2006 Interactive Training Initiative Debriefing Workshop

Yverdon-les-Bains, Switzerland, 4 December 2006

Final workshop on Applied Proteomics Training Initiative – An overview

Session I: Separation techniques
Session II: Mass Spectrometry
Session III: Bioinformatics

Student's feedback
Interview with Hans Voshol, Novartis Institutes for BioMedical Research
Glossary
Acknowledgements

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Final workshop on Applied Proteomics - Tips and Tricks An overview

By Irene Amodei, ICVolunteers

The SPS debriefing session allowed students to evaluate what they had learned during the course

As an alternative to its regular full scale conference and to address an ever growing demand, the Swiss Proteomics Society (SPS) organised, from September through November 2006, an experimental training. Its goal was to promote a closer interaction between all the actors involved in proteomics-related domains in order to share the specific know-how, and to allow parties to familiarise with different techniques and new equipments. A total of **23 trainees** participated, 4 from European countries and the others from the Geneva, Lausanne but also Zurich, Berne and Basel regions. The participants – spanning from students with limited experience to technicians and senior scientists interested in learning new methods – had the choice of **8 short applied courses** (a total of **16 days** of training) hosted by **8 laboratories** all around Switzerland, including the *Ecole Polytechnique Fédérale* of Lausanne, the Department of Clinical Pharmacology of the Berne University, the Swiss Institute of Bioinformatics in Geneva and the Institute for Molecular Systems Biology in Zurich.

The courses aimed at giving participants insight into the main working fields of Proteomics, such as separation techniques, mass spectrometry, phosphoproteomics and bioinformatics.

At the end of the training courses, organisers and participants met for a wrap-up session held in Yverdon-les-Bains on December 4th 2006.

The one-day event provided the opportunity for thorough debate between trainers and trainees, and also an informal and dynamic occasion to evaluate different analysis strategies, and the related results. Besides a detailed presentation of the courses and their outcomes, the meeting offered a useful overview of the advantages, limits, complementarities and overlaps of the current analysis techniques, as well as review of their risks, challenges and future perspectives.

The applied nature of the trainings, the opportunity to work in technologically advanced laboratories, and the effective tips-and-tricks transfer were especially appreciated by all participants.

During the concluding session some critical points were raised: the need to improve the amount of data collected was expressed, as well as the request of a longer training period that would allow a better sample preparation. The different levels of specialisation of the participants and the heterogeneity of their backgrounds was noted, and unevenly interpreted either as an obstacle or as an unprecedented occasion to discover different approaches.

"During the last years every Proteomics laboratory in Switzerland has been dealing with his own problems and trying to solve them summoning its own expertise only," remarked **Jean-Charles Sanchez**, President of SPS. "To dare and share these problems and solutions, is what science is supposed to do and what SPS is all about. From our very beginning in 2000 we have build up a network of experts, merging both academic and commercial profiles, in order to make different goals, missions and contexts interact." The dialogue between academy and industry turned up to be smooth and mutually convenient. "We are all scientists, no matter who the sponsor is" Dr. Sanchez commented. "It's a dynamic synergy that works very well."

SPS wants to dismantle as many barriers as possible; particularly the barrier that usually separates private and public entities, but also the barrier which often stands between trainers and attendees, thus enabling a multi-directional exchange and a better concerted action.

The SPS team acts as a catalyst, said **Reto Stöcklin** from Atheris Laboratories, looking with optimism at the network that has been activated during the workshops: "People who attended the trainings have already started to work together, exchanging information and comments by e-mail. This kind of on-going relationship is very rare after a simple congress."

To ensure continuity to all this is the key challenge. Will the event gain a more international dimension in its future edition in 2008, as many would hope? Will the now more cohesive expert community be able to preserve this spirit of constant exchange and collaboration? Will a simple mailing list or an online forum serve as a sustainable instrument for enabling the information exchange between the members? All this, of course, is just the beginning.

Session Summaries

Session I: Separation techniques

Reporter: Emily S. Fisher, ICVolunteers
Consultant: Alexis Chauvet, University of Geneva, Tatjana M.E. Schwabe, ICVolunteers
Editor: Asta Lim, ICVolunteers

Chair: **Jean-Charles Sanchez** (Swiss Proteomics Society)

Abbreviations: DIGE, two-dimensional gel electrophoresis; **IEF**, isoelectric focusing; **SPS**, Swiss Proteomics Society;

Short presentations by **Hans Voshol** (Novartis Institutes for BioMedical Research, *Subcellular proteomics*), **Peter Lindinger** (University Hospital Basel), **Catherine Zimmerman** (Clinical Proteomics Group, Geneva University, *Shotgun Isoelectric Focusing peptides analysis*), **Ali R. Vaezzadeh** (Clinical Proteomics Group, Geneva University), **Olivier Barré** (Copper Lab, University of Berne, *Two-dimensional liquid separation with the Proteomelab PF2D*).

Throughout the fall of 2006, the Swiss Proteomics Society (SPS) organised separation techniques courses as part of its 2006 Interactive Training Initiative. These courses were aimed at giving participants insight into three different separation techniques for complex samples for proteomic analysis, with emphasis on the pros and cons of each technique. After the completion of each workshop, organisers and participants came together for a debriefing session, moderated by SPS President Jean-Charles Sanchez, to assess both the techniques and the training.

The first course, led by Hans Voshol (Novartis), Axel Ducret (Roche) and Peter Lindinger (University Hospital Basel), focused on subcellular proteomics using the two-dimensional differential gel electrophoresis (2-D DIGE) to analyse the mitochondrial proteome. After briefly touching on purification and fractionation issues, participants used 2-D DIGE to compare three labelled samples – undifferentiated, differentiated, and differentiated and treated (with an insulin sensitizer: rosiglitazone) mitochondria from mouse 3T3 cells. DIGE permits the analysis of up to three samples on the same gel by labeling each sample with a different fluorescent dye prior to the electrophoretic separation and scanning the gel with different wavelengths to visualise the proteins. By analysing overlays of the differently colored images, differences in protein expression can often already be seen by eye and quantified by software analysis. Participants then used mass spectrometry to verify the identity of the differentially expressed proteins and protein isoforms in order to confirm their visual conclusions.

The second course, given by Catherine Zimmermann and Ali R. Vaezzadeh from the Clinical Proteomics Group at Geneva University, introduced shotgun isoelectric focusing (IEF) for peptide analysis. The goal of this hands-on training was to transfer IEF know-how and to discuss shotgun IEF development and data management techniques. Over the course of two days, participants tested the workflow on pre-prepared *Staphylococcus aureus* samples. Limited results and time did not allow for in-depth data analysis, but participants were able to familiarize themselves with two specific programs, Phenyx and ProteinScape.

In the third training, Marc Solioz and Olivier Barré of the Copper Lab at the University of Berne, demonstrated the utility of two-dimensional liquid chromatography with the relatively new Proteomelab PF2D system.This technology allowed participants to first separate proteins into narrow pI range fractions by chromatofocussing, followed by a second chromatographic step on reversed phase material. The Copper Lab is the first in Switzerland to use the Proteomelab PF2D system, recently developed by Beckman-Coulter, which can be used to analyse a wide range of samples, from mammalian cell culture lysates and solid animal tissues to animal biofluids and plant tissue lysates.

At the debriefing session, participants from all three training workshops expressed appreciation for the opportunity to delve further into

separation techniques through hands-on training. Michel Prudent, from the Ecole Polytechnique Fédérale de Lausanne (EPFL), who participated to the course "Subcellular proteomics", noted that it was particularly useful to "get an overview of the two techniques – gels and mass spectrometry" in a real world setting. Participants in the shotgun IEF course also appreciated the chance to familiarise themselves with the technique, learn a few "tricks", and said they hoped to start using such technology in their own labs. Olivier Barré was happy to share his two-years of trials and successes with the new Proteomelab PF2D system with other potential users of the technology.

All participants were pleased with the applied nature of the training courses. If there were any critical comments, it was that participants would appreciate longer courses in the future to ensure sufficient time to complete more complex analyses, especially in the case of the shotgun IEF process, which generates massive amounts of information for analysis.

After the courses presentations, Jean-Charles Sanchez thanked all presenters and participants for their time and consideration. He then led all debriefed participants in a general assessment of the advantages and disadvantages of each of the three separation techniques reviewed. Specifically, he asked course organisers to comment on the protein dynamic range displayed by each technique, the amount of time and sample needed to create sufficient results for analysis, as well as contamination issues. Discussions revealed that, at present, more is known about two-dimensional gels, which are a bit faster and produce statistically viable coefficients of variation. This was attributed to the fact that it is a more mature technique. However, he noted that "gels have their limitations: they tend to identify the same proteins, limiting research, and are not able to deal with hydrophobic proteins". Jean-Charles Sanchez encouraged all presenters and participants to continue working with newer technologies, in order to overcome some of the limitations of 2D gels and further their development and utility in proteomic research. "We still have a lot of work to do in the development of separation techniques", said Dr. Sanchez.

Session II: Mass Spectrometry

Reporter: Tatjana M.E. Schwabe, ICVolunteers
Consultant: Daniel Biass, University of Geneva
Editor: Asta Lim, ICVolunteers

Chair: **Reto Stöcklin** (Atheris Laboratories, Bernex-Geneva)

Abbreviations: ABRF, Association of Biomolecular Research Facilities; **GPF**, gas phase fractionation; **HUPO**, Human Proteome Organisation; **IMAC**, immobilised metal affinity chromatography; **LC**, liquid chromatography; **MS**, mass spectrometry; **RAM**, restricted access media; **SPS**, Swiss Proteomics Society;

Short presentations by **Michael Affolter** (Nestlé Research Centre Lausanne, *Multidimensional LC-MS/MS analysis and gas phase fractionation*), **Philippe Favreau** (Atheris Laboratories Bernex-Geneva, *De novo MS/MS sequencing*), **Manfredo Quadroni** (University of Lausanne, *Analysing protein phosphorylation sites by mass spectrometry*), **Bernd Bodenmiller** (ETHZ Zurich, *Selective isolation and quantitative MS of phosphopeptides*).

The session chaired by R. Stöcklin covered a variety of topics in mass spectrometry, ranging from multidimensional LC-MS/MS analysis and *de novo* MS/MS sequencing to the analysis of phosphopeptides.

While searching for proteins which could add the benefits of mother's milk to bovine milk, M. Affolter's group employed restricted access media (RAM) chromatography, combining size-exclusion with anion-exchange properties, to reduce sample complexity. The resulting fractions were then analyzed for their desired biological activity and the protein composition was determined by LC-MS/MS with gas phase fractionation (GPF). Trainees tested different work-flows in the LC-MS/MS-GPF analysis. GPF, performing several MS scans per sample while focusing on a narrow mass range, requires more material, but can result in better protein identification from the pooled results.

A much closer look at the individual MS spectra was presented by P. Favreau and colleagues, who introduced trainees to *de novo* MS/MS peptide sequencing. This method is usually employed if no hit can be found in a BLAST search or if proteins of an organism whose genome sequence is not available are to be identified. After the overview given by P. Favreau, an enthusiastic student presented her review of the course, highlighting the tricks she had learnt to correctly interpret MS/MS spectra of peptide fragmentations.

The training initiative offered two courses on phosphoproteomics. M. Quadroni's lab aimed to determine the phosphorylation sites of one protein either in a mixture or in isolated form, while B. Bodenmiller, from R. Aebersold's lab, compared in his course different methods for large-scale phosphopeptide identification. Both labs rely on methods to enrich the sample for phosphopeptides, such as affinity chromatography or chemical methods. M. Quadroni presented several possible problems in phosphopeptide analysis, but stressed that the major hurdle was the low abundance not only of the target protein per se, but especially of its phosphorylated forms.

While the different methods for phosphopeptide enrichment, Fe^{3+}-IMAC, TiO_2-resins and phosphoramidate chemistry (PAC) were specific and very reproducible, each method displayed a different subset of phosphopeptides in a common sample, with only approximately one-third overlap. B. Bodenmiller concluded that these methods are complementary and not suitable for a shotgun approach to global phosphoproteome analysis.

In his concluding remarks, R. Stöcklin touched on several emerging points in proteomics and mass spectrometry analyses. While the focus over the last years had been to obtain results from minute amounts of sample and to develop increasingly sensitive methods, several techniques provided the possibility to analyze a large amount of starting material, yielding better results, especially for low abundant proteins. Sample analysis can also be improved by using depletion or enrichment methods, to specifically remove highly abundant proteins from, for example, human serum or to enrich these to obtain the desired proteins or peptides.

An important issue for the complex work-flows and the new techniques in proteomics and MS is validation and reproducibility. HUPO has initiated the development of highly detailed protocols to ensure reproducibility over its associated

proteomics laboratories, which could serve as an example for other groups as well.

It is striking that different approaches in sample preparation and fractionation or in mass spectrometry give complementary results, with only about 50 % overlap between the different workflows. R. Stöcklin raised the question of how many proteins present in a sample could actually be detected with any one technique. He estimated that at most about 10 % of the proteome could be analysed in a single experiment. This leads to two different approaches in proteomics: the (high-throughput) analysis of many samples with a specific protocol or the detailed analysis of one sample with as many techniques as possible.

The chairman suggested that the SPS could look further into this issue, by performing different analyses on the same sample. Hans Voshol (Novartis Institutes for Biomedical Research, Basel) also suggested a concerted action to use the panel of different methods available in the SPS to analyse one sample, taking advantage of the different levels of know-how within the society. He remarked that the issue of data validation was especially important in an industry setting, where large scale financial decisions would be taken according to proteomics data, and that the future of a proteomics laboratory depended on producing robust and commercially interesting data.

Catherine Zimmermann (University of Geneva) commented that the single-sample approach would hardly be feasible for a training initiative, since some of the methods offered in the courses are highly time consuming, and no sample could be analysed with the required controls within the limited amount of time of a course. Rather, this wide analysis could be a new activity, similar to the mass spectrometry contest held earlier by the SPS or the contests organised by the Association of Biomolecular Research Facilities (ABRF).

Session III: Bioinformatics

Reporter: Rana Baydoun, ICVolunteers
Consultant: Béatrice Cuche, University of Geneva
Editor: Asta Lim, ICVolunteers

Chair: **Hans Voshol** (Novartis Institutes for BioMedical Research)

Abbreviations: CV, controlled vocabularies; **HUPO**, Human Proteome Organisation; **MIAPE**, minimum information about a proteomics experiment; **PSI**, proteomics standard initiative; **PTM**, post translational modification; **SPS**, Swiss Proteomics Society

Short presentations by: **Marie-Claude Blatter** (Swiss Institute of Bioinformatics – *The protein sequence databases and the UniProtKP /SwissProt*), **Christine Hoogland** (Swiss Institute of Bioinformatics, *Standardisation efforts in Proteomics*), **Patricia Palagi** (Swiss Institute of Bioinformatics – *Mass spectra analysis*)

Throughout Fall 2006, the Swiss Proteomics Society (SPS) organised three courses on applied bioinformatics with the focus on providing participants with the techniques and know-how to efficiently use bioinformatics tools.

Marie-Claude Blatter delivered a presentation which was three-fold. First, she introduced protein sequence databases, mainly "UniProtKB" and "NCBI-nr" where she stressed the importance for the database user to determine whether the protein had been identified (Swiss-Prot) or only derived from genome projects (TrEMBL). Following which, she discussed Post Translational Modifications (PTMs), where "N-glycosylation" was a featured example. Notably, she highlighted that approximately 6'000 new PTM sites have been annotated in the Swiss-Prot database within the last year. She concluded her presentation with the discussion of CaPSulo, a meta-prediction tool used for subcellular localisation.

An open discussion with the participants followed with special mention of the existence of a tool to find different identifications for the same protein in various databases (http://www.uniprot.org/search/idmapping.shtml).

Swiss-Prot, according to Marie-Claude Blatter, would benefit from the communication and sharing of new results by users. However, the issue of incorporating into Swiss-Prot the results coming from large-scale proteomics experiments raised some questions and will hence remain under further scrutiny.

Christine Hoogland's presentation provided a good overview of standardisation efforts in Proteomics, mainly through two modules, the HUPO Proteomics Standards Initiative (PSI) and the reporting requirements for proteomics (MIAPE).

The Proteomics Standards Initiative was established by HUPO in 2002, with the aim "to define community standards for data representation in proteomics, as well as to overcome the current fragmentation of proteomics data to facilitate data comparison, exchange and verification." The initiative remains an entirely open process. Anyone, including concerned personnel whether in the IT part or experimental part, can contribute.

Christine Hoogland proceeded to introduce MIAPE (the minimum information about a proteomics experiment), which is essentially a list of minimal information and data for an experiment which allows readers to determine if the data is trustworthy. After updating the participants with a list of completed as well as draft-staged MIAPE modules, Dr Hoogland encouraged the attendees to submit their comments and feedback to the related website.

Stressing the importance of establishing data standards, she briefly discussed the variable quality of published proteome data, the proteome databases which are being developed, as well as journals which have expressed interest to publish guidelines on the reporting of proteome data. On a similar note, she expressed the necessity of agreeing on a common set of terminology and implementation of Controlled Vocabularies (CV).

Views were exchanged on the positive developments in the standardisation efforts in the proteomics field, with various PSI standards close to being stabilised and MIAPE still evolving. On a separate note, it was commented that standardising format and reporting requirements should improve the results verification process

and help link complete proteome workflows together. However, establishing standards would still require input from vendors and experimentalists.

The third workshop, lead by Patricia Palagi, was aimed at teaching the participants to use three different types of software, Mascot and Aldente to identify proteins with MS data and Mascot and Phenyx which use MS/MS for protein identification.

She listed the pros and cons of each software but emphasized that the crucial question lies in their user-friendliness, since all software give very equivalent results. Mascot is more commonly used in the market, and beginners prefer it because of its quite simple graphics feature. With Aldente, expert users are able to change more parameters whilst Phenyx presents the advantage of allowing the results to be stored longer with the ability for the data to be compared with the other software.

During the open discussion that followed, Hans Voshol raised the idea that the information obtained through data processing was too raw to allow the biologists to conduct further analysis or extrapolation. He asserted, "Users need more knowledge and less information."

Many trainees and trainers felt that during the course they were constrained by time limitations and that the diversity of the participants' backgrounds caused some difficulty, two aspects which should be addressed for future courses

Student's feedback

23 trainees, most of them from Switzerland, attended the 8 courses organised by the Swiss Proteomics Society this fall and met again during the informal workshop held in Yverdon-Les-Bains on 4 December 2006.

Irene Amodei (right), volunteer reporter from ICVolunteers, talking to Patrizia Arboit.

PATRIZIA ARBOIT, Proteomics Core Facility, Geneva
Technician

"I appreciated the excellent training hosted by the Nestlé Research Center in Lausanne. We were introduced to state-of-art techniques and equipments and learnt various tricks to handle new machines and instruments. Now I think I will be able to start using this new technique in the laboratory I work for. We were only two trainees, with a very different background. My co/trainee was a former Ph.D. student now working on quality control for a private company. We established a good contact, each benefiting from the other's approach and methods. I think that the training was well-structured, proposed at an advanced level, adequately technical and focused."

VLADIMIR CMILJANOVIC, University of Basel
Ph.D student in Chemistry and Chemic-proteomics.

"I attended the Subcellular proteomics training held in Basel which was hosted by Novartis. The course was particularly interesting because it combined three different branches of science: Biology (with the separation of gels and extraction of membranes), Biochemistry (with the merging of gels and the electrophoresis) and Analytical Chemistry (with the use of mass spectrometry and the identification of proteins).
Only two students with a similar level and background attended the course, and this allowed a very effective exchange of knowledge. Our trainer was precise, enthusiastic and stimulating.
I found it a good experience to work with the industry, because we could profit from a state-of-the-art equipment, which was a rare opportunity for us students."

LOÏC DAYON, Ecole Polytechnique Fédérale de Lausanne
Senior scientist on mass spectrometry

"I heard about the course through Professor Manfredo Quadroni, one of my teachers who is also a member of SPS. I chose this course to learn a new technique. I was hosted at the Aebersold laboratory. The quality of the training was good, but I found it was too short. I would have liked the course to last one week, or perhaps for future courses, the course should focus on a reduced topic. Anyway, I am now able to apply the new technique and a lot of tips which I learnt. I also appreciated the opportunity to meet people from different backgrounds and horizons."

Interview with Hans Voshol
Novartis Institute for BioMedical Research

How did the idea of these interactive trainings come up? Was there a need for them?
Proteomics is still a relatively new field and even if Switzerland is a pioneer harboring a large know-how, there is still not enough knowledge exchange between laboratories. So far we have only organised annual congresses to get an overview of the state of studies, research and techniques. But we realised that we needed a different platform to share information and facilitate interactions. Something which is as useful as a congress, but different. That's how we actually got the idea of the 2006 Interactive Training Initiative.

How did you select the labs? How did you build up the network? And how do the labs profit from these trainings?
All labs working on proteomics in Switzerland are directly or indirectly connected to the Society, often directly with members of the SPS Committee. As soon as we started spreading the concept of the training initiative, many came forward and proposed to host trainings.

Everyone pointed out that it was good to work with small yet extremely technical groups. Was it a deliberate choice or a consequence of a lack of participants?
I suppose it was a combination of both. Actually we organised the trainings for a maximum of four. If you want to work efficiently in a lab, and make sure your trainees get something concrete out of it, it is important to limit the number of participants.

How do you judge this initiative? Any comment about the level and variety of trainings? Do you think that there was something missing?
We covered pretty much all major tips and current technologies in the field (from separation, to spectrometry and simple modification). I think it was a good balance.

How do you see the relation between private laboratories and the academic sector?
I work for a pharmaceutical company, so I am not involved in fundamental research. I only do things that are directly applicable to drug discovery. The typical example would be how colleagues in the oncology group uncover a substance that inhibits the growth of tumors cells: they have little idea what that substance actually does and how it kills the cells. They only know that it kills the cells, but not how the process works. If you want to improve this compound, you have to know what happens in the cells and that's almost always within the proteins. That's the typical question that we are asked: find the target of this compound, study the role that proteins play in human cells, so that we can make a better drug and only kill tumor cells, and not all human cells.

What are the benefits for a private laboratory to host this kind of training?
Private companies cannot devote too much time in developing technologies, and we need universities to do that. It is our own interest to educate, spread knowledge and develop skills as any breakthrough will in turn benefit our activities. Private and public sector are complementary in our quest for scientific progress.

Glossary

Chaperones: In biology, chaperones are proteins whose function is to assist other proteins in achieving proper folding. Many chaperones are heat shock proteins, that is, proteins expressed in response to elevated temperatures or other cellular stresses. The reason for this reaction is that protein folding is severely affected by heat and, therefore, some chaperones act to repair the potential damage caused by misfolding. Other chaperones are involved in folding newly made proteins as they are extruded from the ribosome.

Chromatography: Chromatography is a separation method that exploits the differences in partitioning behaviour between a mobile phase and a stationary phase to separate the components in a mixture. Components of a mixture may be interacting with the stationary phase based on charge, relative solubility or absorption.

Differentially expressed proteins: Reference to proteins possessing a different level of expression. Protein expression is a subcomponent of gene expression. It consists of the stages after DNA has been translated into amino acid chains (which are ultimately folded into proteins). Protein expression is commonly used by proteomics researchers to denote the measurement of the presence and abundance of one or more proteins in a particular cell or tissue.

Differentiated sample: Sample from a purified extract of a particular subcellular fraction, i.e. mitochondria.

DIGE: Two-dimensional gel electrophoresis is a form of gel electrophoresis commonly used to analyze proteins. The proteins are separated in the first dimension depending on their isoelectric point. In the second dimension, the proteins are separated based on their molecular weight in a direction of 90 degrees from the first. The result is that the proteins are spread out across a 2-D surface.

Isoforms: In biology, a protein isoform is a version of a protein with some small differences. The discovery of isoforms explains the apparently small number of coding genes revealed in the human genome project: the ability to create catalytically different proteins from the same gene increases the diversity of the genome.

Isoelectric focusing: IEF is a technique for separating different molecules by their electric charge differences. An electric current is passed through a medium, creating a "positive" and "negative" end. Negatively charged particles migrate through a pH gradient toward the "positive" end while positively charged particles move toward the "negative" end. The particles will stop migrating when the reach their pI.

Lysates: A cell lysate refers to the cellular debris and fluid produced by breaking the cell into a homogenous mixture, free of compartimentation.

Mass spectrometry: Mass spectrometry is an analytical technique used to measure the mass-to-charge ratio of ions. It is most commonly used to determine the composition of a physical sample by generating a mass spectrum representing the masses of sample components. The technique has several applications, including identifying unknown compounds by the mass of the compound molecules or their fragments, determining the isotopic composition of elements in a compound, determining the structure of a compound by observing its fragmentation, quantifying the amount of a compound in a sample using carefully designed methods (mass spectrometry is not inherently quantitative), studying the fundamentals of gas phase ion chemistry (the chemistry of ions and neutrals in vacuum), determining other physical, chemical or even biological properties of compounds with a variety of other approaches.

Metabolic proteins: Protein metabolism denotes the various biochemical processes responsible for the synthesis of proteins and amino acids, and the breakdown of proteins (catabolism).

pI: The isoelectric point (pI) is the pH at which a molecule carries no net electrical charge. When a protein is in an electric field, it will migrate until its net charge compensates with the electric field, thus stopping its migration.

Phosphopeptide: a peptide incorporating a phosphate group, typically associated with protein phosphorylation

Reverse phase column: Reverse phase liquid chromatography operates on the principle of hydrophobic interactions which result from repulsive forces between a relatively polar solvent, the relatively non-polar analyte, and the non-polar stationary phase.

Rosiglitazone: Rosiglitazone is an anti-diabetic drug. Its mechanism of action is by activation of the intracellular receptor class of the peroxisome proliferator-activated receptors (PPARs). Apart from its effect on insulin resistance, it appears to have an anti-inflammatory effect.

Undifferentiated sample: Sample from the whole cell and not from a particular subcellular fraction.

Acknowledgements

The SPS 2006 Interactive Training initiative 'Applied Proteomics - Tips & Tricks' was a real success! The Swiss Proteomics Society wishes to thank all those who made this event possible.

First of all, we are deeply grateful to the eleven specialised hosting laboratories in Basel, Bern, Geneva, Lausanne and Zurich, which have accepted to take their time to organize these courses. It is obvious, but nevertheless important, to say that nothing would have been possible without them. It was also a great pleasure to see that we have covered various areas of the proteomics field, from separation techniques to mass spectrometry and bioinformatics.

We would also like to acknowledge ICVolunteers (International Conference Volunteers), an international non-profit organisation specialised in the field of communications. ICVolunteers is the new SPS partner for the organisation of its scientific congress starting this year in Lausanne.

As a test case, ICV has participated in the debriefing workshop in Yverdon-les-Bains (the final step of the SPS 2006 Training initiative) by taking notes, writing summaries of the different sessions and interviewing participants. We would thus like to express our deepest gratitude to the volunteer reporters who provided high quality documents, providing a good overview of the whole event.

We hope that all the participants have enjoyed the courses that they have attended and we invite you to take part of the next SPS event, the 6th SPS scientific meeting to be held in Lausanne in December 2007.

About

Swiss Proteomics Society

The Society (SPS) is a scientific society, according to article 60 of the Swiss Civil Law, established for the public benefit to advance research, development and education in the proteomic sciences. The SPS is a non-profit society, neutral from both political and confessional points of view.

The aim of the SPS is to stimulate and coordinate proteomic activities in Switzerland as well as in other countries, with two major objectives:

- To hold and arrange courses and meetings on matters connected to proteomics;
- To promote the diffusion and exchange of information among people interested in proteomics.

ICVolunteers

ICVolunteers is an international non-profit organisation specialized in the field of communications, in particular languages, conference support and cybervolunteerism. It runs a network of skilled and motivated volunteers to support projects and conferences. Development, exchange of information and service to the society at large are the key elements shared by the communities or organisations involved and by the individuals volunteering though ICVolunteers.

ICVolunteers provided volunteer reporters for the SPS Training event.

Impressum

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