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Label-free quantitative protein profiling of vastus lateralis muscle during human aging

Laetitia Theron, Marine Gueugneau, Cécile C. Coudy-Gandilhon, Didier D. Viala, Astrid Bijlsma, Andrea Maier, Gilian Butler-Browne, Daniel D. Bechet, Christophe C. Chambon

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EuPA2013 Scientific meeting - Posters list and sessions

Release: Sept 6, 2013

Notes: * Abstract number provided by EasyChair was used for the sole purpose of reviewing and edition of congress Proceedings. Please preferably refer to Poster number once the present list is published.

* Late breaking abstract submission is ongoing. These abstracts will be given a Poster number on Sept 23 and authors will be informed directly. All late breaking communications will be presented in Poster session 2

EasyChair Abstract Number	Poster Title & authors	Topic	Poster Number	Session number	Session timing
1	Ourida Alloui-Lombarkia and Saliha Daas-Amiour. Phenolic compounds of Algerian Dates (<i>Phoenix dactylifera</i> L.) and Evaluation in vitro of their Biological Activity	Bioactive substances	P001	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
2	Bevin Gangadharan, Robin Antrabus, Manisha Bapat, Jan Rossa, David Chittenden, Bettina Kampa, Paul Klenerman, Eleanor Barnes, Raymond Dwek and Nicole Zitzmann. New clinical proteomics approaches for discovering biomarkers: Searching for liver fibrosis markers in hepatitis C patients	Disease Biomarkers	P002	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
3	Annarita Farina, Rémy Visentin, Kaspar Z'graggen, Denis Hochstrasser, Pierre Lescuyer and Jean-Louis Frossard. Quantitative proteomic analysis of tissues and fluids from pancreas cystic lesions	Disease Biomarkers	P003	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
4	Katja Witzel and Silke Ruppel. Proteomic Approaches to Understand Plant Growth Promotion Caused by the Endophyte <i>Enterobacter radicincitans</i> sp. nov. DSM 16656	Plant, microbial and model organisms proteomics (IMOP session)	P004	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
6	Florence Gondret, Blandine Guével, Sandrine Tacher, Hélène Gilbert and Emmanuelle Com. Analysis of the liver proteome in response to a genetic divergence in feed efficiency in growing pigs	Plant, microbial and model organisms proteomics (IMOP session)	P005	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
7	Christiane Hedtmann, Ilona Juszcak, Jörn van Buer and Margarete Baier. Functional analysis of the chloroplast antioxidant enzymes in <i>Arabidopsis thaliana</i> accessions	Plant, microbial and model organisms proteomics (IMOP session)	P006	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
9	Ji-Min Li and Hong-Lin Chan. Hyaluronic acid-dependent protection against UVB-damaged human corneal cells	Environmental proteomics & metabolomics	P007	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
11	Julien Peltier, Jean-Pierre Roperch, Stéphane Audebert, Iradj Sobhani and Luc Camoin. Clinical proteomics for the screening, diagnosis and follow-up of ColoRectal Cancer (CRC)	Disease Biomarkers	P008	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
12	José Eduardo Marques Carneiro, Daniele Suzete Persike, Jean-Christophe Cassel, Astrid Nehlig and Maria José Da Silva Fernandes. Carisbamate modifies the proteomic profile of the hippocampus in a model of temporal lobe epilepsy	Disease Biomarkers	P009	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
13	Thierry Salomon, Uyen Nguyen, Francisco Ramirez, Scott Mack, Susan Darling, John Proctor and Annegret Boge. Capillary Electrophoresis for Upstream and Downstream Biopharmaceutical Development	Instrumentation	P010	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
15	Matthieu Garnier, Carrier Gregory, Helene Rogniaux, Gael Bougaran, Elodie Nicolau, Bruno Saint-Jean and Jean-Paul Cadoret. Use comparative proteomics on a selected microalgae provides candidates for biofuel production.	Plant, microbial and model organisms proteomics (IMOP session)	P011	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
16	Mickaël Doué, Gaud Dervilly-Pinel, Fabrice Monteau and Bruno Le Bizec. Comprehensive endogenous steroid profiling through UPLC-, GC- and UPC2-MS/MS. Application to the control of natural hormones abuse in meat producing animals.	Food & environmental analysis	P012	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
17	Aurélien Lardenois, Florence Robriquet, Mélanie Lagarrigue, Blandine Guevel, Thibaut Larcher, Laurence Dubreil, Candice Babarit, Yan Chereh, Charles Pineau, Laëtitia Guevel and Karl Rouger. Exploration of muscle from GRMD dogs transplanted with MuStem cells using « omics » approaches.	Disease Biomarkers	P013	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
18	Marie Méjean, Alain Brunelle and David Touboul. Optimization of supercritical fluid chromatography coupled to mass spectrometry for natural substances analysis	Instrumentation	P014	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
19	Wojciech Cypryk, Tiina Ohman, Eeva-Liisa Eskelinen, Sampsa Matikainen and Tuula Nyman. Quantitative proteomics and bioinformatic analysis of vesicle-mediated protein secretion upon β -glucan stimulation of human primary macrophages	Quantitative Proteomics	P015	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
20	Quentin Enjalbert, Tina Settineri, Christie Hunter, Remco van Soest and Xiang Zhu. Exploring the Sensitivity Differences for Targeted Peptide Quantification in the Low Flow Rate Regime	Quantitative Proteomics	P016	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
22	Olivia Graebner, Yan Luo and Michael Sefkow. Directed mass spectrometry of functional enriched SAHA specific proteins	Functional Proteomics	P017	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
23	Gilles Schnell, Amandine Boeuf, Quentin Bernard, Benoit Jaulhac, Nathalie Boulanger, Alain Van Dorsselaer and Laurence Sabatier. Proteomic analysis of the molecules involved in the Lyme disease	Disease Biomarkers	P018	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
24	Julien Parra, Véronique Legros, Régis Daniel and Florence Gonnet. Biological role of protein sulfation: Identification and characterization by mass spectrometry.	Post-translational Modifications	P019	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
25	Marine Plumel, Thierry Wasselin, Virginie Plot, Jean-Marc Strub, Alain Van Dorsselaer, Christine Carapito, Jean-Yves Georges and Fabrice Bertile. LC-SRM-based absolute quantitation of two novel vitellogenin isoforms in a non-sequenced organism, the leatherback turtle.	Quantitative Proteomics	P020	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
26	Fanny Jumeau, Francisco Jose Fernandez Gomez, Céline Carpentier, Hélène Obriot, Sabiha Eddarkaoui, Sophie Duban-Deweer, Johann Hachani, Frédéric Halgand, Frédéric Chalmel, Sophie Chocu, Claire-Marie Dhanaens, Marie-Laure Caillet, Jean-Marc Rigot, Marie-Claire Peers, Charles Pineau, Luc Buée, Nicolas Sergeant and Valérie Mitchell. Human Sperm Proteome reveals DCDC2C as a new microtubule associated protein of sperm flagellum	Systems Biology	P021	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
27	Ziemianin Gourdet Anna, Plumel Marine, Thiersé Daniel, Evans Alina, Arnemo Jon, Swenson Jon, Fröbert Ole, Gauquelin-Koch Guillemette, Van Dorsselaer Alain, Blanc Stéphane and Bertile Fabrice. Muscle and adipose tissue responses to physical inactivity: a proteomic approach in the hibernating brown bear (<i>Ursus arctos</i>)	Disease Biomarkers	P022	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
29	Szu-Ting Lin and Hong-Lin Chan. Secretomic analysis of potential resistant markers in human uterine cancer cells	Disease Biomarkers	P023	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

31	Angel P. Diz, Edward Dudley, Andrew Cogswell, Barry W. MacDonald, Ellen L.R. Kenchington, Eleftherios Zouros and David O.F. Skibinski. Proteomic Analysis of Eggs from <i>Mytilus edulis</i> Females Differing in Mitochondrial DNA (mtDNA) Transmission Mode	Systems Biology	P024	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
32	Corinne Bure, Alexandre Pinsolle, Sophie Aycirieux, Eric Testet, Maud Cansell and Jean-Marie Schmitter. A Single Run LC/MS/MS Method for Phospholipidomics: application to <i>S. cerevisiae</i> lipidome and marine lecithin	Systems Biology	P025	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
33	Kazutaka Kikuta, Daisuke Kubota, Yoshihisa Suzuki, Hideo Morioka, Yoshiaki Toyama, Akihiko Yoshida, Eisuke Kobayashi, Fumihiko Nakatani, Hirokazu Chuman, Akira Kawai and Tadashi Kondo. A PROTEOMIC ANALYSIS TO IDENTIFY NOVEL PROTEINS RELATED TO MECHANISMS OF TUMOR CELL INVASION IN MYXOFIBROSARCOMA	Disease Biomarkers	P026	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
34	Fabienne Barriere, Marie Claire Nicolai, Marie Pierre Kazek Duret, Olivier Adam and Catherine Manin. Absolute quantification by mass spectrometry of hemagglutinin (HA) for influenza vaccines	Quantitative Proteomics	P027	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
35	Paul Délérés, Franck Vandermoere, Séverine Chaumont-Dubel, Joel Bockaert and Philippe Marin. Impact of 5-HT6 receptor-elicited mTOR activation on neuronal phosphoproteome	Post-translational Modifications	P028	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
36	Aurore Jaffuel, Jérôme Lemoine, Catherine Aubert, Romain Simon, Jean-François Léonard, Jean-Charles Gautier, Olivier Pasquier and Arnaud Salvador. Optimization of Liquid Chromatography - Multiple Reaction Monitoring cubed Mass spectrometry assay for protein quantification: application to aquaporin-2 water channel in human urine	Disease Biomarkers	P029	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
37	Tassadit Ouidir, Frédérique Jarnier, Pascal Cosette, Thierry Jouenne and Julie Hardouin. Characterization of phosphoproteins involved in <i>Pseudomonas aeruginosa</i> PA14 adaptation	Post-translational Modifications	P030	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
38	Jeremy Jeudy, Arnaud Salvador, Romain Simon, Aurore Jaffuel, Catherine Fonbonne, Jean-Francois Leonard, Jean-Charles Gautier, Olivier Pasquier and Jerome Lemoine. MRMCubed (MRM3) optimization for direct quantification of low abundance protein in biological fluids : application to plasma and urine biomarkers	Disease Biomarkers	P031	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
39	Quentin Vanbellingen, Claudia Bich, Nadine Amusant, David Touboul and Alain Brunelle. Study of wood metabolites by TOF-SIMS imaging	Imaging Mass Spectrometry	P032	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
40	Christophe Chambon, Laetitia Theron, Marine Gueugneau, Cecile Coudy, Didier Viala, Astrid Bijlsma, Andrea Maier, Gillian Butler-Browne and Daniel Bechet. Label-free protein profiling of vastus lateralis muscle during human aging	Quantitative Proteomics	P033	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
41	Vivien Berthelot, Gildas Mouta-Cardoso, François Guillonneau, Carine Giovannangeli, Danièle Praseuth and Filippo Rusconi. An integrated analytical workflow aimed at investigating the formation of DNA repair complexes on double-strand breaks	Interactomics	P034	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
43	Laetitia Theron, Cecile Coudy, Thierry Astruc, Michel Hebraud, Didier Remond, Jean-Claude Barthelemy, Daniel Bechet and Christophe Chambon. Human sarcopenia analysis by MALDI imaging	Imaging Mass Spectrometry	P035	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
45	Renata Šnajdrová, Tomáš Ječmen, Kateřina Haladová and Miroslav Šulc. THE STRUCTURAL MAPPING OF HUMAN 14-3-3zeta REGULATORY PROTEIN	Interactomics	P036	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
46	Tomáš Ječmen, Božena Kubíčková, Renata Šnajdrová, Věra Černá, Petr Novák, Petr Hodek, Marie Stiborová, Jiří Hudeček and Miroslav Sulc. CYTOCHROME P450 2B4 AND CYTOCHROME B5 INTERACTION WITHIN MEMBRANE	Interactomics	P037	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
47	Nha Thi Nguyen Huynh, Pélagie Fichter, Grigory Sharov, Clément Potel, Patrick Schultz, Emmanuelle Leize, Valérie Lamour and Noelle Potier. Chemical cross-linking and MALDI-MS for the characterization of intact protein complexes	Interactomics	P038	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
48	Esther Marza, Anne-Aurélien Raymond, Said Taouji, Léo Guignard, Marc Bonneau, Jean-William Dupuy, Jean Rosebaum, Francesca Palladino, Denis Dupuy and Eric Chevet. Endoplasmic Reticulum stress-induced transcription depends on a CDC-48/RUVB regulatory circuit.	Functional Proteomics	P039	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
49	Vibeke Høst, Kristin Hollung, Rune Rødbotten and Eva Veiseth-Kent. Changes in proteolytic activity and protein composition during beef aging	Food & environmental analysis	P040	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
51	Vincent Guérineau, Vincent Huc, David Touboul, Baptiste Boutonnet, Etienne André, Cyril Martini and Alain Brunelle. New methodology for the analysis of highly hydrophobic calixarenes by MALDI-TOF mass spectrometry	Polymers	P041	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
52	Nicolas Barthélemy, Christophe Hirtz, Jerome Vialaret, Susanna Schraen-Maschke, Nicolas Sergeant, Guy Lippens, Isabelle Huvent, Francois Fenaille, Christophe Junot, Sylvain Lehmann and Francois Becher. Toward the absolute quantification of CSF Tau isoforms in the picogram/milliliter range by a simple and cost-effective purification and μ LC-MS/HRMS	Disease Biomarkers	P042	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
53	Lee Gethings, Johannes Vissers, John Shockcor, Robert Tonge, Stephen McDonald, Sandra Kraljevic Pavelic, Mirela Sedic, Maja Lemac, Danica Batinic, James Langridge and Olga Vasieva. Application of multi-omic and functional network analysis for paediatric patients diagnosed with idiopathic nephrotic syndrome	Systems Biology	P043	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
54	Robert Tonge, Suzanne Geenen, Cristian Cojocariu, Lee Gethings, Giorgis Isaac, Johannes Vissers, James Langridge and Ian Wilson. Qualitative and quantitative characterization of the metabolome, lipidome and proteome of human hepatocytes stably transfected with cytochrome P450 2E1 using data independent LC-MS	Systems Biology	P044	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
55	Catherine Brasseur, Julien Bauwens, Cédric Tarayre, Christel Mattéotti, Philippe Thonart, Jacqueline Destain, Micheline Vandebol, Daniel Portetelle, Frédéric Francis, Eric Haubruge, Edwin De Pauw and Jean-François Focant. GCxGC-TOFMS Analysis of Metabolites Produced by Termites on Different Diets: A Step Forward towards Better Understanding of Enzymatic Complexes in Termites and their Common Symbionts	Environmental proteomics & metabolomics	P045	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
57	Andrew Williamson, Steven Ciavarini, Scott Geromanos, Andrew Tudor, Barry Dyson, Lee Gethings, Kelly McMahon, Robert Tonge, James Langridge, Anthony Whetton and Johannes Vissers. A Qualitative and Quantitative Ion Mobility Enabled Data Independent SILAC Workflow	Quantitative Proteomics	P046	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
58	Joomi Ahn, Michael Eggertson, Keith Fadgen, Ying Quing Yu, Robert Tonge and James Langridge. An automated data analysis of hydrogen/deuterium exchange mass spectrometry using DynamX	Instrumentation	P047	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
59	Martial Seveno, Fanny Duhr, Clotilde Mannoury La Cour, Mark Millan, Joël Bockaert, Philippe Marin and Severine Chaumont-Dubel. A proteomic and functional analysis reveals that 5-HT6 receptors modulate neuronal differentiation by recruitment of Cdk5	Functional Proteomics	P048	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
60	J. Will Thompson, Jay Johnson, Giuseppe Astarita, Giuseppe Paglia, Jim Murphy, Geoff Gerhardt, Stephen Cohen, Robert Tonge, James Langridge and M. Arthur Moseley. Comprehensive Profiling of the Proteome, Lipidome, and Metabolome Enabled Using a Prototype UPLC-Compatible Microfluidic Device	Instrumentation	P049	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

61	Coskun Guzel, Johannes Visser, Lennard Dekker, Gerda Zeeman, Robert Tonge, Eric Steegers and Theo Luider. Calcyclin levels determined by high-throughput SRM in serum samples of pre-eclampsia patients	Disease Biomarkers	P050	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
64	Céline Huillet, Géraldine Gleizal, Monique Dupuy, Rafaela Dumas, Olivier Adam and Catherine Manin. Absolute quantification by mass spectrometry of a recombinant protein and two Host Cell Proteins from E. coli for vaccine application	Quantitative Proteomics	P051	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
65	Loïc Dayon and Martin Kussmann. Proteomics of Plasma: Comparison of Analytical Workflows in Terms of Effort, Throughput and Outcome	Disease Biomarkers	P052	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
66	Cécile Perret, Adrian Mihail Stadler, Hélène Nierengarten, Jean-Marie Lehn and Emmanuelle Leize. Cryospray vs electrospray mass spectrometry: study of labile [2x2] grids	Inorganic mass spectrometry	P053	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
67	Olivier Langella, Benoît Valot, Daniel Jacob, Thierry Balliau, Raphaël Flores, Christine Hoogland, Johann Joets and Michel Zivy. Management of MS proteomic data with PROTiCdb : a quantitative comparison between methods of protein extraction	Bioinformatics	P054	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
68	Delphine Feron, Cathy Charlier, Pauline Lehebel, Marianne Coste-Burel, Philippe Moreau, Mohamed Hamidou, Laurent Garderet, François Girodon, Yannick Jacques, Pierre Weigel, Sylvie Hermouet and Edith Bigot-Corbel. Multiplexed antigen microarray for the study of the specificity of monoclonal immunoglobulins in myeloma patients	Disease Biomarkers	P055	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
69	Roxana Martinez-Pinna, Anne Gonzalez de Peredo, Jose Luis Martin-Ventura, Odile Schiltz and Bernard Monsarrat. Label-free quantitative analysis of human plasma-derived microvesicles as a source of biomarkers of atherosclerosis	Disease Biomarkers	P056	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
70	Anne-Aurélien Raymond, Stéphane Claverol, Véronique Neaud, Marc Bonneau and Jean Rosenbaum. A label-free differential quantitative mass spectrometry analysis for the identification of the Reptin interactome in human hepatocellular carcinoma cells: Reptin - DNA-PKcs interaction, regulation, and incidence on DNA damage	Functional Proteomics	P057	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
71	Steven Carberry, Heinrich Brinkmeier and Kay Ohlendieck. Comparative proteomic profiling of soleus, extensor digitorum longus, flexor digitorum brevis and interosseus muscle from the mdx mouse model of Duchenne muscular dystrophy	Disease Biomarkers	P058	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
72	May Hijazi, Elisabeth Jamet and Cécile Albenne. Characterisation of the AGP31 Pro-rich domain using various mass spectrometry approaches	Post-translational Modifications	P059	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
73	Elisabetta Boeri Erba, Pavel Macek, Cyril Dian, Carlo Petosa and Boisbouvier Jerome Boisbouvier Jerome. Native mass spectrometry monitors the assembly of large nanomachines in real-time	Interactomics	P060	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
74	Ikrame Lazar, Manuelle Ducoux-Petit, Bernard Monsarrat, Odile Buret-Schiltz, Catherine Muller and Laurence Nieto. Global label free quantitative proteomics for the identification of exosome-derived adipocyte content and role of these vesicles on melanoma progression.	Functional Proteomics	P061	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
75	Pierre-Edouard Bodet, Cedric Przybylski, Florence Gonnet, Cathy Gomila, Jérôme Ausseil and Régis Daniel. Detection and characterization of glycosaminoglycan sulfated oligosaccharides as biomarkers of mucopolysaccharidoses	Disease Biomarkers	P062	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
76	Ecaterina Lozan, Corinne Buré, Svitlana Shinkaruk, Catherine Bennetau-Pelissero and Jean-Marie Schmitter. Analysis of 17-β-Estradiol by LC-MS/MS	Bioactive substances	P063	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
77	Valérie Cunin, Guiguet-Coradin Helene, Melo-De-Lima Christelle, Seve Michel and Bourgoïn-Voillard Sandrine. Improvements of Sample Preparation Strategies for the Research of Biomarkers in Plasma	Disease Biomarkers	P064	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
78	Nubia Seyffert, Caroline Le Maréchal, Valerie Briard, Julien Jardin, Anderson Miyoshi, Sergine Even, Gwenaël Jan, Nadia Berkova, Richard Thiery, Vasco Azevedo and Yves Le Loir. Staphylococcus aureus proteins differentially recognized by the ovine immune response in mastitis or nasal carriage.	Disease Biomarkers	P065	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
79	Sylvie Michelland, Nathalie Enjolras, Yesim Dargaud, Alice Indalecio, Michel Seve, Claude Négrier and Sandrine Bourgoïn-Voillard. iTRAQ strategy to quantify phosphorylation level of biologically active human factor IX used for the treatment of hemophilia B	Quantitative Proteomics	P066	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
80	Zdenek Kukacka, Michal Rosulek, Miroslava Kopecka and Petr Novak. Study of conformational changes in proteins using chemical cross-linking and mass spectrometry	Quantitative Proteomics	P067	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
81	Brian Mooney, Diwakar Dahal and Kathleen Newton. Changes in the maize mitochondrial proteome correlated with heterosis	Plant, microbial and model organisms proteomics (IMOP session)	P068	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
82	Cédric Przybylski, Meriem Mokaddem, Mehdi Prull-Jahnsen, Els Saesen, Hugues Lortat-Jacob, Florence Gonnet, Régis Daniel and Anne Varenne. Capillary IsoElectric Focusing hyphenated to mass spectrometry as a tool to characterize various forms of the cytokine interferon-γ	Functional Proteomics	P069	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
83	Eva Veiseth-Kent, Mona E. Pedersen, Kristin Hollung, Elisabeth Ytteborg, Grete Baeverfjord, Harald Takle, Torbjørn E. Åsgård, Robin Ørnstrud, Erik-Jan Lock and Sissel Albrektsen. Vertebral columns of Atlantic salmon (Salmo salar) show alterations in protein abundance due to variable dietary P levels	Plant, microbial and model organisms proteomics (IMOP session)	P070	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
84	Cosette Abdallah, Florence Petit, Nazha Sidahmed-Adrar, Marion Bourgeade, François Le Naour and Delphine Pflieger. Quantitative phosphoproteomics of TGF-β signaling pathways activated by Hepatitis C Virus core protein using a triple SILAC approach	Post-translational Modifications	P071	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
85	Fatma Lecourieux, Stéphane Claverol, Christian Kappel, Philippe Pieri, Justine Charon, Marc Bonneau, Eric Gomes, Serge Delrot and David Lecourieux. Direct impact of high temperature on the grapevine berry proteome	Environmental proteomics & metabolomics	P072	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
86	Raphael Voges, Stephanie Corsten, Wolfgang Wiechert and Stephan Noack. Absolute protein quantification by QConCAT during growth of Corynebacterium glutamicum under industrially relevant conditions	Quantitative Proteomics	P073	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
87	Georg Tascher, Agnès Hovasse, Marine Plumel, Valery Shevchenko, Christophe Chesné, Elmar Heinze, Fozia Noor, Christine Carapito, Alain Van Dorsselaer and Fabrice Bertile. Proteomics of the HepaRG cell line for studying drug-induced liver toxicity	Systems Biology	P074	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
88	Delphine Lapaillerie, Ludovic Martin, Jean-Marie Schmitter and Marc Bonneau. Magic Blue: a very fast and sensitive colloidal Coomassie G-250 staining for proteome analysis	Reactivity	P075	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
89	Hana Konecna, Katerina Ornerova, David Potesil and Zbynek Zdrahal. Over thousand of proteins identified in prefractionated beer	Plant, microbial and model organisms proteomics (IMOP session)	P076	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
90	Carine Froment, Romain Roncagalli, Bernard Malissen, Odile Schiltz, Bernard Monsarrat and Anne Gonzalez de Peredo. Large-scale profiling of tyrosine phosphorylation dynamics following TCR activation in primary mouse T-cells	Post-translational Modifications	P077	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

91	Alexis Goichon, Julien Bertrand, Philippe Chan, Stéphane Lecleire, Aude Coquard, Anne-Françoise Cailleux, David Vaudry, Pierre Déchelotte and Moïse Coëffier. Enteral delivery of proteins modulates the duodenal mucosal proteome in humans: focus on proteins involved in cell structure and protein biosynthesis	Bioactive substances	P078	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
93	Hélène Flamant-Waret, Sandrine Bourgoïn-Voillard, Candice Trocmé, Izabel Bérard, Bertrand Toussaint, Karine Botturi, Antoine Magnan, Laurent Nicod, Christophe Pison and Michel Seve. Quantitative Proteomics Approach for the Identification of Biomarkers Predictive of Chronic Lung Allograft Dysfunction (CLAD) after Lung Transplantation	Disease Biomarkers	P079	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
94	Jun Onodera, Masaaki Ubukata, Jone Dane, Akihiko Kusai and Junichi Osuga. Comparative Study of Conventional- and Fast-GCxGC-HRTOFMS Method for Petroleum and Essential Oil Sample	Food & environmental analysis	P080	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
95	Grégoire Harichaux, Cindy Riou, Kathy Soutonie, Aurélien Brionne, Joël Gautron, Valérie Labas, Xavier Druart and Nadine Gerard. Bottom up analysis of Gallus gallus uterine fluid: comparison of two lines of hens and effect of artificial insemination	Quantitative Proteomics	P081	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
96	Sylvia Lehmann, Amandine Hurbin, Michel Seve and Sandrine Bourgoïn-Voillard. Acetylated Proteins Involved in Resistance to EGFR Tyrosine Kinase Inhibitors in Non-Small Cells Lung Cancer	Post-translational Modifications	P082	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
97	Salomé Poyer, Corinne Loutelier, Gaël Coadou, Philipp Hess, Anne Bossée, Florence Mondeguer, Julien Enche, Sophie Gougeon, Carlos Afonso and Marie Hubert. Identification of paralytic shellfish poisons using liquid chromatography and ion mobility coupled to high resolution mass spectrometry	Food & environmental analysis	P083	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
98	Clement Soleilhavoup, Cindy Riou, Guillaume Tsikis, Philippa Kohnke, Valerie Labas, Gregoire Harichaux, Nadine Gerard and Xavier Druart. Proteomic analysis of fluids from the genital tract of ewes during the estrous cycle.	Functional Proteomics	P084	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
99	Maria van Aghoven, David Kilgour, Lionel Chiron, Andrew Soulby, Juan Wei, Marie-Aude Coutouly, Mark Barrow, Marc-André Delsuc, Christian Rolando and Peter O'Connor. New Advances in Two-Dimensional ExD FT-ICR MS	Instrumentation	P085	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
100	Sonja Radau, Marc Vaudel, Florian Beck, Ingo Feldmann, Albert Sickmann, Lennart Martens and René Zahedi. A novel phosphopeptide standard to evaluate data interpretation in a realistic phosphoproteomic environment	Post-translational Modifications	P086	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
102	Juergen Eirich and Stephan Sieber. From natural products to their protein targets: Peptidic photo reactive probes for Affinity-Based Protein Profiling.	Bioactive substances	P087	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
103	Valerie Labas, Isabelle Grasseau, Sabine Alves, Marie Bourin, Karine Cahier, Audrey Gargaros, Grégoire Harichaux, Ana-Paula Teixeira-Gomes, Nadine Gérard and Elisabeth Blesbois. Chicken spermatozoa and seminal plasma proteomic using MALDI-TOF profiling, top down and bottom-up proteomic approaches in order to phenotype semen	Plant, microbial and model organisms proteomics (IMOP session)	P088	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
104	Magalie Duchateau, Daria Julkowska, Inès Subota, Véronique Hourdel, Abdelkader Namane, Julia Chamot-Rooke and Philippe Bastin. Proteomic analysis of Trypanosoma brucei flagella reveals new proteins.	Quantitative Proteomics	P089	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
105	Alex Powlesland, Debbie Baker, Grand Francis, Luise Weigand, Martin Ebner, Linda Hibbert, Tara Mahon, Namir Hassan, Samantha Paston, Jane Harper, Rebecca Ashfield and Bent Jakobsen. A systematic approach to generating immunotherapeutics based on high affinity soluble T cell receptors	Bioactive substances	P090	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
106	Karel Stejskal, Terezie Mandáková, Gabriela Lochmonová, Martin A. Lysak and Zbyněk Zdráhal. Proteomic changes in recently formed hybridogenous Cardamine taxa	Plant, microbial and model organisms proteomics (IMOP session)	P091	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
107	Erman Kocak, Thomas Timm, Julia Grabitzki and Guenter Lochnit. Gel-based proteomic analysis of membrane glycoproteins decorated with phosphocholine from the porcine parasite Ascaris suum	Post-translational Modifications	P092	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
108	Naganand Rayapuram, Ludovic Bonhomme, Jean Bigeard, Kahina Haddadou, Heribert Hirt and Delphine Pflieger. THE HUNT FOR MAPK SUBSTRATES - A PHOSPHOPROTEOMICS APPROACH	Post-translational Modifications	P093	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
109	Jean Bigeard, Naganand Rayapuram, Ludovic Bonhomme, Heribert Hirt and Delphine Pflieger. PHOSPHOPROTEOMICS OF THE CHROMATIN IN ARABIDOPSIS THALIANA SUBJECTED TO BIOTIC STRESS	Post-translational Modifications	P094	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
111	Thomas Timm, Julia Grabitzki, Lisa Ewald, Yavuz Yilmaz and Guenter Lochnit. Phosphocholine (PC)-containing antigens from the parasite Ascaris suum	Post-translational Modifications	P095	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
112	Suvi Ravela, Leena Valmu, Ulf-Håkan Stenman and Outi Itkonen. New LC-MS based assay of serum tumour-associated trypsin inhibitor (TATI) allows simultaneous quantitation and detection of TATI variants	Disease Biomarkers	P096	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
113	Anna Maria Agresta, Antonella De Palma, Sara Motta, Serena Giuliano, Roberta Salvini, Simona Viglio, Anna Bardoni and Pierluigi Mauri. Proteomic approaches to investigate a rare case of human progressive dementia: Nasu-Hakola Disease	Disease Biomarkers	P097	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
114	Mohammad Gulzar, Saïd Bouhallab, Valérie Briard-Bion, Julien Jardin and Thomas Croguennec. Chemical modifications on dry heated alpha-Lactalbumin	Post-translational Modifications	P098	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
116	Yuta Kurota, Yoshihiko Tomita, Tadashi Kondo, Takashi Tajima, Kenta Mukaihara and Naofumi Asano. Cancer Proteomics towards Biomarker Development for Personalized Medicine in Renal Cell Carcinoma	Disease Biomarkers	P099	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
117	Elena Kunold, Nina C. Bach and Stephan A. Sieber. A phosphoproteomics platform to monitor the infection mechanism of human cells with pathogenic bacteria	Plant, microbial and model organisms proteomics (IMOP session)	P100	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
118	Navin Jain, Arpit Bhargava and Jitendra Panwar. Protease-Assisted One-Pot Synthesis and Stabilization of Spherical Silver Nanoparticles: A Novel Template to Study Protein-Nanoparticle Interactions	Interactomics	P101	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
119	Anne-Marie Lomenech, Amande Beaumard, Hayssam Soueidan, Stephane Claverol, Jean-William Dupuy, Sebastien Vilain, Marc Crouzet, Alexis Groppi, Macha Nikolski, Jean-Marie Schmitter and Marc Bonneau. A complexomic study of Pseudomonas aeruginosa using Blue Native PAGE (BN-PAGE) coupled with LC-MS/MS	Interactomics	P102	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

120	Baptiste Porte, Antoine Obry, Frédérique Jarnier, Julie Hardouin, Michelle Hauchecorne, Nicolas Dupré, Clémence Chatelain, Pascal Cosette, Bruno J Gonzalez and Philippe Leroux. Proteomic analysis of mice brain microvessels between pups and adult: A way to unravel neonate vulnerability to injurious processes?	Functional Proteomics	P103	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
122	Clémence Chatelain, Baptiste Porte, Julie Hardouin, Michèle Hauchecorne, Frédérique Jarnier, Stéphane Marret, Pascal Cosette and Philippe Leroux. Proteomic characterization of differentiation in neonate and adult micro-vascular endothelial cells in primo-culture.	Functional Proteomics	P104	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
123	Kéra Nyemb, Julien Jardin, David Causeur, Catherine Guérin-Dubiard, Didier Dupont, Shane Rutherford and Françoise Nau. Quantitative mass spectrometry for nutritional peptidomics: Evaluating the impact of food processing technology by multivariate statistical approaches	Quantitative Proteomics	P105	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
124	Matondo Mariette, Bensimon Ariel, Ching-Yun Chang, Sharon Rashi-Elkeles, Rani Elkon, Meena Choi, Olga Vitek, Yossi Shiloh and Ruedi Aebersold. Investigating ionizing radiation induced modulation of the human cellular proteome using targeted proteomics	Quantitative Proteomics	P106	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
125	Jordane Biarc, Ivan Mikaelian, Philippe Gonzalo, Laurent Fattet, Pierre-Germain Gillet, Ruth Rimokh and Jerome Lemoine. Characterization of an epithelial-mesenchymal transition signature by combining a discovery LC-MS/MS analysis and a label-free quantification.	Quantitative Proteomics	P107	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
126	Zbynek Zdrahal, Ondrej Sedo, David Vinkler, Petr Klempt, Romana Stopkova and Pavel Stopka. Characterization of Odorant Binding Proteins in three species of the genus Apodemus	Systems Biology	P108	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
128	Dominic Helm, Christopher J Hughes, Johannes Pc Vissers, Benjamin Ruprecht, Simone Lemeer, James I Langridge and Bernhard Kuster. Global and targeted proteome analysis on an ion mobility enhanced high duty cycle qTOF	Instrumentation	P109	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
130	Charlotte Corporeau, Claudie Quééré, Julien Normand, Jean-Louis Nicolas, David Tamayo and Stéphanie Madec. Proteomic changes induced by low or high Ostreid Herpes Virus1 load in Pacific oyster <i>Crassostrea gigas</i>	Environmental proteomics & metabolomics	P110	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
132	Thomas Schneider, Sophie Dijon, Ashraf Elamin, Fabio Talamo, Blaine Phillips, Emilija Veljkovic, Gregory Vuillaume, Nikolai Ivanov, Julia Hoeng and Manuel Peitsch. Using iTRAQ Approach to Investigate the Effect of Cigarette Smoke-Induced COPD and Smoking Cessation Effects in C57BL/6 Mice	Quantitative Proteomics	P111	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
133	Sandrine Uttenweiler-Joseph, Alexandre Stella, Bernard Monsarrat, Odile Bulet-Schiltz, Christel Moog-Lutz and Pierre G. Lutz. Quantification of ASB2 proteins by selected reaction monitoring mass spectrometry	Quantitative Proteomics	P112	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
134	Isabel Fernandes, Artur Alves, Bart Devreese, António Correia and Ana Cristina Esteves. Secretome of a cork oak pathogen, <i>Diplodia corticola</i>	Plant, microbial and model organisms proteomics (IMOP session)	P113	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
135	Yohann Couté, Sylvie Elsen, Gwendoline Bellement-Théroué, Guillermina Casabona, Yves Vandenbrouck and Ina Attree. Proteomic analysis of novel hyper-virulent <i>Pseudomonas aeruginosa</i> strain	Quantitative Proteomics	P114	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
137	Sara Motta, Alessandra Martorana, Paola Sperandeo, Fabrizio Basilico, Anna Maria Agresta, Alessandra Polissi and Pierluigi Mauri. MudPIT analysis of <i>Escherichia coli</i> membrane proteome	Plant, microbial and model organisms proteomics (IMOP session)	P115	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
138	Yoann Fillatre, David Rondeau, Antoine Daguin, Alain Jadas-Hecart and Pierre-Yves Communal. The Sampling Method by Evaporation under Nitrogen as a Complementary Approach for the Multiresidue Analysis of 256 Pesticides in Lavandin Essential Oil by LC/ESI/SSRM	Food & environmental analysis	P116	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
139	Jerome Vialaret, Constance Delaby, Christophe Hirtz and Sylvain Lehmann. Implementation of the quantitative mass spectrometry measurement of hepcidin-25 in serum	Disease Biomarkers	P117	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
140	Ludovic Bailly-Chouriberry, Florence Cormant, Patrice Garcia, Albert Kind, Marie-Agnès Popot and Yves Bonnaire. Confirmation of α -cobratoxin in horse plasma by LC-MS/MS with Q-Exactive	Bioactive substances	P118	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
141	Martina Havelkova, David Potesil, Said Hafidh, Jana Fecikova, Vera Capkova, Jan Fila, David Honys and Zbynek Zdrahal. Analysis of Tobacco Pollen Tube Secretome	Plant, microbial and model organisms proteomics (IMOP session)	P119	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
142	Joel Capdevielle, Armelle Buzy, Véronique Mary, Jeanne Stemmelin, Patrick Juvet, Denis Loyaux, Jean-Claude Guillemot and Pascual Ferrara. Proteomic profiling of phospho-Tau in THY-Tau22 transgenic mice	Disease Biomarkers	P120	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
143	Agnès Hovasse, Florence Ploetze, Philippe Bertin, Alain Van Dorsselaer and Christine Carapito. A targeted LC-SRM assay for precise quantification of proteins involved in natural attenuation of an arsenic-rich ecosystem	Quantitative Proteomics	P121	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
144	Natarajan Perumal, Sebastian Funke, Norbert Pfeiffer and Franz Grus. Significant Up-Regulation of Proline-Rich Protein 4 (PRR4) In Human Reflex Tear Proteome	Post-translational Modifications	P122	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
145	Florent Nihoul, Julie Letendre, Tiphaine Monsinjon, Philippe Chan, David Vaudry, Heinz-R. Köhler and Thomas Knigge. Shell colour polymorphism in the White garden snail, <i>Theba pisana</i> (O.F. Müller 1774) is reflected in differential proteomic patterns	Environmental proteomics & metabolomics	P123	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
146	Julie Letendre, Tiphaine Monsinjon, Philippe Chan, Béatrice Rocher, Christophe Minier, David Vaudry and Thomas Knigge. Oestrogen-induced changes in the fish pituitary proteome	Environmental proteomics & metabolomics	P124	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
147	Sebastian Alvaro Vaca Jacome, Raphael Carapito, Nicodème Paul, Alexandre Burel, Ghada Alsaleh, Louise Ott, Siamak Bahram, Alain Van Dorsselaer and Christine Carapito. Differential proteogenomic analysis using LC-MS/MS, label free quantification and personalized proteome databases	Bioinformatics	P125	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
149	Rémi Longuespée, Maximilien Fléron, Marie Claire Gillet, Philippe Delvenne and Edwin De Pauw. Imaging mass spectrometry and proteomics of 3D cell cultures.	Imaging Mass Spectrometry	P126	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
150	Ilona Turek, Sebastian Bartels and Chris Gehring. Interactions of the plant natriuretic peptide AtPnP-A with proteins regulating ROS metabolism	Interactomics	P127	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
153	Sega Ndiaye, Angélique Boedec, François Gray, Florence Lhospice, Claude Villard, Rima Ait-Belkacem, Lyna Sellami, Christian Belmant and Daniel Lafitte. FC antibody fragments analysis using MALDI In Source Decay	Fragmentation	P128	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
154	Frédéric Poussigue, Jérôme Lemoine, Philippe Dugourd and Fabien Chiro. Polyphenol clusters in interaction with peptides – an ion mobility study	Ion mobility	P129	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
155	Gabriel Mazzucchelli, Tyler Zimmerman, Marie-Alice Meuwis, Nicolas Samrgiasso, Dominique Baiwir and Edwin De Pauw. "MELD": a bottom-up method to fully de novo sequence purified proteins	Post-translational Modifications	P130	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

156	Raphael Legouffe, Guillaume Hochart and David Bonnel. Development of High Resolution MSI combined with Metabolomics study to evaluate drug efficacy and Impact onto Biological Environment.	Imaging Mass Spectrometry	P131	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
157	Gregory Hamm, Guillaume Hochart and Raphael Legouffe. Evaluations and application of Quantitative MSI Approaches to small and large molecules analysis in tissue	Imaging Mass Spectrometry	P132	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
158	Ahmad Al Ali, David Touboul, Jean-Pierre Le Caër, Isabelle Schmitz-Afonso, Jean-Pierre Flinois, Catherine Marchetti, Isabelle De Waziers, Alain Brunelle, Olivier Laprèvote and Philippe Beaune. Quantification of 6 cytochrome P450 isoforms in human liver by chromatographic-mass spectrometric coupling	Quantitative Proteomics	P133	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
159	Marianne Tardif, Sabine Brugière, Morgane Mininno, Meryl Mazzoleni, Océane Gigarel, Myriam Ferro, Claude Alban and Stéphane Ravanel. Proteome-wide detection of K/R methylations in Arabidopsis chloroplast	Plant, microbial and model organisms proteomics (IMOP session)	P134	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
160	Séverine Clavier, Xiuxia Du, Rodrigue Marquant, Sandrine Sagan, Gérard Bolbach and Emmanuelle Sachon. Following (R/W)9 Cell Penetrating Peptide track with photocross-linking and mass spectrometry	Interactomics	P135	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
161	Loren Méar, Blandine Guével, Sophie Chocu, Régis Lavigne, Frédéric Chalmel and Charles Pineau. Characterization of the Sertoli cell secretome using Shotgun proteomics and Integrative Genomics	Integrative genomics	P136	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
162	Charlotta Göransson and Marcus Söderquist. Heat inactivation of tissue samples enables reliable measurement of the proteome	Disease Biomarkers	P137	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
163	Issa Diallo, Sylvie Michelland, Clémentine Dupuis, Patrice Faure, Michel Seve and Sandrine Bourgoïn-Voillard. Development of MRM Quantitation Method for Growth Hormone	Quantitative Proteomics	P138	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
164	Clément Fleith, Christine Enjalbal, Sonia Cantel, Jeremie Ciccione, Gilles Subra, Jean Martinez and Ahmad Mehdi. Laser desorption ionization mass spectrometry of peptides on amorphous CHCA-functionalized silica	Instrumentation	P139	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
165	Melinda Rezeli, Ákos Végvári, Thomas Laurell, Oskar Hansson and György Marko-Varga. MRM assay for quantification of apolipoprotein E isoforms in Alzheimer's disease	Quantitative Proteomics	P140	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
167	Sébastien Vachenc, Géraldine Lucchi, Vincent Briaud, Aline Jeannin, Delphine Pecqueur, Pauline Salloignon, Patrick Ducoroy and Caroline Trunzter. Comparison of software solutions dedicated to the discovery of proteomics markers using label-free LC-MS	Bioinformatics	P141	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
168	Mats Borén, Anna Nilsson, Cecilia Eriksson, Beatrice Orback, Marcus Söderquist, Richard Goodwin and Per Andrén. Molecular distribution in heat stabilized tissue using MALDI imaging	Imaging Mass Spectrometry	P142	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
169	F Campos, J Guitard, M Palous, I Meyer, Jy Brossas, A Fekkar, A Detry, D Mazier, C Hennequin and C Marinach. Identification of Cryptococcus neoformans serotypes: from routine to research and back	Plant, microbial and model organisms proteomics (IMOP session)	P143	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
170	Christian Malosse, Joseph Gault, Gerard Pehau-Arnaudet, Corinne Millien, Guillaume Dumenil, Marie-Cecile Ploy and Julia Chamot-Rooke. Screening Type IV Pili from Hyper-virulent Clinical Strains of Neisseria meningitidis Using Top-Down Mass Spectrometry.	Post-translational Modifications	P144	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
171	Anouk Emadali, Sophie Rousseaux, Juliana Bruder-Costa, Claire Rome, Sieme Hamáida, Patricia Betton, Alexandra Debernardi, Sylvie Kieffer-Jaquinod, Florence Combes, Christophe Bruley, Jerome Garin, Myriam Ferro, Rémy Gressin, Mary Callanan and Saadi Khochbin. Identification of a novel biomarker in aggressive lymphoid cancers using a transcriptome-powered targeted proteomics screen	Disease Biomarkers	P145	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
172	Carine Puppo, Luisana Avilan, Elisabetta Miléo, Magali Lorenzi, Jenny Erales, Regine Lebrun, Bruno Guigliarelli, Valerie Belle and Brigitte Gontero. The Intrinsically Disordered Protein (IDP) CP12 and two Calvin cycle enzymes: a fuzzy complex	Systems Biology	P146	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
173	Emmanuelle Claude, Michel Wf Nielsen, Brent Reschke, Robert Tonge and Hilary Major. Rapid imaging of unprocessed chicken bone marrow by LAESI-MS and a T-wave ion mobility equipped Synapt G2-S QTOF	Imaging Mass Spectrometry	P147	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
174	G Palazon, Jy Brossas, L Paris, D Mazier and C Marinach. Identification of new markers of Trypanosoma cruzi disease by proteomic approaches	Plant, microbial and model organisms proteomics (IMOP session)	P148	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
175	Sandeep Kumar Misra, Francine Aké, Xong Fu, Eliane Milohanic, Pascale Cossart, Josef Deutscher, Veronique Monnet, Cristel Archambaud and Celine Henry. Quantitative proteomic analysis identifies PrfA* responsive proteins and phosphoproteins in Listeria monocytogenes	Post-translational Modifications	P149	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
176	Jonathan Williams, Christopher Hughes, Robert Tonge and Jeff Brown. Electrochemical-reduction for enhanced top-down ETD sequencing of peptides and proteins	Instrumentation	P150	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
177	Hanane Kadar, Franck Chiappini, Catherine Guettier, David Touboul, François Le Naour and Alain Brunelle. Characterization of Non Alcoholic fatty liver disease stages by ToF-SIMS imaging	Imaging Mass Spectrometry	P151	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
178	Pierre Le Pogam-Alluard, Béatrice Gargadennec-Legouin, Joel Boustie and David Rondeau. Detection and chemical reactivity of lichen secondary metabolites using in situ DART-MS	Plant, microbial and model organisms proteomics (IMOP session)	P152	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
180	Sergei Saveliev, Marjeta Urh, Ethan Strauss, Mike Rosenblatt, Caroline End, Richard Jones, Michael Ford and Dave Allen. Enhanced protein mass spectrometry analysis with Trypsin/Lys-C mix	Functional Proteomics	P153	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
181	Anna Ziemianin Gourdet, Agnès Hovasse, Christine Carapito, Dominique Jullien, Alain Van Dorsselaer, Christine Schaeffer Reiss and Nükhet Cavusoglu. SRM – based relative quantification of cortical extract protein in different types of human hair	Quantitative Proteomics	P154	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
182	Candice Trocmé, Sandrine Bourgoïn-Voillard, Izabel Bérard, Hélène Flamant-Waret, Bertrand Toussaint, Karine Botturi, Antoine Magnan, Laurent Nicod, Christophe Pison and Michel Seve. Identification of Biomarkers Predictive of Chronic Lung Allograft Dysfunction (CLAD) after Lung Transplantation by Proteomic Technologies	Disease Biomarkers	P155	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
183	Stephanie Kaspar, Sergei Saveliev, Pierre-Olivier Schmit, Mike Rosenblatt, Caroline End, Ethan Strauss, Matt Willetts, Carsten Baessmann and Marjeta Urh. Reference protein extracts for mass spectrometry method development and instrument validation	Instrumentation	P156	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
184	David Cornu, Sandra Blanchet, Manuela Argentin, Jean-Pierre Rousset, Laila Sago, Virginie Redeker and Olivier Namy. Qualitative and quantitative study of the readthrough process in S. cerevisiae	Quantitative Proteomics	P157	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
185	Mark Towers, Laura Cole, Malcolm Clench, Robert Tonge and Emmanuelle Claude. Hierarchical clustering approaches for protein identification directly from tissue sections in a MALDI imaging experiment	Imaging Mass Spectrometry	P158	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

186	Ana Rodrigues, Gabriel Mazzucchelli, Nicolas Smargiasso, Marie-Claire Gillet and Edwin De Pauw. Towards a targeted approach to understand the role of telomeres and telomerase in human cancer biology and evaluate related therapeutic strategies	Quantitative Proteomics	P159	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
188	Alessio Soggiu, Cristian Piras, Emøke Bendixen, Luigi Bonizzi and Paola Roncada. Microbial dynamics into cheese: a functional metaproteomics approach	Plant, microbial and model organisms proteomics (IMOP session)	P160	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
189	Pierre Edouard Bougis, Samuel Granjeaud, Maya Belghazi and Marie-France Martin-Eauclair. Automated scorpion venom mass fingerprinting (VMF) in the nanogram range	Bioactive substances	P161	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
190	Armelle Buzy, Jean-Luc Zacharyus, Stéphanie Olivier-Van Stichelen, Denis Loyaux, Pascual Ferrara and Tony Lefebvre. Identification of β -catenin O-GlcNAcylation and phosphorylation sites in colon cell lines and human colorectal tumors	Post-translational Modifications	P162	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
191	Patrick Pouillet, Guillaume Arras, Florent Yvon, Falaye Camara, Damarys Loew and Emmanuel Barillot. myProMS, a Web Server for Collaborative Processing and Analysis of Mass Spectrometry-based Proteomics Data	Bioinformatics	P163	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
194	Valérie Morineaux, Didier Hilaire, Christelle Mazuet, Julien Enche and Michel R. Popoff. Unambiguous identification of botulinum toxin A subtypes by liquid chromatography-tandem mass spectrometry.	Food & environmental analysis	P164	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
196	Mathieu Dupré, Benoît Gilquin, Christophe Junot, Virginie Brun and Bécher François. Evaluation of a Quadrupole-Orbitrap Mass Spectrometer for the Detection and Quantification of Protein Toxins	Quantitative Proteomics	P165	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
198	Cindy Salvisberg, Nadja Tajouri-Morizur, Pierre R. Burkhard, Patrice H. Lalive and Natacha Turck. Exploring human tear fluids: discovery of new biomarkers for multiple sclerosis.	Disease Biomarkers	P166	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
199	Jordane Biarc, Marion Girod, Quentin Enjalbert, Jeremy Jeudy, Rodolphe Antoine, Jerome Lemoine and Philippe Dugourd. Visible Photodissociation in a Q-Exactive mass spectrometer: specific detection of cysteine-containing peptides.	Fragmentation	P167	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
200	Mathilde Joint, Marilyn Carrier, Cécile Rochette-Egry and Adeline Page. Phosphoproteomic analysis of human nuclear extracts by high resolution nanoLC/Orbitrap Mass Spectrometry	Post-translational Modifications	P168	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
201	Claire Ramus, Jonathan Perot, Flore Mietton, Marie Arlotto, Morgane Champeboux, Yohann Coute and Jérôme Govin. Chromatin dynamics during gametogenesis: using yeast spores and proteomics	Quantitative Proteomics	P169	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
202	Alain Guillot, Florence Blon, Véronique Monnet, Joel Doré and Catherine Juste. A Strategy to go deep and fast into the Collective Proteome of Gut Microbes	Environmental proteomics & metabolomics	P170	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
203	Nannan Tao, Ulrike Schweiger-Hufnagel, Kristina Marx, Stephanie Kaspar, Sabine Jourdain and Anja Resemann. Comprehensive study of O-linked glycans of Erythropoietin	Post-translational Modifications	P171	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
204	Mette Aamand Sørensen, Stine Jacobsen, Louise Bundgaard, Zhi Sun, Erik W. Deutsch and Emøke Bendixen. Assembly of the first build of an Equine PeptideAtlas	Plant, microbial and model organisms proteomics (IMOP session)	P172	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
205	Louise Bundgaard, Stine Jacobsen, Mette Aamand Soerensen, Rob Beynon, Victoria Harman, Lars Jelstrup Petersen and Emøke Bendixen. SRM and QconCAT based analysis of cytokines, acute phase proteins and hypoxia related proteins in the horse	Plant, microbial and model organisms proteomics (IMOP session)	P173	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
206	Thérèse Schembri, François Gray, Mikael Levi, Claude Villard, Stéphane Moreau, Pierre Boissery and Daniel Lafitte. LC-MS/MS for screening and quantifying anti-cancer drugs and metabolites in waste water rejected in Mediterranean sea.	Food & environmental analysis	P174	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
207	Caroline Le-Maréchal, Vincent Peton, Julien Jardin, Valérie Briard-Bion, Stéphanie-Marie Deutsch, Valentin Loux, Hélène Falentin and Gwénaél Jan. An integrative approach of probiotic Propionibacterium freudenreichii Surface proteome	Functional Proteomics	P175	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
208	Stephan Kirsch, Catherine Pech, Halim Guerraoui, Audrey Gabelle, Denis Loyaux and Pascual Ferrara. In-depth screening of neurodegenerative human cerebrospinal fluid proteome	Disease Biomarkers	P176	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
210	Shannon Cornett, Janina Oetjen, Michaela Aichler, Jan Strehlow, Stefan Heldmann, Judith Berger, Michael Gottschalk, Klaus Steinhorst, Jan Hendrik Kobarg, Stefan Wirtz, Stefan Schiffler, Herbert Thiele, Axel Walch, Peter Maass, Theodore Alexandrov, Detlev Suckau, Pierre-Olivier Schmit, Michael Becker and Sabine Jourdain. Acquisition and Analysis of 3D MALDI Imaging Data Sets	Imaging Mass Spectrometry	P177	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
211	Helena Barysz, Juri Rappsilber and Bill Earnshaw. In situ analysis of condensin complex by cross-linking and targeted MS	Functional Proteomics	P178	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
212	Sébastien Brier, Francois Peurois, Karine Jain, Véronique Bordas, Thierry Batard, Nony Emmanuel and Philippe Moingeon. Mapping of B-cell epitopes of the major birch pollen allergen Bet v 1 by using hydrogen/deuterium exchange mass spectrometry	Functional Proteomics	P179	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
213	Sergei Dikler, Jane-Marie Kowalski, Manuel Chapelle, Sabine Jourdain and Shannon Cornett. Novel Workflow Combining MALDI Imaging and LC-MALDI for Obtaining Identification and Spatial Localization of Proteins from Eye Lens Tissue	Imaging Mass Spectrometry	P180	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
215	Jens Fuchser, Eckhard Belau, Soeren-Oliver Deininger, Manuel Chapelle, Sabine Jourdain and Michael Becker. MALDI Imaging of Rat Testis at 10 μ m Pixel Size and 200k Mass Resolution	Imaging Mass Spectrometry	P181	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
216	Patrice Garcia, Isabelle Perot, Ludovic Bailly-Chouriberry, Marie-Agnès Popot and Yves Bonnaire. ITPP detection in plasma and urine samples by LC-MS/MS for horse doping control	Bioactive substances	P182	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
217	Breckenfeld Andreas, Kristina Marx, Andrea Kiehne, Sabine Jourdain and Makus Meyer. In-depth characterization of glycopeptides by combination of CID and ETD fragmentation after charge state enhancement	Fragmentation	P183	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
218	Sebastien Gallien, Sang-Yoon Kim, Adèle Bourmaud and Bruno Domon. Large-scale Quantitative Proteomics Method Based on Parallel Reaction Monitoring	Human Proteome Project (HPP)	P184	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
219	Laure Tonini, Mathilde Beau, Chia-Fang Liu, Alexandre Stella, Carine Froment, David Bouyssie, Wladimir Malaga, Christophe Guilhot, Odile Schiltz and Michel Riviere. Mycobacterium smegmatis glycoproteomics analysis and full extent determination of the Fasciclin protein unusual glycosylation pattern	Post-translational Modifications	P185	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
220	Stephanie Kaspar, Stuart Pengelley, Thorsten Ledertheil, Ralf Hartmer, Wolfgang Jabs, Pierre-Olivier Schmit, Sabine Jourdain and Carsten Baessmann. Increased peptide and protein identification rate for proteomics samples by controlling peptide charge states generated by Captive Spray	Instrumentation	P186	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon

221	Catherine Nury, Virginie Redeker, Sébastien Dautrey, Anthony Romieu, Pierre-Yves Renard, Ronald Melki and Julia Chamot-Rooke. New clickable cross-linkers for studying protein structure: application to the α -Synuclein/Hsc70 complex involved in Parkinson disease	Functional Proteomics	P187	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
222	Thomas Lambour, Bertrand Fabre, Manuelle Ducoux-Petit, François Amalric, Bernard Monsarrat, Odile Burlet-Schiltz and Marie-Pierre Bousquet-Dubouch. Determination of the proteasome complexes composition in a variety of human cell lines	Interactomics	P188	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
223	Gabriel Mazzucchelli, Nicolas Smargiasso, Dominique Baiwir, Edouard Louis, Edwin De Pauw and Marie-Alice Meuwis. Comparison of five serum depletion or fractionation methods applied for clinical biomarkers discovery studies	Quantitative Proteomics	P189	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
226	Serge Urbach, Alexandra Skorupa, Oana Vigy, Séverine Chaumont-Dubel, Jochen H.M. Prehn and Philippe Marin. Angiogenin Induces Modifications in the Astrocyte Secretome: Relevance to Amyotrophic Lateral Sclerosis	Quantitative Proteomics	P190	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
227	Jusal Quanico, Julien Franck, Maxence Wisztorski, Michel Salzet, Robert Day and Isabelle Fournier. Combining Identification and Quantification of Proteins to their Localization Using Parafilm-Assisted Manual Microdissection	Imaging Mass Spectrometry	P191	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
228	Jane Savskov Runager, Cécile Bonnefont, Marianne Overgaard Hesselager, Stine Lønnerup Bislev, Jonas Borch-Jensen and Emøke Bendixen. Pig as a model system for biomedical research	Plant, microbial and model organisms proteomics (IMOP session)	P192	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
229	Arnaud Goyallon, Sophie Cholet, Christophe Junot and François Fenaille. Development of a mass spectrometry-based approach for the profiling of N-glycans in biofluids	Post-translational Modifications	P193	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
230	Loïc Herpin, Emmanuelle Bichon, Laure Beucher, Fabrice Monteau and Bruno Le Bizec. Ultra-high performance supercritical fluid chromatography coupled to time of flight mass spectrometry to monitor β -agonists in animal breeding.	Food & environmental analysis	P194	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
231	Philippe Wolff, Philippe Hammann, Lauriane Kuhn and Johana Chicher. Fast characterization of RNA modifications by MALDI-TOF.	Integrative genomics	P195	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
234	Ūnige A. Laskay, Kristina Srzentić, Tanja Panić-Janković, Michel Monod, Goran Mitulović and Yury O. Tsybin. Middle-Down Proteomic Analysis of Embryonic Proteins Secreted Prior to In Vitro Fertilization	Disease Biomarkers	P196	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
235	Haifa Benmoussa, Sonia Hem, Valerie Rofidal, Mathilde Decourcelle, Jean Benoit Peltier and Yann Froelicher. Comparative proteome and phosphoproteome analysis of style investigate the gametophytic self-incompatibility mechanisms of Citrus clementina.	Quantitative Proteomics	P197	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
236	Florence Petit, Nazha Sidahmed-Adrar, Nassima Benzoubir, Cosette Abdallah, Delphine Pflieger, Marie-Françoise Bourgeade and François Le Naour. Identification of integrin--linked kinase (ILK) as a protein phosphorylated by both HCV core expression and TGF-- β using a quantitative phosphoproteomic SILAC approach	Quantitative Proteomics	P198	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
237	Céline Ribiere, Christophe Chambon, Didier Viala, Mickaël Desvaux and Michel Hebraud. Exploring the Listeria monocytogenes surfaceome by cell envelope shaving and LC-MS/MS analysis	Plant, microbial and model organisms proteomics (IMOP session)	P199	1	Oct 15 - 8:00 to Oct 16 - 12:00 noon
238	Cédric Pionneau, Jean-Yves Brossas, Solenne Chardonnet, Odette Poirier, Mélanie Eyries, Barbara Girerd, David Montani, Marc Humbert and Florent Soubrier. Screening of pulmonary arterial hypertension (PAH) plasma biomarkers using protein fractionation and MALDI-TOF mass spectrometry profiling	Disease Biomarkers	P200	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
240	Frédéric Delolme, Cyril Anastasi, Pasacaline Lécorché, Jimmy Mevaere, Isabelle Zanella-Cléon, Christopher Overall, Vincent Dive and Catherine Moali. N-terminomics reveals new aspects of the activity and specificity of BMP-1/tolloid-like proteinases : consequences for tissue repair and inhibitor design	Functional Proteomics	P201	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
241	Geraldine Lucchi, Emilie Simon, Christine Arnould, Jeannine Lherminier, Patrick Ducoroy and Lionel Bretillon. Proteomic analysis of sub-retinal deposits in Age-related Macular Degeneration	Disease Biomarkers	P202	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
242	Sandra Renier, Christophe Chambon, Ludovic Bonhomme, Michel Hebraud and Mickaël Desvaux. Deciphering the lipoprotein maturation pathway in Listeria monocytogenes by LC-MS/MS label-free quantitative approach	Plant, microbial and model organisms proteomics (IMOP session)	P203	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
244	Barbara Deracinois, Erwan Dupont, Sophie Duban-Deweere, Luc Camoin, Elodie Richard, Matthias Lambert, Bruno Bastide and Caroline Cieniewski-Bernard. Study of the Phosphorylation/O-GlcNAcylation interplay in differentiated C2C12 myotubes: focus on the PI3K/AKT/mTOR pathway.	Post-translational Modifications	P204	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
245	Mårten Sundberg, Margareta Ramström and Jonas Bergquist. Mass Spectrometry-based Proteomics of Dog Cerebrospinal fluid	Plant, microbial and model organisms proteomics (IMOP session)	P205	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
246	Clarissa Dickhut and René Zahedi. Impact of digestion conditions on phosphoproteomics	Post-translational Modifications	P206	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
247	Virginie Brun, Clémence Arrivé, Pascale Delangle, Elisabeth Mintz, Michel Ferrand, Christophe Bruley and Michel Jaquinod. MS-based approaches for studying the pharmacokinetics of an innovative liver-targeted copper-chelator in Atp7b-/- mice used as a model for studies of Wilson's disease.	Disease Biomarkers	P207	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
248	Amandine Anastacio, Solenne Chardonnet, Cédric Pionneau, Christian Federici, Teresa Almeida-Santos and Catherine Poirot. Comparative proteomic analysis of mice ovarian follicles at three different stages during in vitro development	Functional Proteomics	P208	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
249	Aïcha Bagag, Jean-Michel Jault, Nazha Sidahmed-Adrar, Matthieu Réfrégiers, Alexandre Giuliani and François Le Naour. Characterization of hydrophobic peptides in the presence of detergent by photoionization mass spectrometry	Fragmentation	P209	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
250	Camille Garcia, Marwa Ounissi, Audrey Combès, Jean-Michel Camadro and Thibaut Léger. Unraveling the complexity of the HEM14 locus in Saccharomyces cerevisiae: a label-free proteomics approach	Integrative genomics	P210	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
251	Julie Le Faouder, Samira Laouirem, Theodore Alexandrov, Thibaut Leger, Jean-Michel Camadro, Pierre Bedossa and Valerie Paradis. MALDI imaging mass spectrometry of intrahepatic cholangiocarcinoma: a relevant approach for assessment of specific tumor biomarkers	Imaging Mass Spectrometry	P211	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
252	Carole Pichereaux, Marizel Astello, María Del Socorro Santos Diaz, Antonio Reyes-Agüero, Françoise Guéraud, Anne Negre-Salvayre, Bernard Monsarrat, Odile Schiltz, Ana Paulina Barba de La Rosa and Michel Rossignol. Comparative proteomic analysis of Opuntia spp. in relation with its domestication process.	Plant, microbial and model organisms proteomics (IMOP session)	P212	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
253	Marven El Osta, Fabien Remy-Martin, Caroline Truntzer, Wilfrid Boireau and Patrick Ducoroy. The Quantification by SUPRA-MS platform. A multiplexed label-free approach to characterize and quantify markers in Human Plasma, by direct SPRI-MALDI-MS Analysis from Antibody Arrays	Quantitative Proteomics	P213	2	Oct 16 - 12:00 noon to Oct 17 - 16:00

254	Catarina Franco, Bruno Pedras, André Guerra, Sam Dupont and Ana Varela Coelho. Coelomic epithelium as stem cell origin during echinoderm regeneration events? A proteomic characterization	Plant, microbial and model organisms proteomics (IMOP session)	P214	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
255	Grégoire Harichaux, Karine Reynaud, Valérie Labas, Sandra Thoumire, Muhammad Zahid Tahir and Marie Saint-Dizier. Proteomic changes in the oviductal fluid at the time of meiosis resumption and fertilization following a progesterone antagonist treatment in the bitch	Quantitative Proteomics	P215	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
256	Geoffrey Hinsinger, Nathalie Galéotti, Serge Urbach, Nicolas Nabholz, Oana Vigy, Sylvain Lehmann, Valérie Rigau, William Camu, Martial Séveno, Joël Bockaert, Philippe Marin and Eric Thouvenot. Quantitative Analysis of Cerebrospinal Fluid Proteome Reveals Candidate Biomarkers for Multiple Sclerosis Diagnosis and Prognosis	Disease Biomarkers	P216	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
257	Marwa Ounissi, Camille Garcia, Jean-Michel Camadro and Thibaut Léger. Proteomics analysis of the metacaspase MCA1 targets in <i>Candida albicans</i> under apoptosis conditions.	Functional Proteomics	P217	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
259	Elisabete Pires, Isabel Marcelino, Nathalie Vachiéry, Thierry Lefrançois, Gabriel Mazzuchelli, Edwin de Pauw and Ana Coelho. Changes on host cell proteome upon infection with the Rickettsiales <i>Ehrlichia ruminantium</i>	Plant, microbial and model organisms proteomics (IMOP session)	P218	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
260	Sandrine Aros-Calt, Céline Ducruix, Samia Boudah, Guillaume L'Hostis, Bruno Muller, Christophe Junot and François Fenaille. Development of an LC-HRMS-based metabolomic approach to study methicillin-resistant <i>Staphylococcus aureus</i> .	Environmental proteomics & metabolomics	P219	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
261	Cristian Piras, Alessio Soggiu, Viviana Greco, Luigi Bonizzi, Andrea Urbani and Paola Roncada. Shotgun MS analysis of enrofloxacin resistant <i>E. coli</i> isolate	Plant, microbial and model organisms proteomics (IMOP session)	P220	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
262	Bros Pauline, Vialaret Jérôme, Lehmann Sylvain, Gabelle Audrey, Delatour Vincent and Hirtz Christophe. Absolute quantification of beta amyloid peptide 1-38, 1-40 and 1-42 in human CSF by nanoLC-QqQ	Disease Biomarkers	P221	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
263	Magali Court, Guillaume Nugue, Christophe Bruley, François Berger and Virgginie Brun. Investigation of plasma proteome turnover using metabolic labelling and accurate mass and time tag (AMT) strategy	Functional Proteomics	P222	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
264	Rémy Puppo, Goetz Parsieglia, Frédéric Carrière and Régine Lebrun. Rapid Screening Of Cyanobacteria Lipid Composition By TLC-MALDI-ToF	Environmental proteomics & metabolomics	P223	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
265	Mathilde Franci-Allami, Marija Pavlovic, Hélène Rogniaux, Cécile Albenne, Kahina Merah, Richard Sibout, Virginie Lollier, Fabienne Guillon, Elisabeth Jamet and Colette Larré. First identification of cell wall proteins of <i>Brachyopodium distachyon</i> grains	Plant, microbial and model organisms proteomics (IMOP session)	P224	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
266	Miguel Ventosa, Elisabete Pires, André Almeida, Natalie Vachiéry, Thierry Lefrançois, Ana Coelho and Isabel Marcelino. STUDYING EHRlichia RUMINANTIUM PROTEOME: TOWARDS THE IMPROVEMENT OF HEARTWATER VACCINE.	Plant, microbial and model organisms proteomics (IMOP session)	P225	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
267	Christelle Absalon, Sandy Fabre, Claire Mouche, Noel Pinaud, Christiane Venencie, Pierre-Louis Teisseidre, Eric Fouquet and Isabelle Pianet. Isolation and Characterization by HRMS and NMR of a new compound in Red Wine	Food & environmental analysis	P226	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
268	Nazha Sidahmed-Adrar and François Le Naour. The tetraspanin network in the liver	Interactomics	P227	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
269	Samira Laouirem, Julie Le Faouder, Theodore Alexandrov, Denis Mestivier, Thibaut Léger, Xavier Baudin, Mouniya Mebarki, Valérie Paradis, Pierre Bedossa and Jean-Michel Camadro. MALDI imaging mass spectrometry reveals novel ubiquitin modification as a biomarker of cirrhosis progressing to hepatocellular carcinoma	Disease Biomarkers	P228	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
270	Nadezda Kiselova, Dorothe Spillmann and Margareta Ramström. A MALDI-TOF MS-based Method for Analysis of Sulfated Glycosaminoglycans	Post-translational Modifications	P229	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
271	Mathieu Trauchessec, Michel Jaquinod, Virginie Brun, Christophe Bruley, Delphine Ropers, Hidde De Jong, Jérôme Garin, Gwenaëlle Bestel-Corre and Myriam Ferro. Development of an absolute and multiplex MS-based quantification method for <i>E. coli</i> central metabolism enzymes: application for systems biology purposes.	Plant, microbial and model organisms proteomics (IMOP session)	P230	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
273	Maureen Ramero, Mikael Levi and Stephane Moreau. Sensitive assay of free thyroid hormones by online SPE-UHPLC-MS/MS in human plasma	Disease Biomarkers	P231	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
274	Eric Capodanno, Stephane Moreau and Mikael Levi. Rapid simultaneous assay of 25 mycotoxins in a variety of food samples by UHPLC-MS/MS using fast polarity switching.	Food & environmental analysis	P232	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
275	Rawane El Kouba, Cécile Bonnefont, Alain Vignal, Michel Boullier-Oudot, Jean-Pierre Dubois, Julien Arroyo, Christophe Chambon, Nathalie Marty-Gasset, Emmanuelle Labarthe and Caroline Molette. Effects of fasting period duration before slaughtering on the physiology of fatty liver in overfed ducks: proteomics and transcriptomics analyses	Systems Biology	P233	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
276	Simone Lemeer, Benjamin Ruprecht, Heiner Koch, Max Mundt and Bernhard Kuster. Old tools in a new jacket: phosphopeptide enrichment by IMAC, Ti-IMAC and TiO2 columns	Post-translational Modifications	P234	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
277	Fanny Duguet, Marlène Marcellin, Céline Colacios, Odile Schiltz, Bernard Monsarrat, Abdelhadhi Saoudi and Anne Gonzalez de Peredo. Large-scale, label-free quantitative proteomic characterization of regulatory versus conventional T lymphocytes isolated from mouse	Quantitative Proteomics	P235	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
278	Mathilde Louwagie, Kieffer-Jaquinod Sylvie, Véronique Dupierris, Yohann Couté, Christophe Bruley, Jérôme Garin, Alain Dupuis, Michel Jaquinod and Virginie Brun. Introducing AAA-MS, a rapid and sensitive method for amino acid analysis using isotope dilution and high-resolution mass spectrometry.	Quantitative Proteomics	P236	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
279	Jia-Xuan Chen, Florian E. Paul, Miyeko Mana, Kristin C. Gunsalus, Fabio Piano and Matthias Selbach. Analysis of protein-protein interaction by in vivo quantitative proteomics during <i>C. elegans</i> embryogenesis	Interactomics	P237	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
280	Laila Sago, David Cornu and Virginie Redeker. MALDI-MS/MS: advantages and limitations of this top-down approach in the identification and characterization of proteins.	Fragmentation	P238	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
281	Mikael Levi, Maureen Ramero and Stephane Moreau. Fast Screening of Mobile Phases Additives and Solvents for Optimum Sensitivity in LC-MS: Comparison of Ionization Behavior between ESI and HESI	Instrumentation	P239	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
282	Virginie Bertrand, Yi-Shiang Huang, Gabriel Mazzuchelli, Dimitriya Bozukova, Christophe Pagnouille, Marie-Christine Durrieu, Edwin de Pauw and Marie-Claire Gillet. Polymer based intraocular lens adsorbome: a bottom up proteomics study	Quantitative Proteomics	P240	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
284	Olivier Langella, Benoit Valot and Michel Zivy. SIROCCO: a real life solution to the bioinformatics needs for high-throughput proteomics based on standard hardware and free softwares	Bioinformatics	P241	2	Oct 16 - 12:00 noon to Oct 17 - 16:00

286	Edith Nicol, Yannick Lassalle, Stéphane Bouchonnet and Sophie Bourcier. Electron-Induced Dissociation as a complementary tool of CID for structural characterization of pesticides	Fragmentation	P242	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
288	Marianne Ibrahim, Lauriane Kuhn, Philippe Hammann, Ramez Chahine, Zeina Dagher and Emmanuelle Leize-Wagner. Time-course secretome analysis using Label-Free MS1 quantitative proteomic method to reveal differentially expressed proteins in hepatic human cells exposed to benzo(a)pyrene	Quantitative Proteomics	P243	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
289	Yannick Lassalle, Ahmad Rifai, Yasmine Souissi, Carine Clavaguera, Sophie Bourcier, Farouk Jaber and Stéphane Bouchonnet. UV-visible phototransformation of boscalid – structural characterization of photoproducts and potential toxicity	Food & environmental analysis	P244	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
291	Yury Glazyrin, Olga Kolovskaya, Anna Zamay, Ekaterina Spivak, Galina Zamay, Maxim Berezovski and Tatiana Zamay. Identification of the cellular protein targets for antitumor DNA-aptamers	Functional Proteomics	P245	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
292	Florence Roux-Dalvai, Marlène Marcellin, Odile Bulet-Schiltz, Bernard Monsarrat and Anne Gonzalez de Peredo. Global versus Targeted Proteomics: a comparison of LTQ-Orbitrap Velos, 5500QTrap and QExactive instruments for detection and quantification of low abundance proteins	Quantitative Proteomics	P246	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
293	Ali Bouamrani, Céline Leclech, Adrien Mombrun, François Berger and Alim Louis Benabid. From Deep Brain Stimulation to Brain Biomarker Interface Using Micro/Nano – Strategies	Disease Biomarkers	P247	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
294	Dusan Velickovic, David Ropartz, Sylvie Durand, Luc Saulnier, Fabienne Guillon and Héléne Rogniaux. Mapping of polysaccharides in wheat grain cell walls by MALDI imaging	Imaging Mass Spectrometry	P248	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
295	Yutaka Sugihara, Charlotte Weinder, Ákos Végvári and György Marko-Varga. Distribution of kinase inhibitors in malignant melanoma tissue by MALDI mass spectrometry imaging	Imaging Mass Spectrometry	P249	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
296	Raphaël Bilgraer, Sylvie Gillet and Olivier Laprévotte. GLOBAL DIFFERENTIAL PROTEOMIC APPROACH FOR EXPLORING THE HISTONE CODE	Environmental proteomics & metabolomics	P250	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
297	Szilvia Török, Ákos Végvári, György Marko-Varga, Thomas Fehniger, József Tóvári, Sándor Paku, József Timár, Balázs Hegedűs and Balázs Döme. Detection and efficacy of antiangiogenic RTKs in experimental tumors	Imaging Mass Spectrometry	P251	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
298	Francesc Canals, Joan-Josep Bech-Serra, Núria Colomé-Calls, Salvador Martínez de Bartolomé, Jim J. Walters, Kevin B. Ray, Juan Pablo Albar and Proteored-Isciii Consortium. Proteored Multicentric Experiment 8: Quantitative Targeted Analysis in Proteomics. An Assessment Study. (PME8-QTAPAS)	Quantitative Proteomics	P252	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
299	Gabriela Justamante Handel Schmitz, Beatriz Cordenunsi, Teresa Valle, Carlos Labate and João Nascimento. Comparative proteome analysis of the tuberous roots of sweet and bitter cassava (Manihot esculenta Crantz) varieties	Plant, microbial and model organisms proteomics (IMOP session)	P253	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
300	Lyna Sellami, Claude Villard, Matthew E. Openshaw, Roberto Castangia, Jean-Michel Brunel, Pascale Barbier, Omar Belgacem and Daniel Lafitte. Combining LC-MALDI and in-source decay analysis for the characterization of oxidatively modified residues of Tau protein	Post-translational Modifications	P254	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
301	Tiphaine Cecchini, Elodie Degout-Charrette, Yannick Charretier, Ana Mendes-Moreira, Christine Franceschi, Olivier Dauwalder, Tanguy Fortin, Xavier Lacoux, Gilles Zambardi, Nadine Perrot, Dominique Dechaume, Alain Theretz, Victoria Girard, Arnaud Salvador, Géraldine Durand, Sonia Chatellier, Gaspard Gervasi, Jerome Lemoine, Francois Vandenesch and Jean-Philippe Charrier. Rapid detection of beta-lactamases in Gram negative bacteria using Selected Reaction Monitoring Mass Spectrometry	Plant, microbial and model organisms proteomics (IMOP session)	P255	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
302	Alisson Opsomer, Luc Garrigues, Mohamed Benama, Florence Roux-Dalvai, Sebastian Vaca, Annie Adrait, Agnès Hovasse, Amandine Boeuf, Marie-Pierre Bousquet, Alexandre Stella, Christine Schaeffer, Myriam Ferro, Odile Schiltz, Anne Gonzalez de Peredo, Alain Van Dorsselaer, Bernard Monsarrat, Jérôme Garin and Christine Carapito. Establishment of a performance evaluation standard for LC-SRM targeted quantification platforms	Quantitative Proteomics	P256	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
303	Arnaud Goyallon, Francois Perreau, Francois Fenaille, Christophe Junot and Gregory Mouille. Development of a mass spectrometry-based approach for the profiling of N-glycans in plant.	Post-translational Modifications	P257	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
304	Tassadit Ouidir, Frédérique Jarnier, Pascal Cosette, Thierry Jouenne and Julie Hardouin. N-terminal acetylome of Pseudomonas aeruginosa PA14	Plant, microbial and model organisms proteomics (IMOP session)	P258	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
305	Aurelie Tacheny, Marc Dieu and Patsy Renard. Gel-free proteomic analysis of proteins interacting with a regulatory DNA sequence	Interactomics	P259	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
306	Mathilde Decourcelle, Jérémy Duval, Hajar Chouiki, Valérie Rofidal, Sonia Hem and Véronique Santoni. Quantitative label-free of maize endosperm enriched in carotenoids	Quantitative Proteomics	P260	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
307	Manuel Chapelle, Pierre-Olivier Schmit, Sabine Jourdain, Markus Lubeck, Ralf Hartmer, Oliver Raheter and Carsten Baessmann. Characterization of proteomics performance of a novel collision cell for ultrahigh resolution time of flight mass spectrometers (UHR-TOF)	Instrumentation	P261	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
308	Mathieu Riffault, David Moulin, Laurent Grossin, Patrick Netter, Didier Mainard, Jacques Magdalou and Jean-Baptiste Vincourt. Feasibility of label-free relative quantification in proteomics from LC-MALDI data: Application and limits in the investigation of chondrocyte secretion regulation by TGFbeta1	Quantitative Proteomics	P262	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
310	M Bourderioux, C Chhuon, T Nguyen-Khoa, N Cagnard, J F Jais, E Escudier, B Escudier, A Edelman and I C Guerrero. Analysis of urinary exosomes by mass spectrometry: towards clinical application.	Disease Biomarkers	P263	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
311	Virginie Redeker, Laura Pieri, Philippe Chafey, Morgane Le Gall, Guilhem Clary, Willy Bienvenu and Ronald Melki. Proteomic analysis of the cellular response to toxic alpha-synuclein aggregates involved in Parkinson's disease	Post-translational Modifications	P264	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
312	Thierry Sayd, Christophe Chambon, Delphine Centeno and Veronique Santéé-Lhoutellier. Label-free study of peptides released during in vitro digestion of bovine cooked meat	Bioactive substances	P265	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
313	Olivier Pible, François Allain and Jean Armengaud. Phyloproteomics, a new approach for metaproteomics of complex samples	Environmental proteomics & metabolomics	P266	2	Oct 16 - 12:00 noon to Oct 17 - 16:00

314	Sophie Chocu, Frédéric Chalmel, Régis Lavigne and Charles Pineau. Identifying novel molecular actors of spermatogenesis in the rat using Proteomics Informed by Transcriptomics	Integrative genomics	P267	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
316	Jean-Philippe Menetrey, Véronique Dupieris, Myriam Ferro, Jérôme Garin and Christophe Bruley. Proline Studio GUI : a user-friendly, fast and multi-threaded software for visualization and analysis of Proteomics Data.	Bioinformatics	P268	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
317	Evelyne Maes, Geert Baggerman, Dirk Valkenburg, Mathias Wenes, Liliane Schoofs, Massimiliano Mazzone and Inge Mertens. Elucidation of the proteomic signature of macrophages in tumour microenvironments	Quantitative Proteomics	P269	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
318	Emie Durighello, Alain Lorphelin, Laurent Bellanger, Eric Ezan and Jean Armengaud. Francisella tularensis detection in complex media using magnetic immunocapture enrichment and mass spectrometry.	Environmental proteomics & metabolomics	P270	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
319	Matthew S. F. Choo, Roberto Castangia, Omar Belgacem and Anne Dell. Structural elucidation of N-glycans originating from ovarian cancer cells using High Vacuum MALDI mass spectrometry	Disease Biomarkers	P271	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
320	Athanassios Anagnostopoulos, Aggeliki Katsafadou, George Arsenos, Ioannis Skoufos, Athina Tzora, Spiros Karkabounas, George Fthenakis and George Tsangaris. Proteomic analysis of blood and milk from the Greek indigenous Capra prisca goat breed.	Food & environmental analysis	P272	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
321	Sophie Liuu, Emmanuelle Demey-Thomas, Emie Durighello, Gilles Gâteau and Joëlle Vinh. Subtyping of amyloidosis by direct targeted proteomic analysis of fixed biopsy samples	Disease Biomarkers	P273	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
322	Damien Joulié, Jean-Baptiste Boyer, Arnaud Lagorce, Fabrice Confalonieri, Jean Armengaud and Alain Dedieu. New deal from proteomic data for the radioresistant archaeon Thermococcus Gammatolerans.	Plant, microbial and model organisms proteomics (IMOP session)	P274	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
323	Mathilde Beau, Florence Roux-Dalvai, Marie-Laure Renoud, Luc Sensébé, Bernard Monsarrat, Anne Gonzalez de Peredo and Odile Burlet-Schiltz. Large-scale characterization of Adipocyte derived stem cells nuclear proteome by two generation of orbitraps.	Quantitative Proteomics	P275	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
324	Yann Verdier, Iman Haddad, Karim Majzoub, Jules Hoffmann, Jean-Luc Imler and Joëlle Vinh. Dicer2-Argonate2-R2D2 interaction network during antiviral response in D. melanogaster cells.	Functional Proteomics	P276	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
325	Camille Detree, François Lallier, Jean Mary and Fanny Gaillard. Proteomic analysis of the symbiosis of a deep sea hydrothermal vent mussel: Bathymodiolus azoricus	Environmental proteomics & metabolomics	P277	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
326	Chiara Giangrande, Pascal Poncet, Hélène Sénéchal and Joelle Vinh. Characterization of carbohydrates modifications in Grass Pollen Group 13 Allergens.	Post-translational Modifications	P278	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
327	Matthew Openshaw, Yuzo Yamazaki, Omar Belgacem and Takeshi Kawamura. Differentiation of Symmetric/Asymmetric Dimethylated Arginine-containing Peptides using MALDI-TOF-TOF Mass Spectrometry	Post-translational Modifications	P279	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
328	David Bouyssié, Véronique Dupieris, Nicolas Barthe-Dejean, Alexandre Burel, Christine Carapito, Marc Dubois, Laurent Martin, Jean-Philippe Menetrey, Alexandre Walter, Bernard Monsarrat, Odile Burlet-Schiltz, Alain Vandorssaeler, Sarah Cianferani, Myriam Ferro, Jérôme Garin and Christophe Bruley. Proline, a data integration framework and a software suite for mass spectrometry based Proteomics	Bioinformatics	P280	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
329	Nicolas Barthe-Dejean, David Bouyssié, Bernard Monsarrat, Odile Burlet-Schiltz, Jerome Garin and Christophe Bruley. Proline Web GUI: a rich web interface for a remote access to Proline tools, data and related online proteomics resources	Bioinformatics	P281	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
330	Lemoine Jerome, Tanguy Fortin, Jean-Philippe Charrier, Corinne Beaulieu, Elodie Charmette, Frederique Steinbrugger, Come Lepage, Jean Faivre and Genevieve Choquet-Kastylevsky. Biomarker verification: assessment of the performances of LFABP as new CRC marker on 4 independent cohorts of 798 patients, using ELISA, MRM and MRM3. Detection of CRC early stages and adenomas.	Disease Biomarkers	P282	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
331	Marie-Anne Maubert, Elodie Quévrain, Jean Pierre Grill, Dominique Rainteau, Germain Trugnan, Jean Claude Tabet, Joelle Masliah and Carlos Afonso. High-resolution mass spectrometry and partial de novo sequencing constitute a useful approach for determining the profile of chemokine secretion following the stimulation of human intestinal epithelial cells.	Disease Biomarkers	P283	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
332	Giovanni Chiappetta, Shakir Shakir and Joelle Vinh. Profiling the cysteine redox proteome by isobaric Tandem Mass Tag reagents	Post-translational Modifications	P284	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
333	Stéphane Chaignepain, Alfred Améadan, Delphine Lapaillerie, Vincent Parissi, Marc Bonneau and Jean-Marie Schmitter. Chemical crosslinking and mass spectrometry for protein-protein and protein-ligand interaction studies: multifaceted application to the retroviral HIV-1 integrase	Interactomics	P285	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
334	Jennifer Dieppedale, Gael Gesbert, Elodie Ramond, Cerina Chhuon, Iharilalao Dubail, Marion Dupuis, Ida Chiara Guerrero and Alain Charbit. Possible links between stress defense and the tricarboxylic acid cycle in Francisella pathogenesis	Interactomics	P286	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
335	Mehdi Ghaffari, Mahmoud Toorchi, Mostafa Valizadeh and Sedighe Haji Hoseinlou. Proteomic acclimation of sunflower to drought stress	Plant, microbial and model organisms proteomics (IMOP session)	P287	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
336	Arlene Dsilva. The identification of biomarkers potentially predictive for intrauterine growth restriction and macrosomia in term pregnancies	Disease Biomarkers	P288	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
337	Stéphanie Devaux, Dasa Cizkova, Julien Franck, Françoise Croq, Maxence Wisztorski, Lucia Slovinska, Ivana Grulova, Christophe Lefebvre, Isabelle Fournier and Michel Salzet. Proteomic analyses along the rostro-caudal axis of injured spinal cord	Functional Proteomics	P289	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
338	Pierrick Lucas, Hélène Rogniaux, Colette Larré, Virginie Lollier, Charles-Henri Van Nuvel and Dominique Tessier. Benchmarking of peptide retention time prediction algorithms	Bioinformatics	P290	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
339	Jianqing Wu, Pierre-Damien Coureux, Yves Méchulam, Emmanuelle Schmitt and Guillaume van der Rest. Binding regions of the eucaryotic initiation factor 3 (eIF3) subunits unveiled by high resolution mass spectrometry and amide hydrogen / deuterium exchange	Interactomics	P291	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
340	Iman Haddad, Marie Monet-Leprêtre, Céline Baron-Menguy, Maï Panchal, Meriem Riani, Valérie Domenga-Denier, Claire Dussaule, Emmanuel Cognat, Anne Joutel and Joëlle Vinh. Abnormal recruitment of extracellular matrix proteins by excess Notch3ECD in CADASIL	Functional Proteomics	P292	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
341	Emma-Dune Leriche, Marie Hubert-Roux, Martin Grosseil, Catherine Lange, Carlos Afonso and Corinne Loutelier-Bourhis. Direct TLC/MALDI-MS coupling for PAMAM dendrimers analyses	Polymers	P293	2	Oct 16 - 12:00 noon to Oct 17 - 16:00

342	Marlène Marcellin, Claire Ramus, Agnès Hovasse, Anne-Marie Hesse, David Bouyssie, Florence Roux-Dalvai, Sebastian Vaca, Christine Schaeffer, Christine Carapito, Myriam Ferro, Odile Schiltz, Sarah Cianférani, Yohan Couté, Alain Van Dorssaeler, Bernard Monsarrat, Jérôme Garin and Anne Gonzalez de Peredo. Evaluation of different bioinformatics workflows for the detection of variant proteins in complex mixtures by label free quantitative methods	Quantitative Proteomics	P294	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
343	Julien Franck, Celine Meriaux, Dan Bi Park, Jusai Quanico, Young Mok Park, Michel Salzet and Isabelle Fournier. Human Temporal lobe epilepsy: MALDI mass spectrometry imaging and tissue proteomic studies	Imaging Mass Spectrometry	P295	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
344	Ana Maria Gutiérrez, María Fuentes-Rubio, Ingrid Miller and José Joaquín Cerón. GLYCOPROTEIN PATTERNS IN PIG SALIVA USING PHENYL BORONIC ACID LIGAND: INITIAL STUDY	Plant, microbial and model organisms proteomics (IMOP session)	P296	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
345	Karim Arafah, Lida Yang, Nicolas Vancampenhout, Philippe Bulet and Patrice Marche. Differential proteomic analysis using MALDI imaging in a mice model	Imaging Mass Spectrometry	P297	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
346	Véronique Hourdel, Magalie Duchateau, Christian Malosse, Joseph Gault, Marie-Cécile Ploy, Guillaume Duménil and Julia Chamot-Rooke. Proteome Analysis of invasive clinical strains of Neisseria meningitidis Serogroup C	Plant, microbial and model organisms proteomics (IMOP session)	P298	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
347	Eugenio Galano, Erika Mangiapane, Juliusz Bianga, Angelo Palmese, Enrica Pessione, Joanna Szpunar, Ryszard Lobinski and Angela Amoresano. Selective incorporation of selenium as selenocysteine in Lactobacillus reuteri by laser ablation - ICP MS and proteomics approach	Plant, microbial and model organisms proteomics (IMOP session)	P299	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
348	Frederic Chalmel, Laetitia Cloarec, Olivier Sallou, Emmanuelle Com, Regis Lavigne, Lydie Lane and Charles Pineau. PepPSy: a protein prioritization system for the chromosome-centric Human Proteome Project	Human Proteome Project (HPP)	P300	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
349	Rosa Viner, Ryan Bomgarden, Michael Blank, Claire Dauly and John Rogers. Increasing the Multiplexing of Protein Quantitation from 6- to 10-Plex with Reporter Ion Isotopologues	Quantitative Proteomics	P301	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
350	Charles-Henri Van Nuvel, Hélène Rogniaux, Colette Larré, Virginie Lollier, Pierrick Lucas and Dominique Tessier. Relationship between quality of spectra and peptide-spectrum matches	Bioinformatics	P302	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
352	Alain Rouleau, Marven El Osta, Carole Chaix, Patrick Ducoroy and Wilfrid Boireau. Evolution of the biochip-MS readout by using synthetic ligands for the detection and characterization of thrombin	Disease Biomarkers	P303	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
353	Reiko Kiyonami, Michael Senko, Vlad Zabrouskov, Michael MacCoss, Madalina Oppermann, Andreas Hühmer and Claire Dauly. Large scale targeted protein quantification using HR/AM selected ion monitoring with MS/MS confirmation on a novel hybrid, Q-OT-qIT mass spectrometer	Quantitative Proteomics	P304	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
354	Emmanuelle Demey-Thomas, Sophie Liuu, Emie Durighello, Gilles Grateau and Joelle Vinh. Ultrasonic treatment in Proteomic studies: direct processing of biopsy samples for subtyping of amyloidosis.	Disease Biomarkers	P305	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
355	Reiko Kiyonami, Mary Blackburn, Martin Hornshaw, Claire Dauly and Andreas Hühmer. Improved throughput and reproducibility for targeted protein quantification using a new high performance triple quadrupole mass spectrometer	Quantitative Proteomics	P306	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
356	Julie Bertrand, Rima Ait-Belkacem, Amel Boubekr, Claude Villard, Dominique Lombardo, Eric Mas and Daniel Lafitte. MALDI in-source decay imaging for identification of pancreatic cancer biomarkers.	Imaging Mass Spectrometry	P307	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
357	Attila Aranyos. New Tools and Methods for Label-Free Characterization of Biotherapeutic Molecules	Functional Proteomics	P308	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
358	Audebert Stephane, Belotti Edwige, Polanowska Jola, Daulat Avais, Thome Virginie, Lissitzky Jean Claude, Lembo Frederique, Bible Karim, Omi Shizue, Lenfant Nicolas, Gangar Akanksha, Montcouquiol Mireille, Santoni Marie-Josée, Sebbagh Michael, Aurrand-Lions Michel, Angers Stephane, Kodjabachian Laurent, Reboul Jerome and Borg Jean-Paul. The human PDZome: a gateway to PDZ mediated functions	Interactomics	P309	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
359	Claude Villard, Rima Ait-Belkacem, Julie Bertrand, Segha Ndiaye, Lyna Sellami, François Gray, Thérèse Schembri and Daniel Lafitte. MALDI in source decay imaging for identification of biomarkers of solid tumors	Imaging Mass Spectrometry	P310	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
360	Yue Xuan, Jarrett Egerton, Andreas Kühn, Michael Maccoss, Jocelyn Dupuy, Claire Dauly and Markus Kellmann. Data-independent Acquisition (DIA) Analysis on the Q Exactive Mass Spectrometer	Quantitative Proteomics	P311	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
361	Shakir Shakir, Giovanni Chiappetta, Michel Toledano and Joëlle Vinh. Developing a specific multiplex analytical strategy for redox proteomics	Post-translational Modifications	P312	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
362	Vital Vialas, Zhi Sun, Carla Veronica Loureiro, Montserrat Carrascal, Joaquin Abian, Lucía Monteoliva, Eric W Deutsch, Ruedi Aebersold, Robert L Moritz and Concha Gil. A Candida albicans PeptideAtlas	Bioinformatics	P313	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
363	Ana Gil de Bona, Lucia Monteoliva and Concha Gil. COMPARATIVE PROTEOMIC ANALYSIS OF SECRETED PROTEINS AND EXTRACELLULAR VESICLES FROM CANDIDA ALBICANS	Plant, microbial and model organisms proteomics (IMOP session)	P314	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
364	Annamarie Matthes, Marie-Hélène Montane, Benoit Menand, Régine Lebrun, Christian Meyer and Christophe Robaglia. Decoding Target of Rapamycin signalling pathways in Arabidopsis thaliana using ATP-competitive inhibitors and phosphoproteomics	Plant, microbial and model organisms proteomics (IMOP session)	P315	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
365	Cristina Neri, Laura Lovato, Valeria Marzano, Stefano Levi Mortera, Chiara Cavaliere, Anna Laura Capriotti Capriotti, Luisa Pieroni, Antonio Uccelli and Andrea Urbani. Comprehensive identification of the soluble factors involved in mesenchymal stem cells-mediated neuroprotection utilizing the SILAC approach	Systems Biology	P316	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
366	Matthieu Pophillat, Julie Lima Da Silva and Samuel Granjeaud. Sharing DIGE results as simple as a web browser	Bioinformatics	P317	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
367	Aida Pitarch, César Nombela and Concha Gil. Decoding serologic response to invasive candidiasis in non-neutropenic patients: From biomarker discovery to assay validation	Disease Biomarkers	P318	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
368	Syeda S. Quadri, Robert E. Stratford, Stephen M. Boué and Richard B. Cole. Identification of Glyceollin Metabolites in Rats Derived from Conjugation with Glutathione and Glucuronic Acid by On-Line Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometry	Environmental proteomics & metabolomics	P319	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
369	Arnaud Day, Stéphane Fénart, Godfrey Neutelings, Simon Hawkins, Christian Rolando and Caroline Tokarski. Comprehensive identification of cell wall proteins in the flax (Linum usitatissimum) stem	Plant, microbial and model organisms proteomics (IMOP session)	P320	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
370	Sophie Dallongeville, Fabrice Bray, Christian Rolando and Caroline Tokarski. Top down proteomics applied to Cultural Heritage	Environmental proteomics & metabolomics	P321	2	Oct 16 - 12:00 noon to Oct 17 - 16:00

371	Jose A Reales-Calderon, Gloria Molero, Noemí Aguilera, Angel Corbí and Concha Gil. Human monocyte derived macrophages M1 and M2. Differential proteomics upon Candida albicans interaction.	Quantitative Proteomics	P322	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
372	Fabrice Bray, Christine Defer, Dominique Denis, Jean-Jacques Huart, Caroline Tokarski and Christian Rolando. Intact protein analysis to study oxidative stress: application to human plasma Apolipoprotein AI	Disease Biomarkers	P323	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
373	Sara Nasso, David Bouyssié, Marc Dubois, Odile Bulet-Schiltz, Bernard Monsarrat and Ruedi Aebersold. mzR3Db: an optimized file format for the efficient analysis of SWATH-MS data	Bioinformatics	P324	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
375	Samuel Barteau and Olivier Heudi. PROTEIN QUANTITATION - Challenges in developing LC-MS/MS method	Quantitative Proteomics	P325	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
376	Viviana Greco, Alida Spalloni, Alessandro Davoli, Alessio Soggiu, Nicola B. Mercuri, Paola Roncada, Patrizia Longone and Andrea Urbani. Proteomics analysis in spinal cord of SOD1G93A transgenic mice: the involvement of glial cells in motor neurons degeneration of Amyotrophic Lateral Sclerosis	Systems Biology	P326	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
377	Fabrice Bray, Akansha Ashvani Sehgal, Lionel Chiron, Marie-Aude Coutouly, Philippe Pelupessy, Geoffrey Bodenhausen, Marc-André Delsuc and Christian Rolando. 2D FT-ICR MS: a solving method for complex analytical problems	Instrumentation	P327	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
378	Evert-Jan Sneekes, Laurent Rieux, Mauro Depra, Christian Ravnsborg, Dafydd Milton and Remco Swart. Intact protein LC-MS, how to overcome the challenges?	Instrumentation	P328	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
380	Marieke Bruinsma, Hans Frank, Bharath Kumar, Valerie Bentivegna, Martijn Pinkse, Gerrit Melles and Peter Verhaert. QUANTITATIVE COMPARATIVE PROTEOMICS OF AQUEOUS HUMOR FROM HUMAN DONOR EYES FOR OPTIMIZED USE IN TRANSPLANTATION SURGERY.	Disease Biomarkers	P329	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
381	Anne-Catherine Vanhove, Wesley Vermaelen, Bart Panis, Rony Swennen and Sebastien Carpentier. The characterization of the HSP70 family during osmotic stress in a non-model crop via proteomics: beyond the 'usual suspects'?	Plant, microbial and model organisms proteomics (IMOP session)	P330	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
382	Shannon Eliuk, Jeffrey Johnson, Vlad Zabrouskov, Claire Dauly, Patrick Pankert and Nevan Krogan. Global in-depth quantitative proteomic analysis of HIV infected cells using a novel Q-OT-qIT mass spectrometer	Functional Proteomics	P331	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
383	Myriam Ferro, Sophie Le Gall, Lucas Moyet, Daniel Salvi, Sabine Brugière, Daphne Berny, Christophe Bruley and Norbert Rolland. Searching for proteins that follow an alternative targeting pathway to the Arabidopsis chloroplast: a proteomics approach	Plant, microbial and model organisms proteomics (IMOP session)	P332	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
384	Hiba Abdallah, Carine Arnaudguilhem, Farouk Jaber, Hugues Preud'Homme and Ryszard Lobinski. Use of high resolution mass spectrometry for the rapid determination of 25 sulfonamides and their metabolites in animal tissues	Food & environmental analysis	P333	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
385	Hugues Preud'Homme, Juliusz Bianga, Zahia Touat-Hamici, Sandra Mounicou, Kasia Bierla, Ryszard Lobinski, Joanna Szpunar and Laurent Chavatte. ORIGINAL ANALYTICAL STRATEGIES TO INCREASE THE (SELENO)PROTEIN IDENTIFICATION/QUANTIFICATION COVERAGE IN HUMAN CELL LINES	Quantitative Proteomics	P334	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
386	Carine Arnaudguilhem, Nicole Bec, Amina Bouslimani, Christian Larroque, Hugues Preud'Homme and Brice Bouysiere. Use of ICP MS and molecular mass spectrometry to study the metabolization of platinum anticancer drugs during peritoneal carcinomatosis HIPEC treatment	Disease Biomarkers	P335	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
387	Laurent Ouerdane, Federica Aureli, Paulina Flis, Katarzyna Bierla, Hugues Preud'Homme, Nagaraja Prakash and Joanna Szpunar. Complete screening of selenium metabolites in edible plant seeds (cereals and black mustard) by various chromatographic and MS-based techniques.	Inorganic mass spectrometry	P336	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
389	Herbert Thiele, Stefan Heldmann, Judith Berger, Janina Oetjen, Dennis Trede, Ferdinand von Eggeling, Günther Ernst, Orlando Guntinas-Lichius, Peter Maass and Theodore Alexandrov. 3D MALDI Imaging and Integration of Multimodal Images open new horizons in Histopathology	Imaging Mass Spectrometry	P337	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
390	Federica Ciregia, Laura Giusti, Ylenia Da Valle, Angelo Molinaro, Filippo Niccolai, Patrizia Agretti, Teresa Rago, Giancarlo Di Coscio, Paolo Vitti, Fulvio Basolo, Pietro Iacconi, Massimo Tonacchera and Antonio Lucacchini. Presence in the pre-surgical fine-needle aspiration of potential thyroid biomarkers previously identified in the post-surgical one	Disease Biomarkers	P338	2	Oct 16 - 12:00 noon to Oct 17 - 16:00
391	Albert Nemes, David Kreil, Günter Allmaier, Susanne Zeilinger and Martina Marchetti-Deschmann. TRICHODERMA ATROVIRIDE – A Proteomic And Genomic Approach To Identify Regulators Of Mycoparasitism In A Biocontrol Fungus	Environmental proteomics & metabolomics	P339	2	Oct 16 - 12:00 noon to Oct 17 - 16:00