

The Proteomic study of *Thermus thermophilus* HB8

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The latest proteomic technologies permit exact view of cellular and sub-cellular adaptation of a cell and thus can provide a great understanding of cell physiology. Recently, 742 complete microbial genome sequences were opened to the public database (NCBI genome database, <http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi?view=1>, by the end of Aug. 2008). The proteomic approach to the microorganism, especially bacteria, is now well established and a major proteome data are accessible to public database by using MASCOT, SEQUEST or MS-Fit program because of high similarity of amino acid sequence of each protein. Together with transcriptional profiling, the expression or repression of proteomics provides useful clue for interesting candidate proteins or genes which can further validate the function using traditional molecular and biochemical tools.

Thermus thermophilus is thermophilic eubacteria whose physiology was well studied rather than other thermophiles and its genome sequence also completed. Additionally, it contains low number of orfs (about 2,200 ORFs in the chromosome and two plasmids) and the genetic manipulation approach is also well established. Because of this reason, *T. thermophilus* is good model organism for system biology to understand its cellular metabolism and physiology against environmental stimuli under whole cell level. On the other hand, the complete genome sequence reveals that *T. thermophilus* contains ~30% unknown function orfs that prevent complete understanding to its physiology under whole cell level. To investigate and elucidate their cellular function, and understand cellular response against various situations which the cell may be encountered in a variety of environments, the proteome of *T. thermophilus* HB8 was investigated by using nano-LC based FT-ICR/MS and 2-DE based MALDI-TOF analysis.

References

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