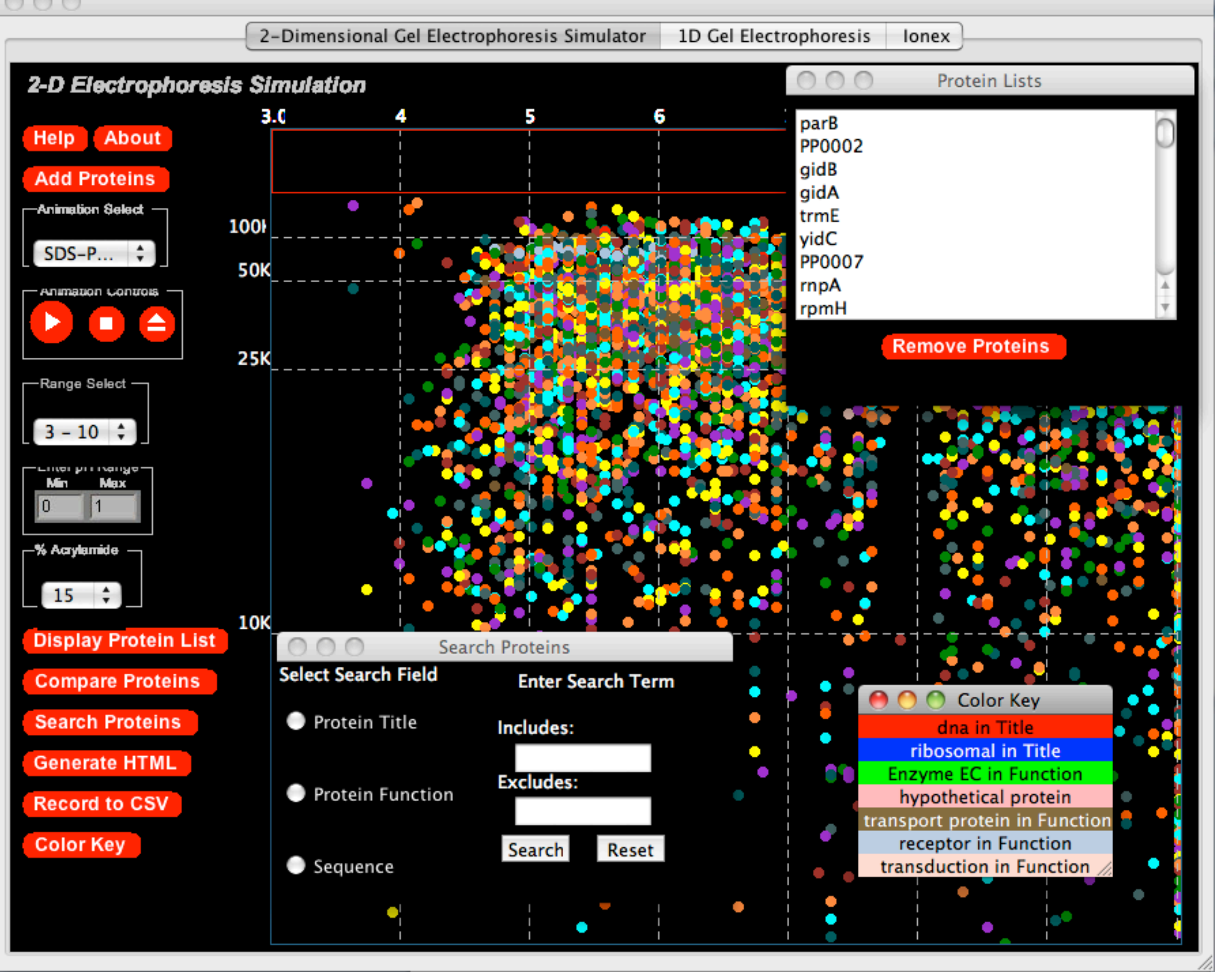
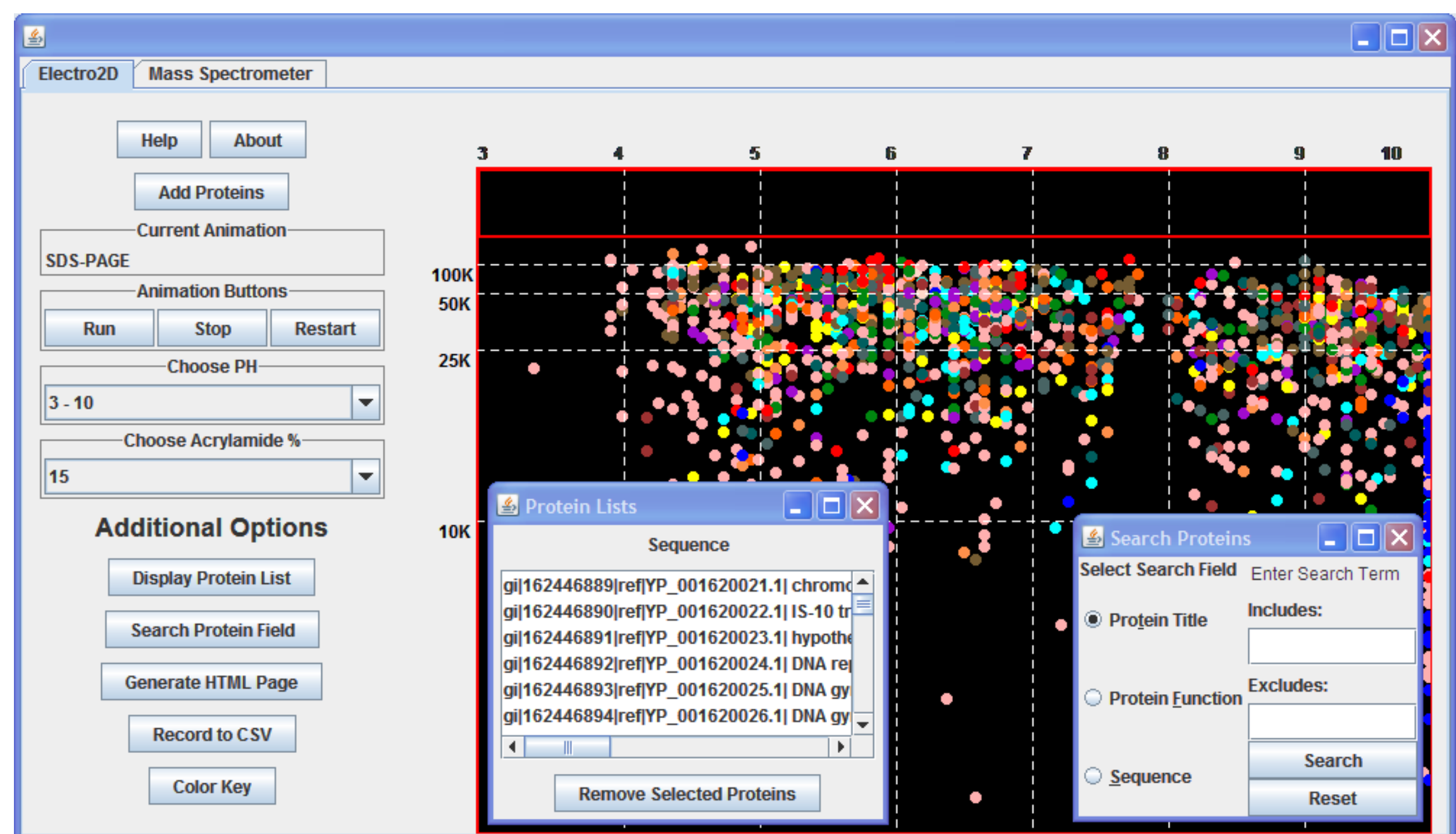


In proteomics, complex mixtures of proteins are separated (usually by chromatography or electrophoresis) and identified by mass spectrometry. 2DE-Tandem MS, a computer program designed for use in the biochemistry, proteomics, or bioinformatics classroom, contains two simulations-2D Electrophoresis and Tandem Mass Spectrometry. These integrated simulations are designed to teach the concept of proteome analysis of simple organisms. 2DE-Tandem MS can be used as a freestanding simulation or in conjunction with a wet lab, to introduce proteomics in the undergraduate classroom, and is available, for free, at <https://sourceforge.net/projects/jbf/>. It was developed using Java Swing therefore, Java must be installed on the host computer, 2DE-Tandem MS functions in Mac OSX, Windows, and Linux, ensuring that every student sees a consistent and informative GUI no matter the computer platform they choose. Future releases will allow peptide sequences to be displayed to aid in the learning process.



The original JBioFramework 2D Electrophoresis simulation on a Macintosh computer.

The original 2D Electrophoresis simulation was updated to be platform independent, compatible with commonly used modern file types for proteome files, and to capitalize on expanded online resources.



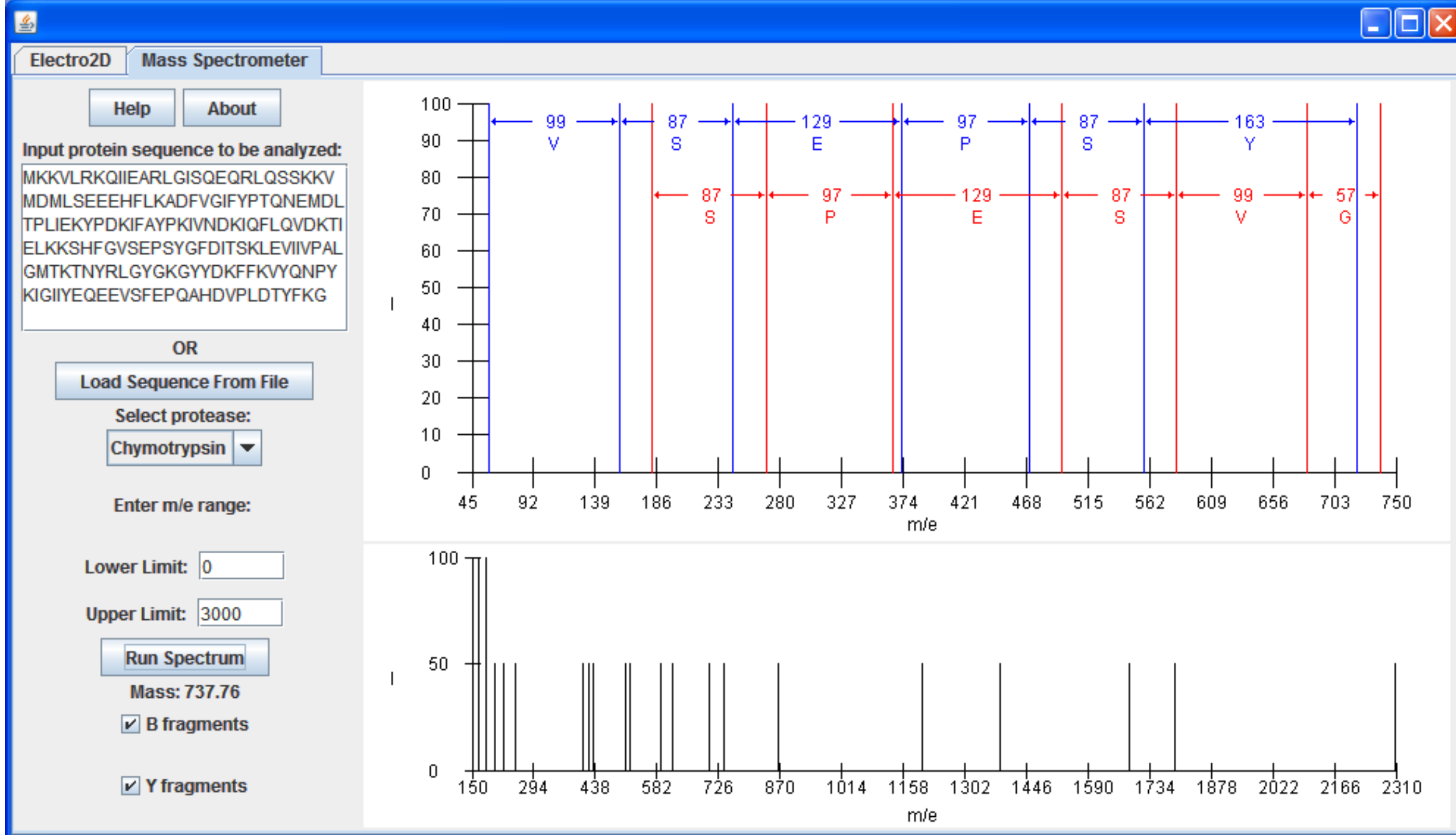
Current JBioFramework on a Windows computer.

After updating the 2D Electrophoresis simulation, a new simulation for Tandem Mass Spectrometry was added to JBioFramework. This new simulation (E2D-TMS) is designed to teach the concept of peptide sequencing and protein identification. The complete program can be downloaded for free at <https://sourceforge.net/projects/jbf/>.

# A Mass Spectrometry Simulation for Biochemistry Education

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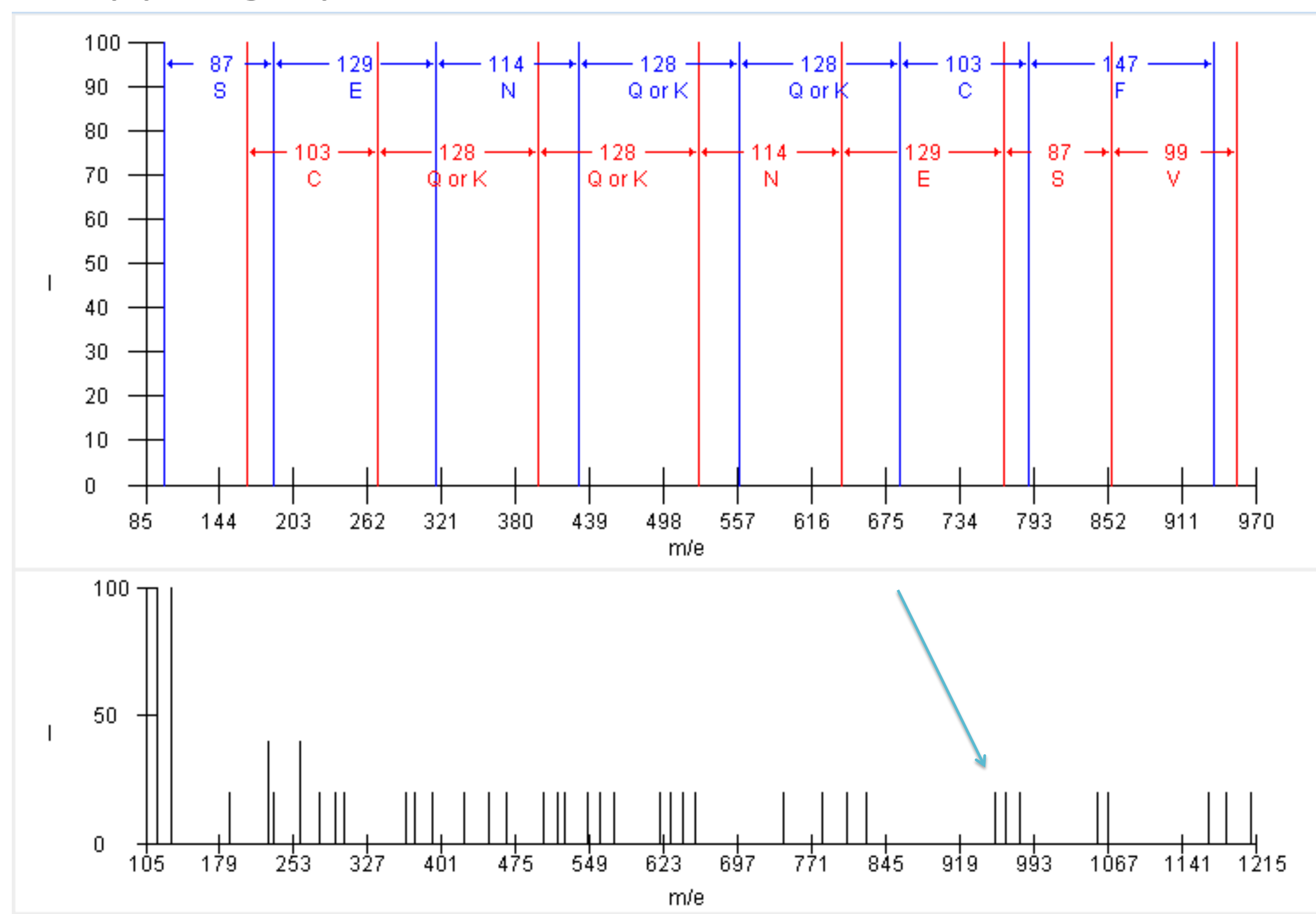
## The Tandem Mass Spectrometry Simulation:



The JBioFramework Tandem Mass Spectrometry Simulation on a Windows Computer.

The tandem mass spectrometry simulation receives input in the form of a peptide sequence from user entry, a FASTA format file, or from the 2D Electrophoresis simulation. Once entered, the user can select from four proteases to digest the peptide sequence, Trypsin, Chymotrypsin, Proteinase K, or Thermolysin.

Once the user clicks the Run Spectrum button the simulation uses the logic of the protease to divide the entered peptide sequence into fragments and displays them in the lower output graph. Clicking on one of these fragment peaks allows its sequence to be read through b- and y- fragmentation in the upper graph.



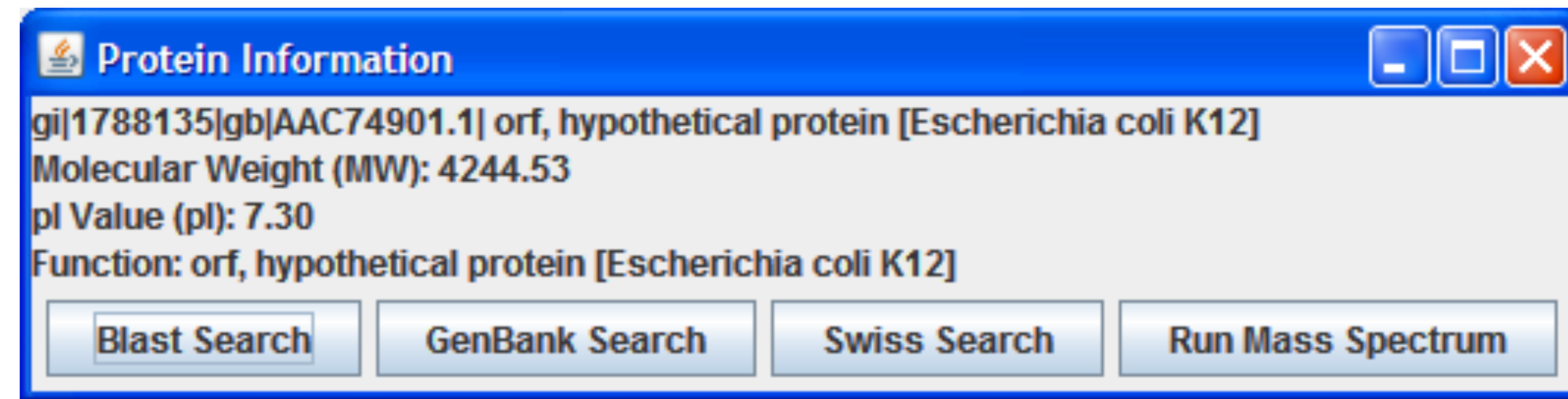
Output and tandem output graphs for peptide sequencing.

## Creating a Familiar Format:

The Tandem Mass Spectrometer simulation interface is designed to resemble the output layout from a real instrument. The y-axis of the initial output graph is a calculated intensity, I, that accurately represents the relative frequencies of each peptide fragment. The x-axis of both graphs plots the mass over charge ratios of each peptide fragment.

## An Integrated Approach:

The 2D Electrophoresis simulation is integrated with the Tandem Mass Spectrometry simulation in that it allows a user to select a protein dot from the gel canvas and send its peptide sequence to the tandem MS simulation.

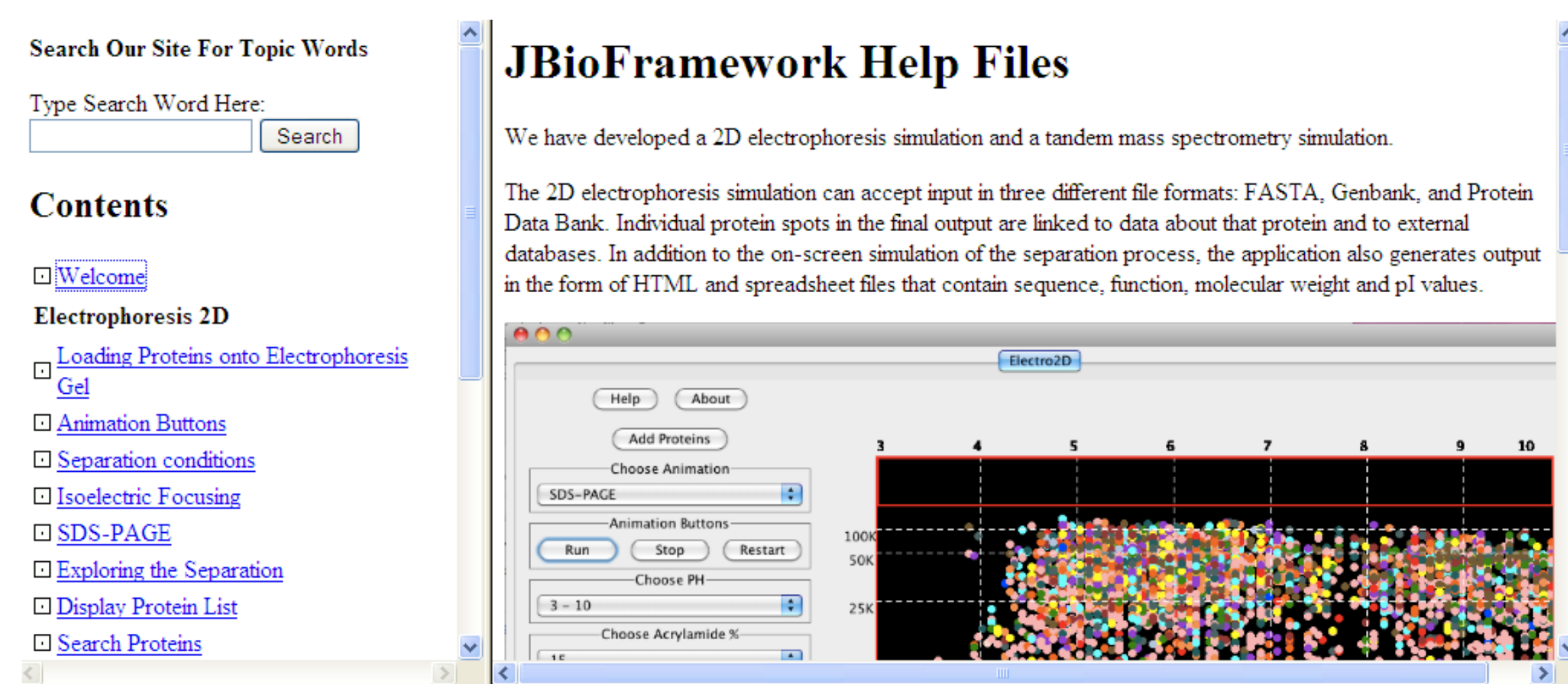


The dialog box that appears when a user clicks on a protein dot in the 2D Electrophoresis simulation.

Students can explore the technique of using tandem mass spectrometry to create the b- and y- fragments used to read the sequence of a fragment of a protein through the mass difference between subsequent peaks. They may then perform online database searches for that deduced sequence to identify the unknown protein.

## Additional Resources:

Extensive help files were created and are available through the program to help students learn about the concepts at work behind the laboratory techniques of 2D Electrophoresis and Tandem Mass Spectrometry.



The Welcome screen of the JBioFramework Help Files.

## Classroom Applications:

Problem sets have also been created to aid in student learning. These worksheets are designed for biology and chemistry classes at two different levels: AP high school/college freshman and upper division for college. They may also be suitable in many other classrooms to introduce proteomics. The problems are designed first to introduce the students to the simulation itself, then to lead them into a deeper study of the concepts and practice of protein separation and identification as practiced in the lab.

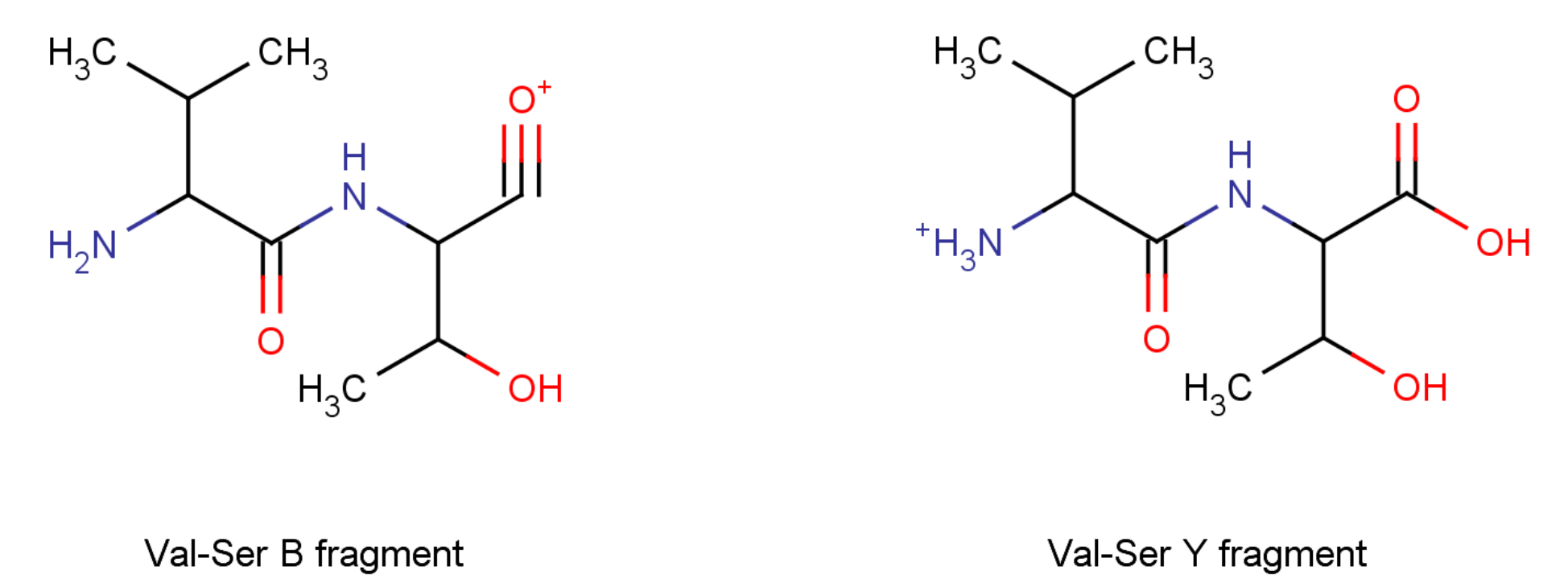
## Creating a Teaching Tool:

The worksheets are designed in a series of simple steps that can be expanded to give the students more freedom. They begin by loading a proteome, selecting separation conditions (for 2DE) and identification conditions (for tandem MS). Students then use the data they have generated to learn more about their proteins with established online resources including NCBI, BLAST, and UniProtKB. The simpler exercises have clear right answers. The more sophisticated problems are more open-ended and can be used to stimulate discussion.

The E2D-TMS application is freely available at <https://sourceforge.net/projects/jbf/>.

## Future Goals

- Update 1D Electrophoresis
- Add chemical drawings of peptide sequences to the tandem mass spectrometer simulation.



An example peptide from a b and y fragment

Allow students to click on a peptide fragment peak, sequence it, and then request a visual drawing of that peptide sequence including backbone and R-group side chains.

- Integrate Chromatography Simulations into the software package.

Develop additional simulations for Ion Exchange Chromatography and Reversed Phase HPLC. Allow interactions between the simulations as seen in the integration between the 2D Electrophoresis simulation and the Tandem Mass Spectrometry simulation.

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