




AccuGENX-ID[®] Identification Report Guide for BacSeq and FunITS

Interpretation

Sample C1234567 - 20131212001 has a closest match of *Staphylococcus pasteuri* 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 *Staphylococcus pasteuri*, with a Species level of confidence.

Section Descriptions

1. Your company name
2. "Ship To" address from your Identification Request Form
3. Unique sample code (C#) assigned by Charles River
4. Your sample ID, as provided on the Identification Request Form
5. Your six-digit Account #, followed by a four-digit alpha numeric code in parenthesis
6. Each Identification Request Form received with samples has a unique number.
7. The due date of your Identification Report
8. Test code for this sample as submitted by the customer
9. Final identification result
10. Confidence level of the identification (Species, Species*, Genus, Family, Class, Order or No Match [for fungi only: the organism was sequenced successfully, but no taxonomic classification could be confidently made based on our current ITS2 fungal library])
11. Your sample and the top 10 closest matches in the Accugenix[®] sequence library.

		223 Lake Drive Newark, DE 19702 Phone: +1.302.292.8888 Fax: +1.302.292.8488 www.criver.com/accugenix		Accugenix[®] AccuGENX-ID[®] Report SOP-GEN-017	
Customer:	1 Valued Customer	Account:	5 110440 (ACC1)		
Address:	2 1023 Mole Drive, Newark, DE 19702, United States				
Accugenix C#:	3 C1234567-20131212001	ID Request Form #:	6 10000		
Customer Sample ID:	4 Example	Due Date:	7 2013-12-12		

Accugenix Database Search Result - BacSeq 8

Identification: **Staphylococcus pasteuri 9**

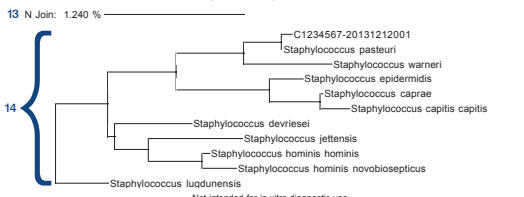
Confidence Level: **Species 10**

Sequence Alignment

}	Alignment: 535 C1234567-20131212001	}
	0.09 % 535 Staphylococcus pasteuri	
	1.21 % 535 Staphylococcus warneri	
	2.34 % 535 Staphylococcus devriesei	
	2.43 % 535 Staphylococcus caprae	
	2.52 % 535 Staphylococcus epidermidis	
	2.62 % 535 Staphylococcus hominis hominis	
	2.62 % 535 Staphylococcus capitis capitis	
	2.80 % 535 Staphylococcus hominis novobiosepticus	
	2.80 % 535 Staphylococcus lugdunensis	

Neighbor Joining Tree

13 N Join: 1.240 %



Prepared By Kerry Falgowski on 2013-12-30 11:56:36
 Reviewed By Emily Huang on 2013-12-30 12:08:47
 CA Alignment By Dan Ryan-Alexander on 2013-12-30 12:13:18
 Page 1 of 1 Rev. 27Jan2014 EH

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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 % 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 1st and 10th 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 21 CFR Part 11