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Iain Rogers
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Dear Iain,

We are writing to you to give you some feedback on our experiences with PEAKS, which we have been using at our institute for the past year.
When we started *de novo* sequencing, we tried out different programs and soon we 'came down to earth again'. Even with excellent tandem mass spectra, the results obtained from most of these programs were often far from satisfactory. Things changed when we employed PEAKS. As a first trial we used auto *de novo* analysis for some known peptides without changing the standard settings and without the use of a database. Just a few seconds later, the right sequences appeared on the first positions of the candidate lists. Afterwards we tried the combination of *de novo* sequencing with database searching. Since then our tandem mass spectra are routinely sequenced by standard database searching and PEAKS.
We were so impressed that we have started to sequence most of our recent data again. PEAKS has helped us to identify unmatched results or confirm ambiguous sequences found by standard database searching methods. As a whole, the sequence coverage increased dramatically for some of the proteins under investigation. The program is not only very fast at processing the data and searching in the databases but also avoids the inconvenience of doing thousands of things manually.
PEAKS has made it possible to identify peptides with the same amino acid composition, but with slightly different sequences that are sometimes difficult to sequence only by database searching. A case in point is the skin protein, elastin. Our group is interested in the characterization of elastin peptides for identifying biomarkers, which could help us to deduce molecular changes that occur on the elastin molecule as a result of pathological disorders or which could help to quantify the protein. Elastin is one of the most internally repetitive human proteins known. Since it is resistant to digestion with trypsin, less substrate specific enzymes, such as elastase have to be used. Many elastin peptides produced by elastase digestion are small and similar in amino acid composition. Unambiguous identification of such peptides would have been extremely difficult without the combined use of automated *de novo* sequencing and database searching.
PEAKS is very accurate and powerful software with an innovative user interface. The program lives up to its promises and helps us to save a lot of time.

Sincerely,

Christian E.H. Schmelzer

Melkamu Getie