EDMAN SEQUENCING RESEARCH GROUP

Of the Association of Biomolecular Resource Facilities

Newsletter

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Including an update from the 12th International meeting

ABRF 2008 Salt Lake City

- Enabling Technologies in the Life Sciences -

From the ESRG: "Thank you to all who participated in the 2008 study."

Inside the ESRG 2008 Study

By Brian Hampton

"Do you have problems sequencing an N-terminally histidine-tagged protein?"

That was the question at the heart of the ESRG study this past year. Not surprisingly the answers to that question from the ESRG members last spring were "yes," "no" and "sometimes". So the group designed a study that would provide a scientific basis for investigating this question.

But as in many of the ESRG studies, the initial hurdle that must be overcome is - where to obtain the samples for the study. The last two years members of the ESRG themselves have produced the study samples. This year Wendy Sandoval with the help of Jessica Huard and Liza Ingle all of Genentech were able to prepare two N-terminally tagged protein constructs that were eventually sent out to twenty seven laboratories for analysis. This was a busy time for Wendy and the ESRG as we were just getting the final samples prepared when the study was announced in September.

More than half of the labs that requested the samples turned in their results. The data was compiled and analyzed during December and January to give participants as much time as possible to return their data for inclusion in the study.

The ESRG 2008 study results were presented February 11 at the ABRF 2008 International meeting in Salt Lake City, Utah. Serving his first year on the ESRG, Steve Smith of the University of Texas Medical Branch presented the poster, and Wendy Sandoval presented the talk titled "ESRG Study 2008: Investigation into poly-amino acid N-terminal tags and their effects on automated Edman degradation."

This study isn't finished. More work should be planned to investigate this phenomenon.

The ESRG session at the ABRF 2008 meeting was well attended. Following the oral presentation many of those in the audience gathered for a lively discussion that centered around the main observations of the study: the high degree of lag following the His-tag sequence and what appeared to be preview in the form of increased background from those amino acids present in the protein sequence immediately following the His-tag.

Another topic of discussion was about what would make a good study for 2009. Suggestions ranged from determining the best techniques for obtaining sequence read lengths in excess of 50 cycles and several people called for further investigation of the His-tag sample toward improving the sequencing efficiency through the His-tag.

The ESRG is interested in getting feedback from the people who operate Edman sequencing facilities and anyone who is interested in the technology. You can find contact information for ESRG members and additional information about past studies on the ABRF website http://www.abrf.org/index.cfm/group.show/EdmanSequencing.29.htm.

The ESRG Members for 2007

Rich Thoma (Co-chair) - Monsanto Inc.
Brian Hampton (Co-chair) - University of Maryland
Peter Hunziker - University of Zurich
Joe Leone - Pfizer Inc.
Klaus Linse - University of Texas, Austin
Wendy Sandoval - Genentech Inc.
Steve Smith - University of Texas Medical Branch
Nancy Denslow (EB Liaison) - University of Florida

TRIBUTE

From approximately 1946 through 1957 Pehr Edman elucidated and refined the chemistry still in use today for the stepwise degradation of proteins allowing for the determination of their amino acid sequences. A biographical memoir of Pehr Edman can be read at http://www.science.org.au/academy/memoirs/edman.htm and a historical treatment of Edman's work is contained in Chapter 3 "Pehr Victor Edman: A Solitary Genius" (Birger Blombäck) in "Selected Topics in the History of Biochemistry. Personal Recollections. VII, Volume 42" (Elsevier) Excerpts can be viewed at Google Books