

Absolute quantification of viable bacteria abundances in food by next-generation sequencing : quantitative NGS of viable microbes

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EUKARYOME: the rRNA gene reference database for identification of all eukaryotes

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Seasonal dynamics of bacterial composition and functions in biological treatment of coking wastewater

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The development of gut microbiota in critically ill extremely low birth weight infants assessed with 16S rRNA gene based sequencing

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Trophoblast derived extracellular vesicles specifically alter the transcriptome of endometrial cells and may constitute a critical component of embryo-maternal communication

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Use of PCR-denaturing gradient gel electrophoresis for the discrimination of Candida species isolated from natural habitats

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