

Identification of *Methanococcus jannaschii* Proteins in 2-D Gel Electrophoresis Patterns by Mass Spectrometry

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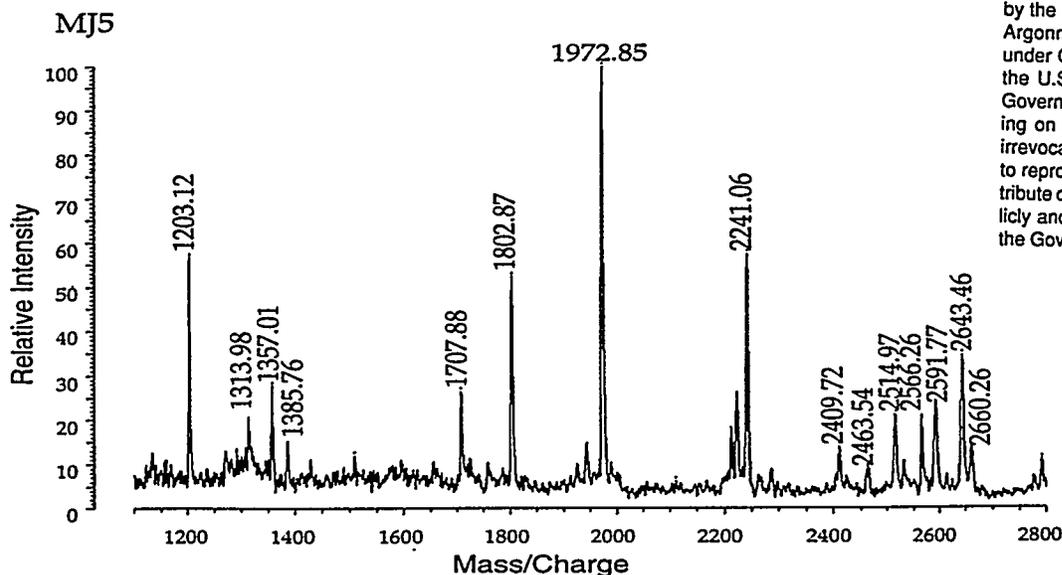
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Introduction

The genome of *Methanococcus jannaschii* has been sequenced completely and has been found to contain approximately 1,770 predicted protein-coding regions. When these coding regions are expressed and how their expression is regulated, however, remain open questions. In this work, mass spectrometry was combined with two-dimensional gel electrophoresis to identify which proteins the genes produce under different growth conditions, and thus investigate the regulation of genes responsible for functions characteristic of this thermophilic representative of the methanogenic Archaea.

Methods

The proteins of *Methanococcus jannaschii* were separated by 2-D gel electrophoresis and detected using Coomassie blue or silver stain. A number of protein spots were chosen at random, excised from the gel, destained by 25 mM ammonium bicarbonate/50% acetonitrile, and digested *in situ* with trypsin. The resulting peptides were then recovered using 50% acetonitrile/5% TFA, and analyzed by Kratos Kompact mass spectrometry. α -Cyano-4-hydroxycinnamic acid was used as the matrix.



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Figure 1. MALDI MS spectrum of the tryptic digest of a *M. jannaschii* protein (MJ5).

Results

Different staining methods were compared for their compatibility with mass analysis. A modified silver staining protocol turned out to be the method of choice due to its high protein detection