

# Accugenix Identification Report Guide



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## Sequencing Identification Report

SOP-GEN-017

Customer: ① Accugenix, Inc. Account: ⑤ 110440 ( ACC1 )  
Address: ② 223 Lake Dr., Newark ,DE, 19702, USA  
Accugenix C#: ③ C1010056-20100607001 ID Request Form #: 100007 ⑥  
Customer Sample ID: CM Sample - 051010 ④ Due Date: ⑦ 2010-06-07

### Accugenix Database Search Result - BacSeq ⑧

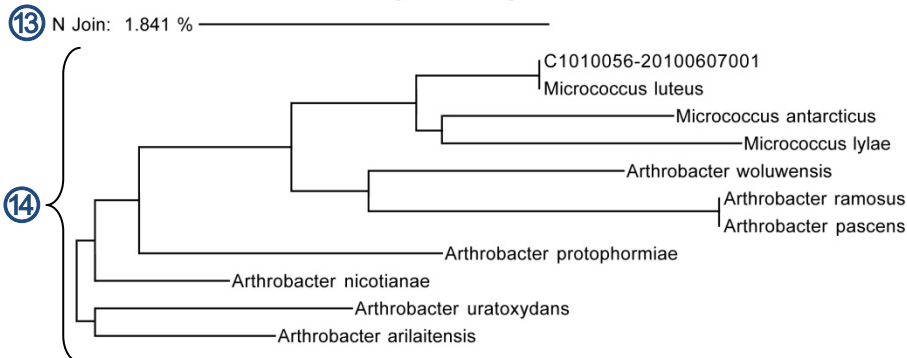
Identification: **Micrococcus luteus** ⑨

Confidence Level: **Species** ⑩

#### Sequence Alignment

Alignment: 504 C1010056-20100607001  
0.00 % 504 Micrococcus luteus  
1.99 % 503 Micrococcus antarcticus  
2.38 % 505 Micrococcus lylae  
3.17 % 505 Arthrobacter woluwensis  
3.17 % 504 Arthrobacter nicotianae  
3.37 % 506 Arthrobacter uratoxydans  
3.37 % 504 Arthrobacter ramosus  
3.37 % 504 Arthrobacter pascens  
3.67 % 504 Arthrobacter arilaitensis  
3.97 % 504 Arthrobacter protophormiae

#### Neighbor Joining Tree



Not for Use in Invitro Diagnostics

⑮

Prepared By Jacqueline L. Miller on 2010-06-02 15:06:05  
Reviewed By Emily Huang on 2010-06-02 15:21:12  
QA Approved By Mary E. Beird on 2010-06-02 15:26:14

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## Interpretation

Sample C1010056-20100607001 has a closest match of *Micrococcus luteus* and links directly to it in the Neighbor Joining Tree. Both the sample and its closest match have identical sequences in the first 500 base pair region of the 16S gene. The result is *Micrococcus luteus*, with a Species level of confidence.

1. Your company name
2. "Ship To" address from your Identification Request Form
3. Unique sample code (C#) assigned by Accugenix
4. Your sample ID, as provided on the Identification Request Form
5. Your 6-digit Account #, followed by a 4-digit alpha-numeric code in ( )
6. Each ID Request Form received with samples has a unique number
7. The due date of your Identification Report
8. Test code for this sample, indicating a bacterial or fungal result
9. Final identification result
10. Confidence level of the identification (Species, Species\*, Genus, Family, Class, Order or No Match)
11. Your sample and the top 10 closest matches to the Accugenix sequence library
12. The result of the alignment represents the percent genetic difference, or # of nucleotide differences, between the unknown sample sequence and the library entry sequence
13. The 1.841% value is the length of the line next to it; similar to a legend on a map, it provides a horizontal distance scale for the Neighbor Joining Tree; the % value is somewhat arbitrary but falls between the % differences of the 1<sup>st</sup> and 10<sup>th</sup> closest matches
14. Neighbor Joining Tree – visually represents the genetic differences between your isolate and its 10 closest matches
15. Electronic signatures in compliance with FDA regulation CFR 21 Part 11