

Resource Summary Report

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Using sequins in metagenome experiments.

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.bic3kayn>

Authors: Tim Mercer

Summary: Metagenome sequins are a set of synthetic DNA controls that reflect the sequence complexity, GC content, phylogenetic diversity and abundance of a natural microbial community. The sequins are 'spiked-in' to your DNA sample, which together undergo to library preparation, sequencing and analysis. The sequins can then be distinguished from your sample DNA in the output library by their synthetic sequence, and analyzed as internal controls. Sequins are compatible with all standards library preparation and sequencing methods. This protocol describes the laboratory steps required to re-suspend and spike the sequins into your DNA sample, as well as the bioinformatic steps required to analyze sequins in your output library. For further details on the design, validation and use of sequins, we refer users to 'Synthetic microbe communities provide internal reference standards for metagenome sequencing and analysis' by Hardwick et. al., (2018) Nature Communications.

Affiliations: Garvan Institute of Medical Research

External URL: <http://www.sequinstandards.com>

Version: 1

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