

Soil & Environmental field gathers a wide range of samples such as soils, plants, animal, microorganisms, wastewater etc. and often mixed. This makes the sample preparation step complex.

In some cases, the sample preparation method must be able to dissociate soft or hard matrices from microbial communities inside them. In other cases, living microorganisms have to be extracted from the matrices. Moreover, the targeted molecules are often in low concentration then big quantities of sample have to be proceeded at once in order to increase the detection limit.

To meet these needs, Precellys® homogenizers provides a high speed sample disruption based on bead-beating in 2, 7 and 15mL associated to a wide range of lysing kits for the extraction of RNA, DNA, proteins but also living microorganisms from various matrices within minutes with high reproducibility, high throughput and no cross-contamination.



AVAILABLE PRECELLYS® TOOLS

Equipment: Precellys® Evolution, Precellys® 24, Cryolys®

Lysing matrix for soil & environment samples (soils, plants, wastewater...) : SK38 2mL and 7mL, CK14 2mL and 7mL, CK28 2mL, 7mL and 15mL, VK05 0,5mL and 2mL, VK01 2mL, VKMix 7mL

APPLICATION NOTES AVAILABLE

DNA extraction from soils, Genosol, National Institute for Agronomic Research (France)

Analysis of the genetic resources of soil microbial communities with Precellys® 24.

Environmental Biomarkers Analysis, Laboratory of Industrial and Environmental Toxicology ULCO, Dunkerque / ILIS –Lille II (France)

DNA extraction from mosses for long term accumulation and bioaccumulation assessment of organic and inorganic pollutants.

Metabolomic study of the red algae *Chondrus crispus*, MetaboMER, Metabolomic Platform, FR2424 CNRSUPMC, Station Biologique de Roscoff, Roscoff, (France)

Cryogrinding of red algae *Chondrus crispus* with the combo Precellys® 24 and Cryolys® for whole metabolome extraction.

Protein extraction from tough marine phytoplankton, Environmental Proteomics (Canada)

Protein extraction from tough recalcitrant marine phytoplankton for quantitative analysis of protein composition.

Metabolomic study from clam gill, Key Laboratory of Coastal Zone Environment Processes, CAS; Shandong; Provincial Key Laboratory of Coastal Zone Environment Processes, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai (China)

Metabolites extraction from clam gills to assess the sensitivity of three pedigrees of Manila clam to the acute mercury exposure.

RNA extraction from pufferfish torafugu with Minilys®, Laboratory of Marine Biochemistry, University of Tokyo (Japan)

RNA extraction from pufferfish torafugu with Minilys® in the frame of a global study on the mechanisms involved in the biological processes in relation to energy metabolism, stress responses and cell signaling pathway .

SCIENTIFIC PUBLICATIONS AVAILABLE



[1] Viviane Radla, *et al.* Drying and rewetting events change the response pattern of nitrifiers but not of denitrifiers to the application of manure containing antibiotic in soil, *Applied Soil Ecology* Volume 95, November 2015, Pages 99–106

[2] Charlotte R. Hewins, *et al.* Seasonal variation in mycorrhizal fungi colonizing roots of *Allium tricoccum* (wild leek) in a mature mixed hardwood forest, *Mycorrhiza*, August 2015, Volume 25, Issue 6, pp 469–483

[3] Silvia Gschwendtner, *et al.* Effects of Elevated Atmospheric CO₂ on Microbial Community Structure at the Plant-Soil Interface of Young Beech Trees (*Fagus sylvatica* L.) Grown at Two Sites with Contrasting Climatic Conditions, *Microbial Ecology*, May 2015, Volume 69, Issue 4, pp 867–878

[4] Joaquín M. Ayarza, *et al.* Expression of stress-related proteins in *Sediminibacterium* sp. growing under planktonic conditions, *Journal of Basic Microbiology*, April 2015

[5] T. I. Chernov, *et al.* Assessment of diversity indices for the characterization of the soil prokaryotic community by metagenomic analysis, *Eurasian Soil Science*, April 2015, Volume 48, Issue 4, pp 410–415

[6] R. Quintãa, *et al.* Growth and nitrogen uptake by *Salicornia europaea* and *Aster tripolium* in nutrient conditions typical of aquaculture wastewater, *Chemosphere* Volume 120, February 2015, Pages 414–421

[7] Simon M. Dittami, *et al.* Molecular probes for the detection and identification of ichthyotoxic marine microalgae of the genus *Pseudochattonella* (Dictyochophyceae, Ochrophyta), *Environmental Science and Pollution Research*, October 2013, Volume 20, Issue 10, pp 6824–6837

[8] Anke Stükena, *et al.* Novel hydrolysis-probe based qPCR assay to detect saxitoxin transcripts of dinoflagellates in environmental samples, *Harmful Algae*, Volume 28, August 2013, Pages 108–117

[9] Pål A. Olsvika, *et al.* Transcriptional profiling in burbot (*Lota lota*) from Lake Mjøsa—A Norwegian Lake contaminated by several organic pollutants, *Ecotoxicology and Environmental Safety*, Volume 92, 1 June 2013, Pages 94–103

[10] Simon M. Dittami, *et al.* Seasonal dynamics of harmful algae in outer Oslofjorden monitored by microarray, qPCR, and microscopy. *Environ Sci Pollut Res*, January 2013

CONCLUSION

The use of Precellys® Homogenizers (Precellys® Evolution, Precellys® 24 and Minilys®) significantly decreases the time spent on sample preparation of environmental samples such as leaves, soils, algae, or wastewater. Thanks to dedicated lysing kit, Precellys® increases detection limits with efficient grinding and maintain also high quality RNA, DNA, proteins extraction. In addition, the 15mL option of Precellys® Evolution allows to process big quantities of samples in minutes with high reproducibility.

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