

# Scientists develop method for comprehensive proteome analysis

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Investigators at Burnham Institute for Medical Research (Burnham) have deciphered a large percentage of the total protein complement (proteome) in *Schizosaccharomyces pombe* (*S. pombe*) fission yeast.

Laurence Brill, Khatereh Motamedchaboki, Ph.D. and lead investigator Dieter Wolf, Ph.D., developed the novel method, used to identify 4,600 proteins in the organism, using an array of sophisticated techniques. The research was published online on March 9 in the journal *Methods*.

"Analysis of the proteome of an organism tells us so much more than simple DNA sequence analysis," said Dr. Wolf. "Proteome analysis gives us a snapshot of what proteins are being expressed in the cell at any given point in time. This can tell us how [protein](#) expression changes in response to certain stimuli and in disease states, which may help identify new biomarkers for diseases. We are now applying the methodology to protein profiling of human [stem cells](#) in collaboration with Burnham's stem cell program director, Evan Snyder."

The method developed by Burnham scientists involved digestion of the proteins into smaller [peptides](#), then separation of the peptides based on electrostatic charge using strong anionic exchange chromatography. The peptides were further separated by molecular weight using high pressure liquid chromatography. Each of the individual peptides was detected and identified using mass spectrometry and database analysis. DNA analysis of the yeast's genome predicts 5027 proteins. The team identified 4,600 proteins, which is not quite the entire proteome. The remaining 400 are

only expressed during *S. pombe*'s mating state.

*S. pombe* is often used as a model organism to study DNA damage response and repair, cell division, stress responses and other aspects of cellular biology.

Source: Burnham Institute

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