# Identification of the PEG-Induced Proteins by 2D-Gel Electrophoresis and Mass Spectrometry in *Sphingopyxis macrogoltabida* strain 103

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## ABSTRACT

***Cell-free extracts from a PEG 4000-utilizing bacterium, Sphingopyxis macrogoltabida strain 103, grown on glucose and PEG 4000 medium were separated into cytoplasmic, membrane-bound and signal protein fractions. Each fraction was analyzed by two-dimensional polyacrylamide gel electrophoresis (2D-PAGE). A total of 19 differentially-expressed proteins by PEG were in-gel trypsin digested and the digestion mixtures were analyzed by MALDI-TOF mass spectrometry to determine the molecular masses of the resulting tryptic peptides. Ten proteins in the cytoplasmic fraction showed homology to fatty acyl CoA synthetase, IEA two-component response regulator, permease, LacI-transcription regulator, galactinol synthase, coenzyme PQQ synthesis protein, transcription regulator, translation-initiation factor like protein, CheY-like two-component response regulator and hypothetical protein. Three proteins in the membrane-bound fraction were identified as LysR-transcription regulator, GutR-transcription regulator and two-component response regulator. Six proteins in the signal protein fraction were polyphosphate kinase, ATP sulfurylase, amino acid permease, sigma-54 dependent transcription regulator, fatty-acid-CoA ligase and LysR-transcription regulator. These proteins are expected to be relevant to PEG metabolism by S. macrogoltabida strain 103.***

**Key words:** PEG degradation, *Sphingopyxis macrogoltabida*, 2D-PAGE, MALDI-TOF mass spectrometry

## INTRODUCTION

Polyethylene glycols [PEGs, $HO(CH_2\text{-}CH_2O)_nH$] are man-made polymers that have been widely used as commodity chemicals in various industrial products such as pharmaceuticals, cosmetics and lubricants and as raw materials in the synthesis of nonionic surfactants and polyurethanes. Since they are water-soluble,