Abstract Submitted
for the MAR07 Meeting of
The American Physical Society

RAId_DbS: Method for Peptide ID using Database Search with Accurate Statistics[1] GELIO ALVES, ALEKSEY OGURTSOV, YI-KUO YU, NCBI/NLM/NIH — The key to proteomics studies, essential in systems biology, is peptide identification. Under tandem mass spectrometry, each spectrum generated consists of a list of mass/charge peaks along with their intensities. Software analysis is then required to identify from the spectrum peptide candidates that best interpret the spectrum. The library search, which compares the spectral peaks against theoretical peaks generated by each peptide in a library, is among the most popular methods. This method, although robust, lacks good quantitative statistical underpinning. As we show, many library search algorithms suffer from statistical instability. The need for a better statistical basis prompted us to develop RAId_DbS. Taking into account the skewness in the peak intensity distribution while scoring peptides, RAId_DbS provides an accurate statistical significance assignment to each peptide candidate. RAId_DbS will be a valuable tool especially when one intends to identify proteins through peptide identifications.

[1] This reasearch was supported by the Intramural Research Program of the NIH/DHHS

Yi-Kuo Yu
NCBI/NLM/NIH

Date submitted: 20 Nov 2006 Electronic form version 1.4