

## **Exploration of proteomics data in the "omic" context using the Annotation, Mapping, Expression and Network suite of tools (AMEN).**

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High-throughput genome biological experiments yield large and multifaceted datasets that require flexible and user-friendly analysis tools to facilitate their interpretation by life scientists. Many solutions currently exist, but they are often limited to specific steps in the complex process of data management and analysis and some require extensive informatics skills to be installed and run efficiently. In this context, we developed AMEN, an innovative unified suite of tools for molecular systems biological data analysis freely available at the Sourceforge portal and running on all operating systems. This solution enables biological and medical researchers with basic bioinformatics skills to manage and explore genome annotation, chromosomal mapping, protein-protein interaction, protein-gene regulation, expression profiling and proteomics data. During this keynote presentation, concrete examples will be given and will illustrate the integration and exploration of proteomics data with other "omic" field.