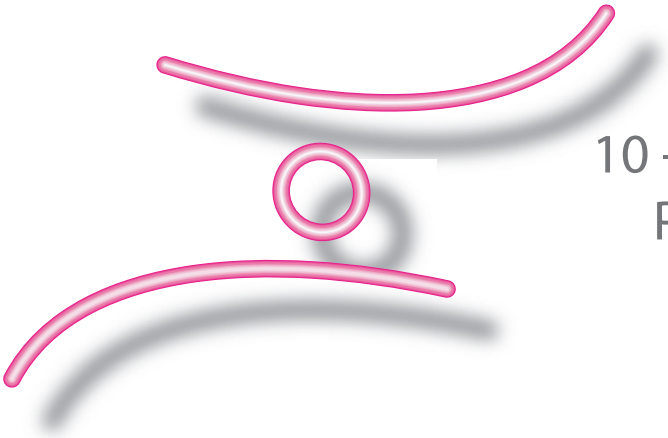
Proteomics and Human Proteome

From bench to bedside



10 - 13 February, 2009
Pamplona, Spain

Joint Congress of the Spanish Proteomics Society
and the Latinamerican Human Proteome
Organization

SEPROT
SOCIEDAD ESPAÑOLA DE PROTEÓMICA

LAHUPO
Latinoamerican Human
Proteome Organization

Congress Venue
Faculty of Sciences, University of Navarra
http://unav.es/proteomicsmeeting

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PROTEÓMICA

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Abstract Book

of the

Joint Congress of the Spanish Society and the Latin American Human Proteome Organization

Welcome Address of the Sociedad Española de Proteómica (SEProt)

La SEProt cumple 5 años

El próximo 13 de abril (Acta Fundacional) o 9 de diciembre (Registro de Asociaciones) nuestra Sociedad cumple 5 años. Parece que fue ayer pero hace ya cuatro años que la actual Junta Directiva, la primera elegida en Asamblea General durante el I Congreso de la SEProt celebrado en Córdoba (13-17 febrero 2005), dirige la marcha de nuestra Sociedad. Atrás queda también el II Congreso (Valencia, 10-14 2007) que consolidó la decidida vocación internacionalista de la SEProt, tanto en el plano europeo –contribuyendo actualmente de manera destacada en los órganos de dirección y comités de la Federación Europea de Sociedades de Proteómica– como en el ámbito latinoamericano. El III Congreso que este 2009 celebramos en Pamplona tiene también un punto de mira en el fortalecimiento de las relaciones entre países separados por el Océano Atlántico pero culturalmente cercanos. Hubo intentos de acercamiento anteriores, incluyendo la posibilidad de creación de una red multinacional de temática proteómica que no prosperó por reticencias de alguna Sociedad de Proteómica a un supuestamente encubierto "neocolonialismo cultural". No caeré en la tentación de comentar este sinsentido, aunque tampoco cejaré en promover el fortalecimiento de lazos proteómicos entre ambos lados del charco... En nuestro país, en este primer lustro de existencia de nuestra Sociedad, se han consolidado algunos programas de educación a través de becas de asistencia a cursos nacionales e internacionales de formación en el ámbito de la Proteómica, merced a la saneada economía de la SEProt, consecuencia directa de la excelente gestión por parte de nuestro Tesorero David Andreu de los ingresos por cuotas individuales y corporativas.

Reconocer la excelencia investigadora premiando contribuciones de especial relevancia es una de las tareas más gratas de una Sociedad científica. Así lo han entendido también las empresas del ramo que han apoyado esta iniciativa patrocinando diversos galardones. Gabriel Padrón (Centro de Ingeniería Gené-

tica y Biotecnología, La Habana, Cuba) recibió en Valencia el Premio SEProt-Promega "por su contribución al desarrollo de la espectrometría de masas y su aplicación a la revolución proteómica". Applied Biosystems patrocinó los premios SEProt-ABI para pósters presentados por grupos no españoles. Durante el III Congreso se otorgarán los premios SEProt a un artículo publicado durante el bienio 2007-2008 y a un trabajo original presentado en forma de panel al Congreso. Esta tercera edición, al igual que las anteriores, está patrocinada por Bruker Biosciences Española S.A. El III Premio SEProt está dedicado a la memoria de José Luis López Rodríguez, entrañable y excelente proteómico de *Mytilus*, de la Universidad de Santiago de Compostela, que nos dejó tempranamente el pasado 12 de octubre. Sus muchas virtudes han sido comentadas por quienes más le conocieron en el portal electrónico de la SEProt. Dándo su nombre a nuestro galardón queremos también rendir un sentido y público homenaje institucional a nuestro compañero José Luis.

Durante el pasado congreso, nuestra Sociedad otorgó membresía de Honor a John B. Fenn, galardonado con el Premio Nobel de Química en 2002 por su trabajo pionero en el desarrollo de la ionización de macromoléculas mediante electronebulización (Proteómica 0:11-14, julio 2007). Otra técnica esencial de la Proteómica es la ionización mediada por radiación láser y asistida por una matriz (MALDI). Este método de ionización fue desarrollado simultánea e independientemente por Koichi Tanaka (Shimadzu, Japón) y por Franz Hillenkamp y Michael Karas (a la sazón en la Universidad de Münster, Alemania) durante los años 80 del pasado siglo. Los avatares del destino, quizás forzados por la presión de la poderosa compañía japonesa, hicieron que Tanaka compartiera con Fenn el Premio Nobel que la Academia Sueca negó a los alemanes. Nuestra Sociedad, nombrándoles Socios de Honor, ha querido sumarse a la lista de instituciones que reconociendo esta injusticia histórica han rendido honores a Hillenkamp y Karas. Me alegra y enorgullece también Peter Roepstorff, pionero de la espectrometría de masas biológica, testigo y actor privilegiado de la transición Química de Proteínas-Proteómica, y maestro de proteómicos, haya aceptado ser Miembro de Honor de la SEProt.

El artículo 25c de nuestros Estatutos especifica que "el nombramiento de los Socios de Honor corresponde a la Asamblea General, a propuesta de, al menos, diez Socios Ordinarios. El nombramiento se refrendará en votación secreta, debiendo alcanzar un número de votos favorables de, al menos, dos tercios de la totalidad de los miembros de la Junta Directiva. La decisión favorable deberá ser refrendada por la Asamblea General por mayoría simple". Quisiera desde esta tribuna proponer la candidatura a Socios de Honor de dos pioneros de las

técnicas proteómicas, Jasna Peter-Katalinić (http://impb.klinikum.uni-muenster.de/research/peterkatalinic/index.html) y Pier-Giorgio Righetti (Electrophoresis 27 [8]: 1435-1692 [No. 8 April 2006] Special Issue: Dedicated to Professor Pier Giorgio Righetti at his 65th Birthday). Jasna ha contribuido durante los últimos 25 años al desarrollo de la glicoproteómica; Pier-Giorgio, prolífico e imaginativo innovador de las técnicas de separación y su aplicación a la proteómica, ha publicado más de 450 artículos originales. A él debemos la invención de las tiras de gradiente de pH inmovilizado o la reciente técnica de "democratización" de proteomas complejos o ProteoMiner comercializado por BioRad.

Suenan tambores que anuncian la necesidad de renovación. Y no sólo porque así lo marquen nuestros estatutos, sino porque el funcionamiento de toda Sociedad se rige por ciclos que garantizan el progreso de las ideas. Seguimos siendo una Sociedad joven, muy joven, que necesita el apoyo de todos sus socios. La Junta Directiva que surja de la Asamblea General en Pamplona va a necesitar el apoyo de *proteómicos* experimentados y aprendices de brujo para seguir contribuyendo al desarrollo de nuestra disciplina, en España y fuera de nuestras fronteras. Muchos han sido los logros conseguidos en este quinquenio, pero muchos siguen siendo los proyectos iniciados que aun necesitan el espaldarazo de la consolidación. En julio del 2007 vio la luz el número 0 de la revista Proteómica y unos meses después (febrero del 2008) se publicó el número 1 con ocasión de las Primeras Jornadas Bienales de Proteómica (Sitges, 21-22 febrero 2008). Estas iniciativas, revista y Jornadas, han tenido como principales valedores a los *Jesuses*, Jorrín y Vázquez, respectivamente. Conociendo el entusiasmo que siempre han demostrado hacia la SEProt, seguro que no yerro en el convencimiento de que ambos seguirán brindando su colaboración en esos proyectos de capital importancia para la SEProt.

Aprovecho esta ocasión para despedirme como Presidente de la SEProt y desearle al nuevo Presidente, que será elegido por la Asamblea General durante el III Congreso, las mismas satisfacciones, sensación de compañerismo que yo he experimentado durante estos cuatro años al frente de la Junta Directiva. A Ángela, Concha, David, Jesús J., Jesús V., José Manuel, Juan Pablo, y Fernando, mi reconocimiento y gratitud por vuestra dedicación y apoyo. ¡Haber trabajado con vosotros por nuestra Sociedad compensa con creces el tiempo y esfuerzo robado a otras actividades! A la nueva Junta Directiva le esperan nuevos retos, como la tarea de profesionalizar la Secretaría Técnica de la Sociedad, incluyendo asesoría fiscal, y la edición de un libro en castellano sobre Proteómica. Todos los que impartimos Cursos de Doctorado, de Licenciatura, de especialización, Másters, etc., seguramente coincidiremos en la necesidad de disponer de una monografía

en nuestro idioma que recoja la historia, el desarrollo de la tecnología, así como los principios y aplicaciones de la Proteómica. Podemos esperar a que alguien lo haga o ponernos manos a la obra. Somos muchos los que pensamos que podemos y debemos hacerlo desde la SEProt. Como siempre, cualquier sugerencia y ayuda serán más que bienvenidas. ¿Seguimos hablando en Pamplona?

Juan J. Calvete
Presidente de la SEProt

Welcome Address of the Latin American Human Proteome Organization (LAHUPO)

Buenos Aires, December, 2008

Dear Colleagues

On behalf of the Latin American Human Proteome Organisation (LAHUPO) Congress Organizing Committe, we would like to invite you to join the Congress of the Spanish Proteomics Society (3rd SEPROT) and the Latinoamerican Human Proteome Organisation (2nd LAHUPO), to be held in Pamplona, Spain, 10-13 February, 2009.

We have prepared the Scientific Program to put a central focus in the Proteomics and Human Proteome: "From bench to beside".

We look forward to welcoming you in Pamplona, to enjoy the wisdom and experience of outstanding HUPO scientists and Iberoamerican Colleagues.

With Warm Regards,

Mario Hugo Genero,
Congress Co-Chair-LAHUPO President

Andrea Sabina Llera,
LAHUPO secretary

Welcome Address of the Organizing Committee of the SEProt and LAHUPO Congress

Pamplona, January, 2009

Dear colleagues,

It is my great pleasure to welcome you all, on behalf of the Scientific and the Organizing Committees, to the 3rd Congress of the Spanish Proteomics Society and the 2nd Latin American Human Proteome Organisation that are celebrated conjointly in Pamplona.

Despite the rapid advances experimented over the last few years, Proteomics is still at its infancy. It is a discipline with a tremendous future that offers all kind of opportunities to analyze biological systems with unprecedented efficacy to generate new concepts in biology, identify new diagnostic and therapeutic targets and study drug effects in cell biology. The challenge of defining and understanding proteomes in the context of cell biology is huge and requires a multidisciplinary effort to ensure innovative technical developments, the generation of biological information as well as the integration and interpretation tools to transform the information in biological knowledge. We sincerely hope to have been able to create an ideal environment where international experts could discuss all these aspects generate new ideas and establish productive scientific interactions.

The venue of the meeting is the University of Navarra, in particular the Faculty of Sciences that during this year 2009 celebrates its 50th anniversary. I do really thank to our University for all the support and facilities provided to organise this event. We are also in debt with our sponsors, DIGNA, ANAIN, Gobierno de Navarra, Plan Tecnológico de Navarra, BioRad, Sigma, GE Healthcare, AB, Thermo, Waters, Genoma España, Bruker, SODENA, Beckman-Coulter, Agilent, Promega, Ministerio de Ciencia e Innovación, for their generosity making possible this adventure. I would like to thank very, very, very much the effort and enthusiasm of people involved in the organisation of the congress, especially to Leticia, Jokin, Kike, Javier, Elsa y María. And last but not least, I

thank you all for coming to Pamplona to share your outstanding research; you are the real meeting.

I wish you a pleasant and productive stay in Pamplona and since that life is not only science, don't forget to spare some time visiting Pamplona, it will amaze you, and discover the end of the history of this small roman village. Be careful with the small and charming bars of the old town, they are pretty addictive...

Fernando J. Corrales

Hillenkamp, Karas, Roepstorff, 3 *Nobel* Honorary Members of SEProt

The development of mass spectrometry has contributed to biological research in a similar manner as the development of particle accelerators has driven the advance of atomic physics. Mass spectrometers and storage rings both represent machines that domesticate, respectively, macromolecular ions and subatomic particles long enough to reveal their properties. The invention in 1929 by Ernest O. Lawrence of the circular particle accelerator, which he referred to as his "proton merry-go-round", but which became better known as the cyclotron, opened the doors to investigate the structure and properties of atoms. More than four decades before, in 1886, Eugen Goldstein observed rays in gas discharges under low pressure that travelled through the channels in a perforated cathode toward the anode, in the opposite direction to the negatively charged cathode rays. Goldstein called these positively charged anode rays "Kanalstrahlen". Wilhelm Wien (1911's Nobel Laureate "for his discoveries regarding the laws governing the radiation of heat") found that strong electric or magnetic fields deflected the canal rays and, in 1899, constructed a device with parallel electric and magnetic fields that separated the positive rays according to their charge-to-mass ratio. English scientist J.J. Thomson later improved on the work of Wien by reducing the pressure to create a mass spectrograph. Thomson succeeded in causing electric deflection because his cathode ray tubes were sufficiently evacuated that they developed only a low density of ions. Thomson measured the mass-to-charge ratio of the cathode rays by measuring how much they were deflected by a magnetic field and how much energy they carried. Thomson's separation of neon isotopes by their mass was the first example of mass spectrometry, which was subsequently improved and developed into a general method by Thomson's student F. W. Aston and by A. J. Dempster in 1918 and 1919 respectively. Thompson is credited for the discovery of the electron and of isotopes, and also for the invention of the mass spectrometer. He was awarded the 1906 Nobel Prize in Physics. Francis William Aston, a British chemist and physicist, won the 1922 Nobel Prize in Chemistry "for his discovery, by means of his mass spectrograph, of isotopes, in a large

number of non-radioactive elements, and for his enunciation of the whole-number rule". In 1918, Arthur Jeffrey Dempster, a Canadian-American physicist, developed the first modern mass spectrometer, allowing physicists to identify compounds by the mass of elements in a sample, and determine the isotopic composition of elements. Dempster's mass spectrometer was over 100 times more accurate than previous versions, and established the basic theory and design of mass spectrometers that is still used to this day. Dempster's research over his career centered around the mass spectrometer and its applications, leading in 1935 to his discovery of the uranium isotope ^{235}U. This isotope's ability to cause a rapidly expanding fission nuclear chain reaction allowed ten years latter the development of the atom bomb.

Mass spectrometry is an analytical technique that identifies the chemical composition of a compound based on the mass-to-charge ratio of charged particles. The ratio of charge to mass of the particles is calculated by passing them through electric and magnetic fields in a mass spectrometer. This apparently simple experimental design underlays one of the most resolutive technique for unravelling the chemical structure of a vast array of substances, from simple molecules to complex macromolecules, with the sole requirement of being able to ionize them. Molecules are built by a unique spatial combination of atoms, and mass is amongst the most fundamental characteristics of matter. Hence, an accurate measure of the mass represents a unique feature that characterize any substance. Further, isobaric substances can be distinguished by mass spectrometry through identification of reporter ions generated by fragmenting their unique structures.

In 1989, half of the Nobel Prize in Physics was awarded to Hans Dehmelt and Wolfgang Paul for the development of the ion trap technique in the 1950s and 1960s. An ion trap is a combination of electric or magnetic fields that captures ions in space. Fast scanning, selective mass filtering, and the possibility of exciting ions to investigate their structures has led to a revolution in mass spectrometry. However, techniques for ionization have been key to determining what types of samples can be analyzed by mass spectrometry. Among the many ionization techniques developed during the first half of the last century, including electron ionization (EI) and chemical ionization (CI) used for gases and vapors; inductively coupled plasma (ICP) sources (used primarily for metal analysis); field desorption (FD), fast atom bombardment (FAB), atmospheric pressure chemical ionization (APCI), secondary ion mass spectrometry (SIMS), etc., two techniques often used with liquid and solid biological samples include electrospray ionization (invented by John B. Fenn[1,2]) and matrix-assisted laser desorption/

ionization (MALDI, developed simultaneously in the 1980's independently by Koichi Tanaka[3,4] (at Shimadzu Corporation, Japan) and Franz Hillenkamp and Michael Karas[5,6] at that time at the Institute of Medical Physics and Biophysics within the Medical Faculty at the University of Münster, Germany.

Long before the 1980's, there had been investigation into the use of optical energy, not limited to laser light, to achieve ionization of organic compounds. Because this was limited to compounds that could be vaporized without being decomposed, very few compounds could be ionized. When a solid phase organic compound was irradiated with a laser, the organic compound absorbed the laser light, providing enough energy for desorption. Further, when the positive and negative charges of the particle are not in balance, it could be measured as an ion. However, in this case, since the laser light is absorbed directly into the analyte,the molecular bonds may be broken due to the increased internal energy. In the 1980's, "desorption to gas phase by rapid heating" gained attention. In short, if a given compound "AB" is heated, it is assumed that "AB" will be released to the gas phase as intact "AB" as well as fragmented "A" and "B". To perform this rapid heating, various heating methods were devised. However, a high enough temperature could not be achieved quickly enough to obtain intact vaporization of macromolecules, such as proteins. Since the time width of a pulse laser itself is between a nanosecond to several microseconds, rapid heating would seem possible using a focused beam to generate energy at high density and high speed. However, this would require a medium to enable its conversion into thermal energy. The term matrix-assisted laser desorption ionization (MALDI) was coined in 1985 by Franz Hillenkamp, Michael Karas and their colleagues. These researchers found that the amino acid alanine could be ionized more easily if it was mixed with the amino acid tryptophan and irradiated with a pulsed 266 nm laser[5]. The tryptophan was absorbing the laser energy and helping to ionize the non-absorbing alanine. Peptides up to the 2843 Da peptide melittin could be ionized when mixed with this kind of "matrix"[6]. The breakthrough for large molecule laser desorption ionization came in 1987 when Tanaka and his co-workers used what they called the "ultra fine metal plus liquid matrix method" that combined 30 nm cobalt particles in glycerol, a formulation adapted from the Fast Atom Bombardment (FAB) MS method, developed by Michael Barber and colleagues and which was widely used in the 1980's to achieve ionization of thermally labile compounds, with a 337 nm nitrogen laser for ionization. Using this laser and matrix combination, Tanaka was able to ionize biomolecules as large as the 34,472 Da protein carboxypeptidase-A, and another ion having a mass number exceeding 100,000[4]. Karas and Hillenkamp were subsequently able to ionize the 67 kDa protein albumin using a nicotinic acid

matrix and a 266 nm laser[7]. Further improvements were realized through the use of a 355 nm laser and cinnamic acid derivatives as the matrix[8].The availability of small and relatively inexpensive nitrogen lasers operating at 337 nm wavelength and the first commercial instruments introduced in the early 1990s brought MALDI to an increasing number of researchers[9]. Today, mostly organic matrices are used for MALDI mass spectrometry[10].

Professors Franz Hillenkamp and Michael Karas have received, individually or jointly, several scientific awards for the development of the MALDI technique: the Mattauch-Herzog award of the Arbeitsgemeinschaft Massenspektrometrie (1990) (to MK); the award of the American Society for Mass Spectrometry for "A distinguished Contribution in Mass Spectrometry" (1997) (MK & FH); the "Molecular Bioanalytics" award from the German Society for Biochemistry and Molecular Biology (2000) (MK & FH); the Association of Biochemical Research Facilities award for "Recognition of the outstanding contribution to biomolecular technologies" (FH, 2003; MK, 2006); the Thompson Medal of the International Mass Spectrometry Society (2003) (FH); the Fresenius Award of the Gesellschaft Deutscher Chemiker e.V.(2003), the Karl-Heinz Beckurts Award of the German Helmholtz Association (2003) (MK & FH), the Torbern Bergman Medal of the Swedish Chemical Society (Analytical Division) (2006) (MK & FH). Notwithstanding these honors, Profs. Karas and Hillenkamp have every right to feel frustrated by the fickleness of fate. In 2002, the Nobel Prize in Chemistry was awarded to John Bennett Fenn for the development of electrospray ionization (ESI) and Koichi Tanaka for the development of soft laser desorption (SLD. Many researchers in the field, me among them, felt aggrieved and even defrauded when Karas and Hillenkamp's contribution was not considered by the Nobel Committee of Swedish Academy of Science. Two years ago, the Spanish Proteomics Society proudly confered upon Prof. John Fenn its first Honorary Membership in recognition of his pioneering research in the development of electrospray ionization of macromolecules, an essential tool in Proteomics. Now, we feel very honored for Professors Michael Karas and Franz Hillenkamp having accepted the nomination to become also Honorary Members of SEProt and to deliver Plenary Lectures at its 3rd. Congress.

The Spanish Proteomics Society also happily acknowledges the seminal work of Prof. Peter Roepstorff in the fields of Protein Chemistry and its modern version, Proteomics in its most broader sense. Peter is not only a priviledged witness but also a principal starring of the transition from Protein Chemistry to Proteomics. A few years ago, on occasion of his 65th birthday, Ole N. Jensen, Albert J.R. Heck, and Franz Hillenkamp wrote a brief biography of Peter Roepstorff in

the International Journal of Mass Spectrometry[11]. I have reproduced here some paragraphs from this article in the believe that this act of cut-and-paste will not be considered plagiarism.

Peter Roepstorff founded, and until recently headed, the Protein Research Group at the University of Southern Denmark, where the main research focus is the development of methods for protein mass spectrometry and proteomics, including techniques for the determination of post-translational modifications. Throughout his career Peter has been searching for new challenges in protein chemistry and mass spectrometry. His early work in the late 1960's and early 1970's led to methods for peptide sequencing and for the determination of novel posttranslational modifications, including the discovery of gammacarboxyglutamic acid. Prof. Roepstorff is not only rightly considered a founder of what started as mass spectrometry of proteins and then became proteomics; he remains one of the most eminent developers and experts. He has co-authored more than 400 scientific articles and book chapters, one of the most cited being a paper suggesting the nomenclature for mass spectrometric peptide fragmentation[12]. A paper on the measurement of Kd's by mass spectrometry became also a well-cited classic. To cite just one more example, the TiO2 phosphopeptide enrichment method developed in Roepstorff's lab led revolution in an area of intense research, phosphoproteomics.

From early on, Peter initiated research projects with biotech and pharma companies in Denmark and abroad. Around 1993 the Protein Research Group and the Münster group joined efforts to tackle a seemingly hopeless problem, the MALDI-MS of nucleic acids. The project was not successful enough to convince the EU bureaucracy to continue funding it, but the core ideas developed then are now the basis for a commercial use by Sequenom Inc.

Peter is a well-respected attendee of many meetings as he is always very open in giving his opinion and (un)asked advise. He is also an outstanding mentor, having always promoted education and training. The high scientific level, the friendly atmosphere, and the international ambience of the laboratory is a big inspiration for all students and colleagues and has made Roepstorff's Protein Research Group known all over the world as an excellent training site. Numerous graduate students and post docs from all over the world have received education in the Protein Research Group, and many of them are now heading proteomics laboratories in different countries. In 2005 he transferred the responsibility for the Protein Research Group to the next generation in order to get more time for research. This has allowed him to realize one of his dreams: participating in a major Danish Marine Biology Expedition, Galathea 3, where he was scubadiving

in tropical coral reefs in the search for new fluorescent proteins. Typical for Peter, who always teaches colleagues and students to go for the fun-experiment, which often brings you the most exciting results and new insights.

The famous statement *Pigmaei gigantum humeris impositi plusquam ipsi gigantes vident*, is attributed to Isaac Newton. The vision and work of Michael Karas, Franz Hillenkamp, and Peter Roepstorff on mass spectrometry undoubtly represent solid pillars upon which biological mass spectrometry is continuously being developed.

Juan J. Calvete
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SEProt President

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The Spanish Proteomics Society

proudly confers upon

Prof. Michael Karas

Honorary Membership

for a distinguished career, and particularly in recognition of his pioneering research in the development of matrix-assisted laser-desorption ionization of macromolecules, an essential tool in Proteomics.

Prof. Michael Karas is hereby granted all the Rights, Honors, and Privileges thereunto appertaining.

Given on occasion of the Joint 3rd Congress of the Spanish Proteomics Society and the Latin American HUPO, in Pamplona (Spain), the tenth day of February, two thousand and nine

Jesús V. Jorrín
Secretary

EPRO

Juan J. Calvete
President

The Spanish Proteomics Society

proudly confers upon

Prof. Franz Hillenkamp

Honorary Membership

for a distinguished career, and particularly in recognition of his pioneering research in the development of matrix-assisted laser-desorption ionization of macromolecules, an essential tool in Proteomics.

Prof. Franz Hillenkamp is hereby granted all the Rights, Honors, and Privileges thereunto appertaining.

Given on occasion of the Joint 3rd Congress of the Spanish Proteomics Society and the Latin American HUPO, in Pamplona (Spain), the tenth day of February, two thousand and nine

Jesús V. Jorrín
Secretary

EPRO

Juan J. Calvete
President

The Spanish Proteomics Society

proudly confers upon

Prof. Peter Roepstorff

Honorary Membership

For a distinguished career in protein chemistry, biological mass spectrometry and proteomics, and for having promoted education and training in these disciplines for over 40 years.

Prof. Peter Roepstorff is hereby granted all the Rights, Honors, and Privileges thereunto appertaining.

Given on occasion of the Joint 3rd Congress of the Spanish Proteomics Society and the Latin American HUPO, in Pamplona (Spain), the thirteenth day of February, two thousand and nine

Jesús V. Jorrín
Secretary

EPRO

Juan J. Calvete
President

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CONVOCATORIA DEL *TERCER PREMIO JOSÉ LUIS LÓPEZ RODRÍGUEZ DE LA SOCIEDAD ESPAÑOLA DE PROTEÓMICA*

Pamplona, Julio de 2008

La *Sociedad Española de Proteómica* (*SEProt*) convoca la tercera edición del PREMIO SOCIEDAD ESPAÑOLA DE PROTEÓMICA destinado a reconocer la labor en el campo de la Proteómica de un científico que desarrolle su actividad en España. El premio, patrocinado por **Bruker BioSciences Española S.A.** (http://www.bruker.es), está dotado con 2000 € y una placa conmemorativa, y será entregado por un representante de Bruker Española durante el 3er Congreso de la SEProt que se celebrará en la Facultad de Ciencias de la Universidad de Navarra conjuntamente con la Latinamerican Human Proteome Organisation (LAHUPO) entre los días 10-13 de Febrero de 2009 (http://www.unav.es/proteomicsmeeting/index.html). En la presente convocatoria se otorgarán **dos galardones** que en ningún caso podrán ser compartidos. Una mitad del premio (1000 €, diploma acreditativo y la placa conmemorativa) será para **una publicación científica** relacionada con cualquier desarrollo o aplicación de la Proteómica. La otra mitad del premio (1000 €, diploma acreditativo) será para una contribución en forma de **panel** al 3er Congreso de la SEProt. Las decisiones de los jurados serán inapelables. Los Premios no podrán concederse al mismo científico dos veces y podrán quedar desiertos si así lo decidiese el jurado.

La elección de la publicación científica merecedora del galardón será realizada por un jurado de expertos designado a tal efecto por el Presidente de la SEProt. Solo podrán optar al Premio científicos españoles que sean o no socios de la SEProt. La labor investigadora deberá haber sido realizada en España y haber sido publicada entre Enero de 2007 y Diciembre de 2008. Los candidatos deberán remitir 3 copias del trabajo **en formato electrónico** al Secretario de la SEProt (Jesús V. Jorrín, Dpto. Bioquímica y Biología Molecular, Edificio Severo Ochoa (C6), Campus de Rabanales, Universidad de Córdoba, 14014 Córdoba. bf1jonoj@uco.es). Deberán, asimismo, adjuntarse los datos personales y profesionales del candidato, y un breve resumen de las razones que, a juicio del candidato, debieran ser consideradas por el jurado. **La fecha límite para la recepción de los trabajos será el 31 de Diciembre de 2008**. La decisión se tomará antes del 15 de Enero de 2009 y será dada a conocer en el programa final del congreso y a través del portal electrónico de la SEProt. El galardonado será invitado a participar en el 3er Congreso de la SEProt exento del pago de las tasas de inscripción y a publicar un artículo en la revista Proteómica.

La elección del ganador(a) del Premio SEProt a la contribución en formato panel presentada al 3er Congreso de la SEProt se efectuará entre los primeros firmantes del estudio por un jurado designado a tal efecto por el Presidente de la Sociedad Española de Proteómica. Solo podrán optar al Premio científicos españoles sean o no socios de la SEProt. La labor investigadora considerada deberá haber sido realizada en España y ser inédita o, en todo caso, no haber sido publicada con anterioridad a Diciembre de 2008.

Juan J. Calvete – Presidente de la SEProt

AWARD ANNOUNCEMENT

The Spanish Proteomics Society (SEProt) announces an award, sponsored by Applied Biosystems, for a poster presented at the SEProt-LAHUPO Congress. The Prize carries a € 500 monetary award and a diplome.

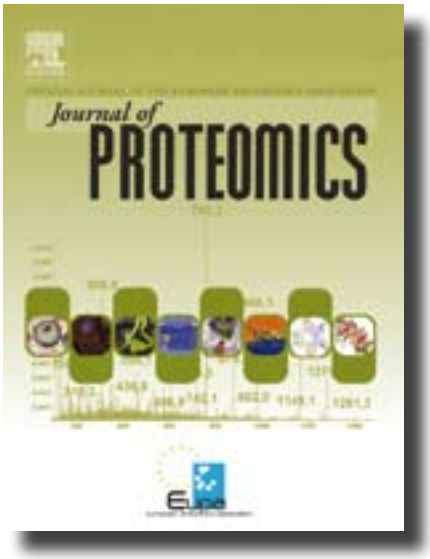
Selections will be based on the scientific excellence and/or tecnical innovations in the field of Proteomics. Award recipients will be chosen by the Poster Award Committe formed by three members of the SEProt Board.

Awards will be presented to the winners by Susanna Baqué, PhD, Senior Manager Sales & Support, Mass Spectrometry Systems, during the SEProt and General Meeting Session.

Good Luck!

Pamplona, January, 2009

Juan J. Calvete
SEProt President



The proceedings of the Proteomics and Human Proteome meeting will be published as a special issue of the Journal of Proteomics. The journal operates an online submission and peer review system that allows authors to submit articles online and track their progress via a web interface. The Journal of Proteomics will only publish in this special issue original research articles describing novel research work presented at the meeting. Also manuscripts submitted for this issue must not have been, nor will be, submitted for publication elsewhere at any time during its consideration by the Journal of Proteomics.

Authors should submit their manuscripts via the online system on or before March 15, 2009. No manuscript will be accepted after this date.

Detailed instructions for authors as well as information on aims and scope of the journal can be found at

http://www.elsevier.com/wps/find/journaldescription.cws_home/713351/description#description

To submit manuscripts to the special issue "Proteomics and Human Proteome: From Bench to Bedside", the article type SI: Proteomics and Human Proteome should be selected.