



Mass Spectrometry
and Proteomics Facility

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Tim Blacker
Bioinformatics Solutions Inc.
145 Columbia St. W, Suite 2B
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Dear Tim,

I am writing to describe how the software PEAKS has positively impacted our Facility in our day to day operations. Our Facility is the Core Mass Spectrometry and Proteomics Facility at The Ohio State University and the hub Facility for the Ohio State Mass Spectrometry Consortium. We serve a very diverse research community ranging from the College of Medicine, Pharmacy, Chemistry, Biochemistry Veterinary Medicine and others. While routine proteomic analyses is a main service we offer, non-routine samples are quite frequently analyzed here. Non-routine samples include samples with modifications such as phosphorylation, samples requiring *de novo* sequencing, foot printing etc. The modifications analyzed in this Facility range from phosphorylation, acetylation, modified amino acids and glycosylation. It is important to have processing software available to readily incorporate analysis of these unique samples. The PEAKS software has been extremely useful in this regard, I have really liked the flexibility to input new modifications and use the pre-programmed ones within the same data file. I purchased PEAKS for the purpose of processing the non-routine samples, but have also found to prefer it over search engines available on the web for routine samples.

The features I particularly like the most in PEAKS include the ability and ease in viewing the mass spectra from a pkl file, the ease in processing each spectra individually or the entire data file at once, the accuracy of the results, the ease in manipulating the spectra multiple times with different processing parameters, the simplicity in searching and reading the results and the comprehensive help files. A typical *de novo* project usually took me 2 – 5 days to process using Proteinlynx. Each MS/MS spectra had to be processed by hand from the chromatogram window, smoothed, and MaxEnt'ed before copy/pasting the spectra in Proteinlynx. From there, it was a constant struggle to get accurate sequence assignments. I often would find myself resorting to using a calculator to figure the b/y series by hand. If a data file had 20 MS/MS switches, it would take an enormous amount of my time to process the data and get the results to the researcher. I can do a couple *de novo* projects from start to finish in a morning or afternoon. My productivity has increased times since using PEAKS software to process data.

I am also very impressed with the software's ability to process the data accurately. Even poor quality data has generated enough sequences to be useful. I have compared search

results of routine protein ID's between Mascot, Genomic Solutions and PEAKS. The PEAKS results are always comparable and often superior. The PEAKS searches often match more peptides in a sequence for increased sequence coverage and definitely pull out modifications from the sequences more efficiently than search engines freely available on the web. As a result we certainly will use this software for both routine searches and non-routine analyses and hope to be able to include in our FY 05 budget to purchase another license for the lab.

Sincerely,

A handwritten signature in blue ink that reads "Kari B. Green Church". The signature is written in a cursive style with a large, stylized initial "K".

Dr. Kari B. Green-Church
Associate Director
CCIC Mass Spectrometry and Proteomics Facility