

Guiding you to successful LC-MS/MS solutions

Register now to attend our free All Molecule Seminar

Metabolism

Structural elucidation using mass spectrometry can be greatly simplified using both MSⁿ, accurate mass data together with software tools for data processing. Sample analysis may involve three key stages (i) identifying differences between samples which may be trivial to complex. Sophisticated tools such as SIEVE can be used to find low levels of compounds in biological matrices such as urine. (ii) Ion trap and hybrid LTQ Orbitrap instruments are used to acquire MSⁿ and accurate mass data. (iii) Automated software tools such as Mass Defect Filtering, with MetWorks and Mass Frontier are then used to facilitate data interpretation. Examples will describe how our hardware and software tools can be applied to solve structural problems.

Bioanalysis

Experience has shown that matrix effects can influence LC-MS/MS based bioanalytical assays leading to erroneous results. As LC-MS/MS has gained wide-spread acceptance, matrix effects have become a major concern and requires careful evaluation during bioanalytical method validation. Turboflow technology based methods offer a clear advantage in terms of reducing ion suppression effects and coupled to advanced selectivity techniques such as FAIMS and H-SRM, combine to yield highly robust bioanalytical methods. Along with the advantages presented by LCQuan2.5 software and the latest features of the Watson 7.3 LIMS release, Thermo Fisher Scientific's comprehensive GLP bioanalysis solution for the pharmaceutical and CRO industries will be discussed in this seminar.

Environmental

Exposure to pesticides, antibiotics and veterinary drugs in food and environment is a significant health concern. As these chemicals become more potent, lower limits of detection (LOD) become critical. The emerging technique of choice for identification and quantification of these substances is LC-MS/MS. This presentation will focus on the solutions available from Thermo Fisher Scientific. Specific emphasis will be on EQuan which is a turnkey solution for the on-line enrichment and analysis giving the customer significant time savings over off-line techniques. In addition, data from the TSQ Quantum Access will be discussed showing the benefits of QED MS/MS technology, which allows Quantitation and full scan structural confirmation 'on-the-fly'.

We invite you to participate and exchange ideas.

Register now!

For additional information, and to register, please write to Monique at sales@alpha-analytical.com.sg or ring us at 6567-8885.

Kindly RSVP by 20th April 2007 (Friday).

Come join us on

27th April (Friday), 0830am – 1230pm
Lunch is provided

**Swissotel Merchant Court Hotel
Ballroom (Section A)**
20 Merchant Road,
Singapore 058281

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Seminar Agenda

- 08:30 AM **Registration (Ballroom-Section A)**
- 09:00 AM **Welcome / Introduction**
Dr. Charles Liu – Thermo Fisher Scientific
- 09:15 AM **Solving Analytical Challenges in Metabolism: Use of MSⁿ, Accurate Mass and Software Tools.**
Dr. Julian Phillips – Thermo Fisher Scientific
- 10:00 AM **Tea Break (15 mins)**
- 10:15 AM **Matrix Effects & Ion Suppression challenges in Bioanalysis:- Impact of new CDER Guidelines; TurboFlow, FAIMS, LCQuan 2.5, & Watson 7.3**
Dr. James Kapron – Thermo Fisher Scientific
- 11:00 AM **Quantum Analysis of Environmentally Hazardous compound**
Dr. Jonathan Beck – Thermo Fisher Scientific
- 11:45 AM **Large-scale protein characterization: Do we need it? What do we learn from it?**
Dr. Manfred Raida (Senior Research Scientist) – Institute of Molecular and Cell Biology (IMCB), Experimental Therapeutics Centre (ETC)
- 12:30 PM **Buffet Lunch at Ellenborough Market Cafe (1 hour)**