



Mycobacterium tuberculosis H37Rv, complete genome

Sequence ID: NC_000962.3 Length: 4411532 Number of Matches: 1

Range 1: 1128091 to 1129179 GenBank Graphics

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Score             Expect  Identities          Gaps         Strand
2012 bits(1089)   0.0     1089/1089(100%)     0/1089(0%)   Plus/Plus

Query  1        ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  60
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Sbjct  1128091  ATGTTGCGCCTGGTAGTCGGTGCGCTGCTGCTGGTGTTGGCGTTCGCCGGTGGCTATGCG  1128150

Query  61       GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  120
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Sbjct  1128151  GTCGCCGCATGCAAAACGGTGACGTTGACCGTCGACGGAACCGCGATGCGGGTGACCACG  1128210

Query  121      ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  180
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Sbjct  1128211  ATGAAATCGCGGGTGATCGACATCGTCGAAGAGAACGGGTTCTCAGTCGACGACCGCGAC  1128270

Query  181      GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  240
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Sbjct  1128271  GACCTGTATCCCGCGGCCGGCGTGCAGGTCCATGACGCCGACACCATCGTGCTGCGGCGT  1128330

Query  241      AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  300
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Sbjct  1128331  AGCCGTCCGCTGCAGATCTCGCTGGATGGTCACGACGCTAAGCAGGTGTGGACGACCGCG  1128390

Query  301      TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  360
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Sbjct  1128391  TCGACGGTGGACGAGGCGCTGGCCCAACTCGCGATGACCGACACGGCGCCGGCCGCGGCT  1128450

Query  361      TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  420
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Sbjct  1128451  TCTCGCGCCAGCCGCGTCCCGCTGTCCGGGATGGCGCTACCGGTCGTCAGCGCCAAGACG  1128510

Query  421      GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  480
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Sbjct  1128511  GTGCAGCTCAACGACGGCGGGTTGGTGCGCACGGTGCACTTGCCGGCCCCCAATGTCGCG  1128570

Query  481      GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  540
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Sbjct  1128571  GGGCTGCTGAGTGCGGCCGGCGTGCCGCTGTTGCAAAGCGACCACGTGGTGCCCGCCGCG  1128630

Query  541      ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  600
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Sbjct  1128631  ACGGCCCCGATCGTCGAAGGCATGCAGATCCAGGTGACCCGCAATCGGATCAAGAAGGTC  1128690

Query  601      ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128691  ACCGAGCGGCTGCCGCTGCCGCCGAACGCGCGTCGTGTCGAGGACCCGGAGATGAACATG  1128750

Query  661      AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  720
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Sbjct  1128751  AGCCGGGAGGTCGTCGAAGACCCGGGGGTTCCGGGGACCCAGGATGTGACGTTCGCGGTA  1128810

Query  721      GCTGAGGTCAACGGCGTCGAGACCGGCCGTTTGCCCGTCGCCAACGTCGTGGTGACCCCG  780
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Sbjct  1128931  GACGGAAGCATCTGGGACGCGATCGCCGGCTGTGAGGCCGGTGGCAACTGGGCGATCAAC  1128990

Query  901      ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  960
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Sbjct  1128991  ACCGGCAACGGGTATTACGGTGGTGTGCAGTTTGACCAGGGCACCTGGGAGGCCAACGGC  1129050

Query  961      GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1020
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Sbjct  1129051  GGGCTGCGGTATGCACCCCGCGCTGACCTCGCCACCCGCGAAGAGCAGATCGCCGTTGCC  1129110

Query  1021     GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  1080
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Sbjct  1129111  GAGGTGACCCGACTGCGTCAAGGTTGGGGCGCCTGGCCGGTATGTGCTGCACGAGCGGGT  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 *buffer* : 200µl

Etanol absolut : 200µl

W1 *buffer* : 400µl

Wash buffer : 600µl

Elusion buffer : 100µl

B. Komposisi Larutan Stok Primer

a. Primer *Forward*

Massa primer kering : 18,4 nmol

Volume ddH_2O : 184 µl

Konsentrasi stok : 100 µl (184 µl)

Pengenceran larutan stok:

$V_1N_1 = V_2N_2$

$V_1 \cdot 100 = 100\ \mu l \cdot 10$

$V_1 = 10\ \mu l$ → **Volume ddH_2O = 90 µl**

b. Primer *Reverse*

Massa primer kering : 20,6 nmol

Volume ddH_2O : 206 µl

Konsentrasi stok : 100 µl (206 µl)

Pengenceran larutan stok:

$V_1N_1 = V_2N_2$

$V_1 \cdot 100 = 100\ \mu l \cdot 10$

$V_1 = 10\ \mu l$ → **Volume ddH$_2$O = 90 µl**

D. Komposisi PCR *Mix*

Enzim *mytaq red* : 25 µl

Primer *forward* : 1 µl

Primer *reverse* : 1 µl

ddH$_2$O : 13 µl

Sampel DNA : 10 µl

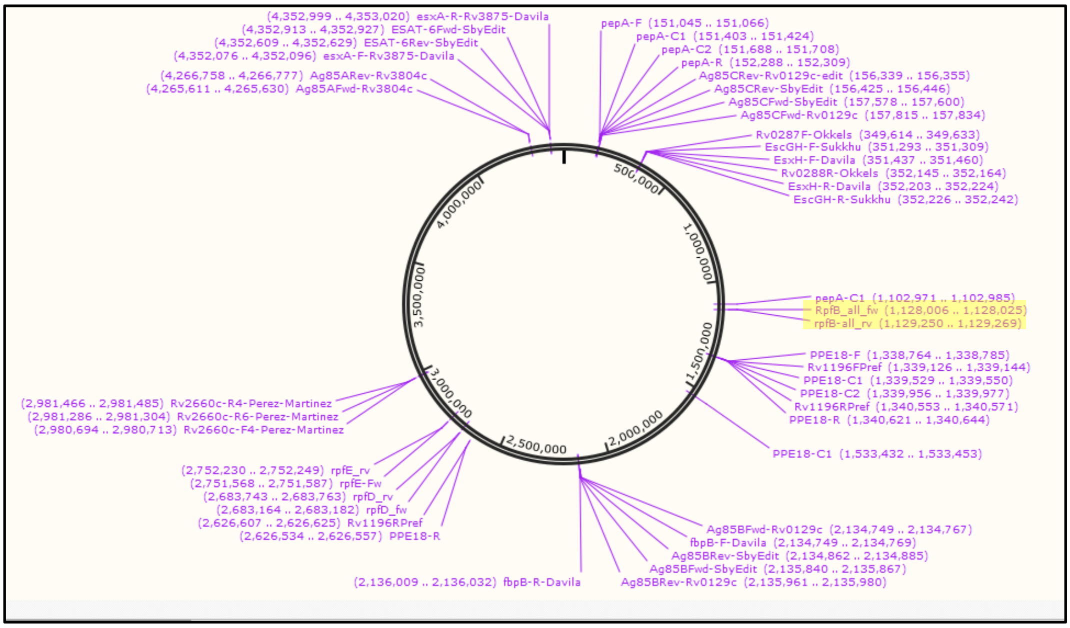
Volume Total : 50 µl

E. Komposisi Gel Agarosa

Berat agarosa : 2 gram

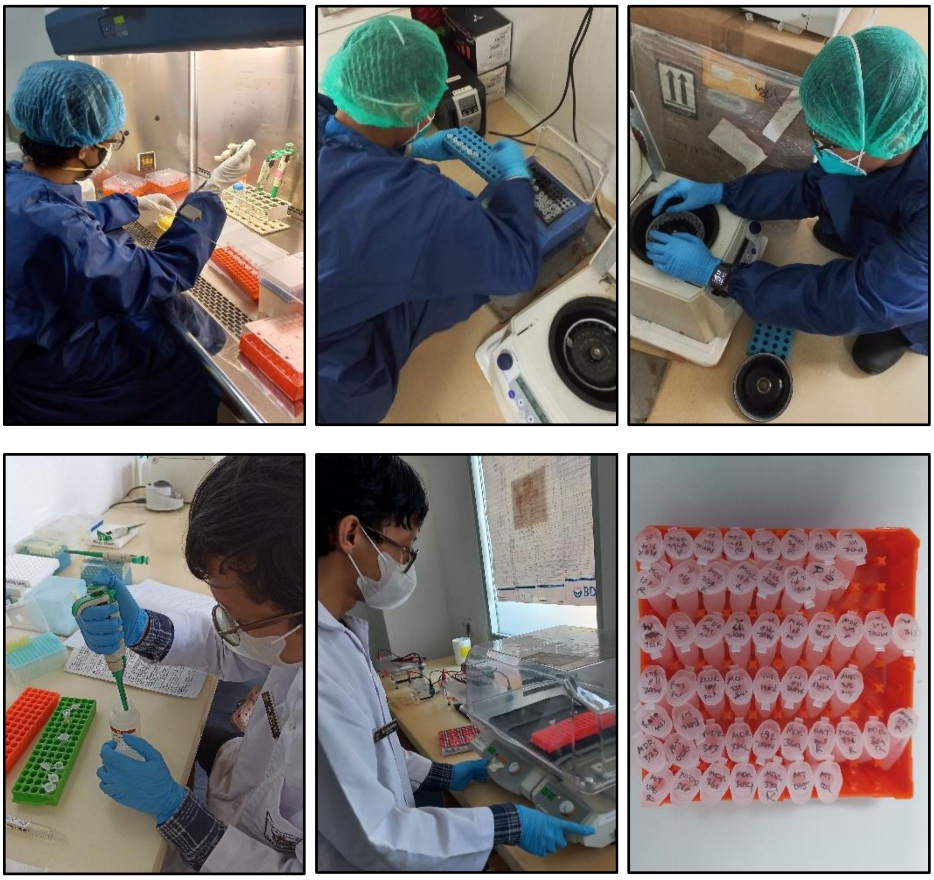
Volume TBE *buffer* : 100 ml

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

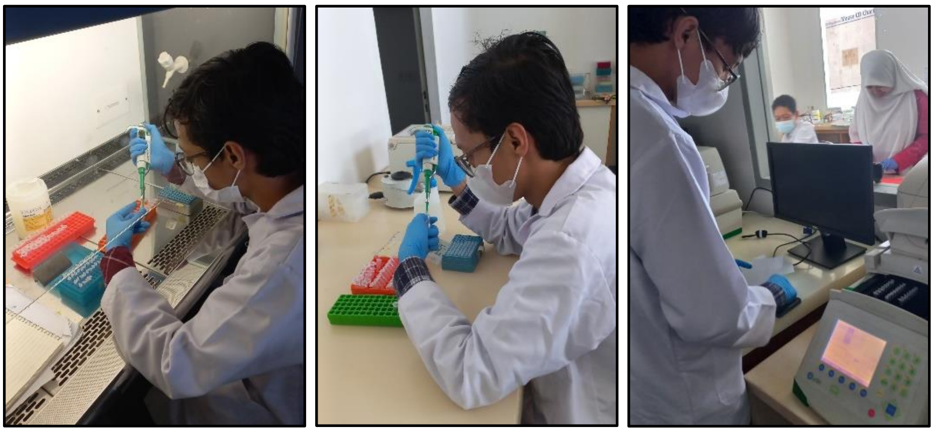


Lampiran 6. Dokumentasi Penelitian

A. Ekstraksi DNA



B. Amplifikasi Gen Rpf-B



C. Elektroforesis