



## Akonni Biosystems Publication List

1. D. P. Chandler, A. Kukhtin, R. Mokhiber, C. Knickerbocker, D. Ogles, G. Rudy, J. Golova, P. Long and A. Peacock. 2010. Monitoring microbial community structure and dynamics during in situ U(VI) bioremediation with a field-portable microarray analysis system. *Env. Sci. Technol.* 44: 5516-5522.
2. S. G. Bavykin, V. M. Mikhailovich, V. M. Zakharyev, Y. P. Lysov, J. J. Kelly, O. S. Alferov, I. M. Gavin, A. V. Kukhtin, J. Jackman, D. A. Stahl, D. Chandler, and A. D. Mirzabekov. 2008. Discrimination of *Bacillus anthracis* and closely related microorganisms by analysis of 16S and 23S rRNA with oligonucleotide microarray. *Chemico-Biol. Interactions* 171(2): 212-235.
3. E. M. L. Starke, J. C. Smoot, W. Jer-Horng, W.-T. Liu, D. P. Chandler, and D. A. Stahl. 2007. Saliva-based diagnostics using 16S rRNA microarrays and microfluidics. *Ann. NY. Acad. Sci.* 2007 1098: 345-361.
4. M. Doran, D.S. Raicu, J.D. Furst, R. Settmi, M. Schipma and D. P. Chandler. 2007. Oligonucleotide Microarray identification of *Bacillus anthracis* strains using support vector machines. *Bioinformatics* 23(4): 487 - 492.
5. D. P. Chandler, D. S. Schabacker, S. Bavykin and I. M. Gavin. 2007. Leaving the surface behind: At the intersection of protein microarrays and mass spectrometry. In: *Functional Protein Microarrays in Drug Discovery*. P. Predki, Ed., CRC Press. Boca Raton, FL. pp. 199-216.
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7. D. S. Schabacker, I. Stefanovska, I. Gavin, C. Pedrak, and D. P. Chandler. 2006. Protein array staining methods for undefined protein content, manufacturing quality control, and performance validation. *Anal. Biochem.* 359(1): 84-93.
8. E. M. L. Starke, J. C. Smoot, L. M. Smoot, W.-T. Liu, D. P. Chandler, H. H. Lee, and D. A. Stahl. 2006. Technology development to explore the relationship between oral health and the oral microbial community. *BMC Oral Health* 6 (Suppl. 1): S10.
9. Bavykin SG, Lysov YP, Zakhariyev V, Kelly JJ, Jackman J, Stahl DA, Cherni A. Use of 16S rRNA, 23S rRNA, and *gyrB* gene sequence analysis to determine phylogenetic relationships of *Bacillus cereus* group microorganisms. *J Clin Microbiol.* 2004 Aug;42(8):3711-30. Erratum in: *J Clin Microbiol.* 2006 Jul;44(7):2676.
10. Eyers L, Smoot JC, Smoot LM, Bugli C, Urakawa H, McMurry Z, Siripong S, El-Fantroussi S, Lambert P, Agathos SN, Stahl DA. Discrimination of shifts in a soil microbial community associated with TNT-contamination using a functional ANOVA of 16S rRNA hybridized to oligonucleotide microarrays. *Environ Sci Technol.* 2006 Oct 1;40(19):5867-73.
11. Siripong S, Kelly JJ, Stahl DA, Rittmann BE. Impact of prehybridization PCR amplification on microarray detection of nitrifying bacteria in wastewater treatment plant samples. *Environ Microbiol.* 2006 Sep;8(9):1564-74.
12. Lee HH, Smoot J, McMurray Z, Stahl DA, Yager P. Recirculating flow accelerates DNA microarray hybridization in a microfluidic device. *Lab Chip.* 2006 Sep;6(9):1163-70. Epub 2006 Jul 13.
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