1.

Record Nr.	UNINA9910467594603321
Titolo	ISTFA 2015 conference proceedings from the 41st International Symposium for Testing and Failure Analysis : November 1-5 2015, Oregon Convention Center, Portland, Oregon, USA / / organized by ISTFA/2015, Electronic Device Failure Analysis Society (EDFAS), ASM International
Pubbl/distr/stampa	Materials Park, Ohio : , : ASM International, , [2015] ©2015
ISBN	1-5231-0206-3 1-62708-103-8
Descrizione fisica	1 online resource (536 pages) : illustrations (some color)
Soggetti	Electronics - Materials - Testing Materials - Testing Electronic apparatus and appliances - Testing Semiconductors - Testing Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Cover title.

2.

Record Nr.	UNINA9910220053503321
Autore	A. Murat Eren
Titolo	New Insights into Microbial Ecology through Subtle Nucleotide Variation
Pubbl/distr/stampa	Frontiers Media SA, 2016
Descrizione fisica	1 online resource (133 p.)
Collana	Frontiers Research Topics
Soggetti	Microbiology (non-medical)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	The 16S ribosomal RNA gene commonly serves as a molecular marker for investigating microbial community composition and structure. Vast amounts of 16S rRNA amplicon data generated from environmental samples thanks to the recent advances in sequencing technologies allowed microbial ecologists to explore microbial community dynamics over temporal and spatial scales deeper than ever before. However, widely used methods for the analysis of bacterial communities generally ignore subtle nucleotide variations among high-throughput sequencing reads and often fail to resolve ecologically meaningful differences between closely related organisms in complex microbial datasets. Lack of proper partitioning of the sequencing data into relevant units often masks important ecological patterns. Our research topic contains articles that use oligotyping to demonstrate the importance of high-resolution analyses of marker gene data, and providides further evidence why microbial ecologists should open the "black box" of OTUs identified through arbitrary sequence similarity thresholds.