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Results. Analysis of clean sequences. In total, 819,834 high-quality sequences were obtained after raw data quality trimming. The average length of the high-quality sequences ranged from 394 bp to 395 bp (Table I). The calculated rarefaction curves (Fig. 1) and coverage values (Table II) prompted that the libraries were abundant enough to the bacterial diversity analysis in all the tissues that ...

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Polish Journal of Microbiology 2017, Vol. 66, No 4, 419-425 ORIGINAL PAPER * Corresponding author: P. Lisiecki, Department of Pharmaceutical Microbiology and Microbiological Diagnostics, Chair of Biology and Biotechnology, Medical University of Łódź, Łódź, Poland; e-mail: pawel.lisiecki@umed.lodz.pl Introduction

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Polish Journal of Microbiology 2013, Vol. 62, No 2, 121-129 ORIGINAL PAPER Introduction Repair of DNA damages by base excision is one of the main strategies used by the cell to defend against exogenous or endogenous genotoxic stress. These damages have the potential to cause cell death or mutation.

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The strain were deposited in the collection of the Institute of Fermentation Technology and Microbiology (LOCK 105), Lodz University of Technology, Poland. Additionally, 126 Salmonella sp. strains were used: three reference strains from American Type Culture Collection (ATCC, USA) and 123 environmental strains from the collection of Proteon Pharmaceuticals SA (Table III).

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1 Department of Antibiotics and Microbiology, National Medicines Institute, Warsaw, Poland ; Department of Pharmaceutical Microbiology, Medical University of Warsaw, Warsaw, Poland. PMID: 30451441 PMCID: PMC7256845 DOI: 10.21307/pjm-2018-044 Abstract Probiotic bacteria have been used as a health-promoting factor for a very long time. Nowadays, products containing probiotic bacteria are ...