

197d The Microbial Proteome Project: a Database of Microbial Protein Expression in the Context of Genome Analysis

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This project, funded through the U.S. Department of Energy Microbial Genome and Genomics:GTL programs, is focused on the detection and characterization of differential protein expression in microbial systems relevant to the goals of the Office of Biological and Environmental Research. As part of this effort, relational databases are being used to assimilate and integrate the data collected. The Microbial Proteome Project knowledgebase currently includes experimental details and two-dimensional electrophoresis (2DE) proteome data for 11 different microbes (*Deinococcus radiodurans*, *Geobacter sulfurreducens*, *Geobacter metallireducens*, *Methanococcus jannaschii*, *Prochlorococcus marinus*, *Pyrococcus furiosus*, *Psychrobacter* sp.5, *Rhodopseudomonas palustris*, *Rhodobacter sphaeroides*, *Shewanella oneidensis*, and *Synechocystis* sp. PC), over 8000 2DE images that are accessible to authenticated users, and the identifications of 575 *S. oneidensis*, 400 *G. sulfurreducens*, and 77 *G. metallireducens* proteins together with the peptide mass data used to obtain these identifications. As part of the overall goal of this project is to provide a public resource of protein expression information for microbes in the context of genome sequence, a public website (<http://GelBank.anl.gov>) has been designed to provide access to proteome analysis results as they become validated and published. GelBank includes the complete genome sequences of approximately 130 microbes along with numerous tools that provide the capability to search the sequence databases for specific protein functions and amino acid sequences. This site also includes web applications pertinent to 2DE analysis, such as titration curves for collections of proteins and 2DE pattern animations. The database is currently populated with protein identifications from the Argonne Microbial Proteomics studies and will accept data input from outside users interested in sharing and comparing results from proteome experiments. This growing knowledgebase provides the opportunity for comparison of proteomes across species as well as the assessment of differential cellular responses to a variety of growth conditions.