

Mass Spectrometry & Spectroscopy

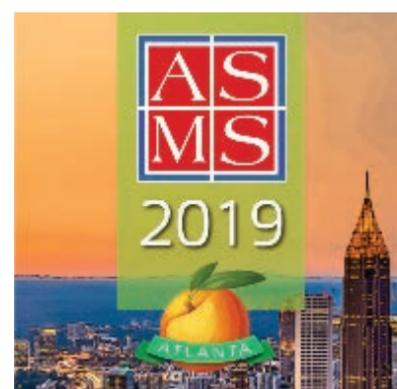
67th ASMS Conference on Mass Spectrometry and Allied Topics held in Atlanta from June 2nd to 6th, 2018 at the Georgia World Congress Center, Atlanta, Georgia USA.

Trevor Hopkins, International Labmate Contributing Editor for Chromatography and Spectroscopy.

A hot (30°C+) and humid Atlanta, Georgia was the venue for the 67th ASMS Conference.

Young scientists were again featured prominently in the ASMS programme with an Undergraduate Students and First Time (at ASMS) Graduate Students meeting on Sunday from 4:00 - 4:45 pm which covered 'Plan Your Strategy: What to See and Do at ASMS'; and a Special Program for Undergraduate Students with a Sunday, 7:30 - 9:00 pm, Poster competition in the Exhibit Hall and a Monday, 11:30 am - 1:00 pm, 'Meet the Experts' session with free lunch, where lunch tables were reserved for undergraduate students in the Exhibit Hall.

The conference started early for many enthusiastic attendees; with one-and two-day short courses beginning on Saturday and Sunday 1st and 2nd of June from 9:00 am to 4:30 pm; on Sunday, the four tutorial lectures, which was started in 2017, were held in two parallel sessions starting at 5 pm. In one parallel pathway, Stephen Blanksby from the Queensland U. of Technology & Gavin Reid from the University of Melbourne presented 'Lipidomics' and Enrico Davoli from the Mario Negri Institute presented 'Targeting Imaging'. In the other pathway, Michal Sharon from the Weizmann Institute discussed, 'Native Mass Spectrometry' and Birgit Schilling of the Buck Institute presented 'Data Independent Acquisition'.



The brief opening ceremony was followed by a very informative, data rich and interesting lecture, which contained zero reference to mass spectrometry yet hosted some 4,000 ASMS participants with standing room only - twenty deep at the rear, entitled 'Transitioning the World Energy for All Purposes to Stable Electricity Powered by 100% Wind, Water, and Sunlight' by Mark Z. Jacobson, Stanford University.

Mark graduated with both a B.S. in Civil Engineering, BA in Economics, and an MS in Environmental Engineering from Stanford University (1988) followed by an MS (1991) and PhD (1994) in Atmospheric Science from the University of California at Los Angeles. His work has focused on better understanding air pollution and global warming problems and developing large-scale clean, renewable energy solutions to them. Toward that end, he has developed and applied three-dimensional atmosphere-biosphere-ocean computer models and solvers to simulate air pollution, weather, climate, and renewable energy. He has also developed roadmaps to transition countries, states, cities, and towns to 100% clean, renewable energy for all purposes and computer models to examine grid stability in the presence of high penetrations of renewable energy. In 2019 Mark was voted as one of the world's top 100 people in climate change.

Mark's lecture discussed the energy plans he has developed over the last ten years to completely switch over to clean renewable energy. He proposed that there are three driving forces to this; Air Pollution, Global Warming and Energy Security. His proposal was to electrify, cool and heat employing wind, water and solar sources, The data provided in the forty five minute talk was compelling and left the audience feeling why hasn't this been done already. His home is totally powered by solar and has no natural gas supply so he heats, cooks', powers his two cars etc. and claims his payback for the upfront capital outlay is 5-10 years.

This was followed by the Opening Reception, located in the poster-exhibit hall, an opportunity to meet up with exhibitors, colleagues and old friends whilst eating and drinking. Hors d'oeuvres stations scattered through the exhibit/poster hall (enough for dinner!), free 'SweetWater 420 - a tasty West Coast style Extra Pale Ale accentuated with a stimulating hop character' brewed locally in Atlanta by the SweetWater Brewing Company and a cash bar for wine were all available. Technical posters were not posted until Monday morning.

Monday saw ASMS start for the early risers with a choice of 17 breakfast seminars, hosted by the corporate members, starting at 7:00 am and the oral presentations, exhibition and posters starting in earnest at 08:30 with a total of 384 oral presentations running in 8 parallel sessions of the scientific programme over the four days (32 sessions daily running concurrently) and culminating on Thursday with the closing plenary lecture entitled 'Chemistry of Food and Soft Drinks' by Lilly D'Angelo of Global Food & Beverage Technology Associates.

This year there was a whopping 3133 posters (compared to 3279 in 2018, 2889 in 2017 and 2982 in 2016) displayed during the week with an allowed one-hour non-overlapping lunch break. All presenters were now scheduled for 3 hours with odd-number posters presented between 10:30 - 11:30 am PLUS 12:30 - 2:30 pm and even-number posters presented 10:30 am - 12:30 pm PLUS 1:30 - 2:30 pm. A new feature this year promoted by ASMS was the use of QR Code Signs for Poster Presentations, permitting people interested in specific

posters to register their interest from the ASMS mobile app. The poster topics covered ranged from instrumentation and imaging to native MS in structural biology cannabis testing and protein topics aplenty, ensuring that if you did not utilise a prior selection process of some sort you would miss out on many interesting topics and have very sore feet. If you weren't walked and talked out by 17:00 then there were 18 Workshops (up from 15 in 2018) running daily Monday to Wednesday from 17:45 to 19:00 leaving just one hour for dinner before the Corporate Hospitality suites swung into action at 20:00; providing endless finger foods, snacks, refreshments and conversation - all lasting until 23:00.

Attendance was down slightly (~6%), compared to the ASMS 2018 conference, at 6,675 attendees (see Table 1 for recent history) with attendees from 52 countries plus all 50 US States and Puerto Rico. There were 180 (191 in 2018) exhibit booths.

Year	Location	Total Attendees
2012	Vancouver	6,277
2013	Minneapolis	6,140
2014	Baltimore	6,913
2015	St. Louis	6,100
2016	San Antonio	6,276
2017	Indianapolis	6,338
2018	San Diego	7,147
2019	Atlanta	6,675

Table 1. Historical Attendances

ASMS Awards

2019 John B. Fenn Award for a Distinguished Contribution in Mass Spectrometry

The ASMS Award for a Distinguished Contribution in Mass Spectrometry was renamed to honour the memory of John B. Fenn, who shared the 2002 Nobel Prize for the development of electrospray ionisation, and was an active member of ASMS from 1986 until his passing in 2010.

The 2019 John B. Fenn ASMS Award for a Distinguished Contribution in Mass Spectrometry was awarded to Dr John R. Yates for his development of automated, large-scale interpretation of peptide tandem mass spectral data.

Dr Yates, a Professor in the Department of Molecular Medicine, The Scripps Research Institute developed the SEQUEST algorithm and laid a critical foundation for the field of proteomics that has enhanced the accuracy and effectiveness of mass spectrometry permitting the understand important biological and clinical questions.

Further software developments by Dr Yates continue to empower molecular and cellular biology research, including peptide and protein quantitation, identification of posttranslational modifications, and the use of DNA sequences to enable proteogenomic methods.

Al Yergey MS Scientist Award

Dr Jeffrey Shabanowitz, a Principal Scientist in the Hunt Laboratory at the University of Virginia, was the recipient of the new Al Yergey MS Scientist Award. The Al Yergey Mass Spectrometry Scientist Award is sponsored by ASMS to recognise dedication and significant contributions to mass spectrometry-based science by 'unsung heroes'. This award is named in memory of Al Yergey a well-respected scientist who was known as a dedicated mentor.

Dr Shabanowitz has worked with Professor Donald Hunt at the University of Virginia for forty years and has coauthored more than 330 peer-reviewed scientific papers and is the co-inventor on ten patents. The methods and instrumentation he helped to develop played a major role in the development of peptide sequence analysis by tandem mass spectrometry which now underpin the field of proteomics, and have led to major breakthroughs, especially in immunology and epigenetics research.

Biemann Medal

The Biemann Medal is awarded to an individual early in his or her career to recognise significant achievement in basic or applied mass spectrometry. Dr Sarah Trimpin, Professor of Chemistry at Wayne State University was awarded the 2019 Biemann Medal for her discovery and development of novel ionisation processes. Dr Trimpin's observation of highly charged protein ions in an atmospheric pressure MALDI experiment led to her discovery that ionisation can occur by passing compounds through the mass spectrometer inlet. She demonstrated that this approach provides sensitivity often better than electrospray ionisation or MALDI.

Through her studies, Dr Trimpin discovered solid matrices that spontaneously produce multiple charged ions when exposed to vacuum (termed matrix-assisted ionisation, MAI) needing no heat, nebulising gases, laser, or voltage with a very low chemical background achieved for a variety of compounds, including proteins as large as bovine serum albumin (66 kDa).

Ron A. Hites Award Outstanding Research Publication in JASMS

The Ron Hites Award, which includes \$2,000 and a certificate, is awarded to a scientist for an original outstanding research publication, based on its novelty, technical and presentation quality, potential stimulation of future research and the impact on other future applications.

The 2019 Award was presented to Dr Julia Laskin from Purdue University and her co-authors for their paper entitled '**Towards High-Resolution Tissue Imaging Using Nanospray Desorption Electrospray Ionization Mass Spectrometry Coupled to Shear Force Microscopy**'; Son N. Nguyen, Ryan L. Sontag, James P. Carson, Richard A. Corley, Charles Ansong, and Julia Laskin; J. Am. Soc. Mass Spectrom. (2018) 29:316Y322.

New Product Roundup

In the interests of impartiality companies introducing new instruments and products are again listed in alphabetical order, we have attempted to feature the majority of new product introductions for 2019.

Agilent Technologies

The new Agilent **InfinityLab LC/MSD iQ** System, released at ASMS, incorporates 'designed-in' smart features, software, and hardware. The Agilent InfinityLab Liquid Chromatography/Mass Selective Detector iQ (LC/MSD iQ) system provides mass detection for quick confirmation of compounds providing more specificity and selectivity than a UV detector - even for chromatographically unresolved compounds.

The InfinityLab LC/MSD iQ system is designed to sit beneath the Agilent's InfinityLab HPLC instruments stack introduced in 2018, saving lab space. The system is designed to be serviced without dismantling the stack and the new InfinityLab Flex Bench MS enables mobility with easy access to all the modular system components.

New software features include an Auto Acquire mode for method setup and routine operation utilises the OpenLab CDS Software. A new release of Agilent's MassHunter WalkUp Software for open-access drug discovery and chemistry labs has a touch-screen enabled interface and preconfigured analyses and reports.

Other new Agilent products, include the 6546 LC/Q-TOF System provides the acquisition of high-resolution data across a wide dynamic range and includes Q-RAI (Quadrupole-Resolved All Ions), a data-independent acquisition mode that reduces the complexity of MS/MS spectra. An updated MassHunter Software Suite was launched with the 6546 system.



Figure 1. InfinityLab LC/MSD iQ.

Bruker

The main introduction of ASMS in 2019 for Bruker was the new **timsTOF fleX™** mass spectrometer which includes a software-switchable MALDI source adapted to the ESI timsTOF Pro™ platform.

The new, combined ESI/MALDI capability is reported to enable spatially-resolved omics, SpatialOMx™, on a single instrument. The timsTOF fleX has a 10kHz SmartBeam™ 3D laser with pixel fidelity for rapid, label-free MALDI imaging at high-spatial resolution, preserving the 4D proteomics and phenomics sensitivity of the timsTOF Pro in ESI mode.

With the SpatialOMx approach, researchers can see spatial molecular distributions in tissues from MALDI imaging, to guide 4D omics molecular expression studies, e.g. on proteins, low-level cancer antigen peptides, lipids, glycans, metabolites, or xenobiotics, which cannot be observed by traditional staining or labelling techniques. MALDI-guided SpatialOMx permits the specific targeting of cell sub-populations for subsequent ESI-TIMS/PASEF-based data dependent acquisition (DDA) or data independent acquisition (DIA) 4D proteomics or 4D lipidomics/metabolomics. Both can now be performed on a single instrument.



Figure 2. timsTOF fleX™

Bruker also launched IntelliSlides™ specifically designed to automate timsTOF fleX workflows. The IntelliSlides come pre-inscribed with software-readable 'teach marks' on the conductive surface to indicate where to place the tissue sample, a bar code and tracking number. With specialised software, IntelliSlides now make MALDI Imaging even easier. The SciLS Lab 2020 MALDI imaging software, now integrated with MetaboScape5.0 for automated annotations of lipids and metabolites in tissue molecular images in spatialOMx.

4D Phenomics and 4D Proteomics Innovations

Bruker's timsTOF™ Pro launched in 2018 for nLC-TIMS-MS/MS 4D proteomics has been further enhanced by combining PASEF with DIA, in diaPASEF for high sensitivity bottom-up proteomics. While the duty-cycle of DDA PASEF dramatically improved sensitivity and depth of coverage using short nanoLC runtimes, the stochastic nature of DDA results in missing values, an issue significantly improved by diaPASEF workflows, or by match-between-runs (MBR) for ddaPASEF.

The diaPASEF workflow, shown at ASMS 2019 as a work-in-progress workflow available to methods development customers, uses overlapping windows in the ion mobility spectrum to trigger MS/MS, efficiently using the quadrupole to transmit the precursor ions at high sensitivity. The new diaPASEF workflow typically results in a 30% improvement, now with over 7,000 proteins identified in a 120 minute single-shot experiments with 200 ng of HeLa digest injected. Data analysis, including 4D feature alignment in mass, retention time, ion mobility and intensity, is performed using the new Mobi-DIK software, which is based on the OpenMS software.

New Consumables and Software for 4D Proteomics

Bruker and PreOmics GmbH announced a co-development and co-marketing agreement for PreOmics iST sample preparation technology on the timsTOF Pro. The iStageTip (iST) technology removes detergents, polymers, salts, lipids and other contaminants. New iST protocols enable sample preparation with a significant time advantage (over 40 hrs saved) compared to common protocols.

For proteomics software, Bruker and Genedata announced a partnership for the Genedata Expressionist software platform, which supports the timsTOF Pro 4D omics format.

New Ultra-high Sensitivity 4D Lipidomics Workflow

Bruker announced advances to its ultra-high sensitivity **4D lipidomics** workflows on the timsTOF Pro and timsTOF fleX platforms, showing high-sensitivity measurements using LC-TIMS-MS/MS. Optimisation of the PASEF 4D lipidomics methods now enables double the number of identified lipids in a single-shot analysis. This workflow employs nanoLC-TIMS-PASEF to quantify approximately 500 lipids with high quantitative accuracy and reproducibility from just a few thousand cells, in addition to building a library of more than 1,000 accurate CCS values from human plasma, mouse liver and human cancer cells.

Sciex

Sciex released the following new products and technologies at ASMS.

Acoustic Ejection Mass Spectrometry (AEMS) technology, incorporating the Open Port Interface and Acoustic Droplet Ejection, is introduced before commercialisation and is stated to be Echo MS upon commercialisation.

In early testing, AEMS technology has reportedly shown the potential to reduce screening times, from 115 days to 4 days for 1 million compounds due to reductions in analysis time.

Additional reported achievements of AEMS technology include:

- Up to **50x faster sample analysis**, delivering rich data sets and reducing the risk of missing lead compounds
- Accelerated speed of analysis, capable of up to **3 samples per second** – 180 samples/min, 11,000 samples/hour, 260,000 samples/day
- **Low CV's quantification (5-8%)**, hence high reproducibility regardless of the matrix
- **Sample analysis direct from the plate** - No liquid chromatography required, eliminating potential carry over and errors

Sciex Triple Quad™ 5500+ LC-MS/MS System – QTRAP® Ready

The Sciex Triple Quad™ 5500+ LC-MS/MS System – QTRAP® Ready, is said to couple triple quadrupole and QTRAP® functionality in a single system to provide higher data confidence from the same sample. The QTRAP® functionality can be implemented at any time by activating a field upgradable license.

Combining the two instruments produces an instrument with increased efficiency and dynamic range.

Features of the Sciex Triple Quad™ 5500+ LC-MS/MS System – QTRAP® Ready include:

- **Increased Polarity Switching Time:** Increased efficiency of positive and negative ion analysis in the same acquisition – with 5 msec in MRM and Scheduled MRM™. Analyse more analytes in a single run with good data quality
- **Linear Dynamic Range of up to 6 orders:** Produces highly precision, quantified data to see low-level trace detection through to excessively abundant analytes in any application
- **QTRAP® functionality:** 12,000 Da/sec enables fast qualitative confirmation of analytes in parallel with MRM quantitative data

TripleTOF® 6600+ LC-MS/MS System - featuring Scanning SWATH® Acquisition and OneOmics™ Project in Sciex Cloud

The **TripleTOF® 6600+ LC-MS/MS System** is built for flexible large-scale precise quantification. The instrument incorporates simplified low-flow source technology to produce accessible, sensitive and robust quantification; while multiple software improvements increase robustness and maximise system uptime. The key features of the TripleTOF® 6600+ LC-MS/MS System include:

- **OptiFlow® Turbo V Source:** A single source for all low-flow applications, with flow rates of 100 nL/min – 200 µL/min, the OptiFlow Turbo V Source enables long-term operations to study large sample cohorts
- **Up to 100 Hz MS/MS Scan Speeds:** Delivers unique qualitative and quantitative capabilities, from fast targeted quantification (MRMHR) to highly multiplexed data-dependent (DDA) and data-independent methods (SWATH)
- **Analyst® TF Software 1.8:** Scheduled ionisation and target TIC function give the user temporal control over the number of ions entering the system, eliminating the acquisition of unwanted data and maximising system uptime

Also introduced with the TripleTOF® 6600+, was **Scanning SWATH® Acquisition**. Scanning SWATH creates a digital data record of all detectable analytes, capturing more detail about potential markers than its predecessor. Utilising a sliding Q1 window scanned across the mass range, Scanning SWATH produces 4D data where the correlation between fragment and precursor provide better confidence.

Sciex also introduced a new generation of **OneOmics™, now integrated into Sciex Cloud**. A shared SWATH® approach by integrating customers data into a cloud-based environment aimed at efficiently translating big data generated from proteomics, metabolomics, and genomics workflows into meaningful biological results.

Shimadzu Corporation

Shimadzu Corporation introduced the following new products at ASMS 2019:

Announced the release of the MALDImini™-1 which is a compact MALDI digital ion trap mass spectrometer. The MALDImini-1 reportedly fits in a space the size of a piece of paper, while allowing fast high-sensitivity measurements and detailed structural and qualitative analyses over a wide mass range, even with sub-microlitre sample volumes.

The small footprint and lower power requirements allow it to be plugged into a conventional AC power supply due to a unique Digital Ion Trap (DIT) technology, with a new design of laser optics, sample stage, and vacuum exhaust system.

The MALDImini-1 can be placed next to the sample preparation area, allowing for a convenient workflow, the sample and matrix are simply spotted on the sample plate, dried, and loaded into the instrument. Taking around five minutes this setup enables users to conduct and repeat even in-depth structural analyses quickly.

The new digital ion trap uses rectangular wave RF to allow ion trapping up to 70,000 Da. This capability, when combined with a MALDI source, enables high-sensitivity MSn analysis in a broad range of applications. The MS/MS and MS3 functionality of the DIT allows researchers to perform comprehensive structural analyses, such as direct glycopeptide analysis, post translational modification analysis, and branched glycan structural analysis. The unit easily integrates with powerful processing tools to analyse data, such as MASCOT for identifying protein digests, SimGlycan™ for processing MSn data for glycans, and eMSTAT Solution™ for statistical analysis.



Figure 3. Shimadzu MALDImini™-1

Shimadzu also announced the release of the **Cell Culture Media Analysis Platform, C2MAP™-2030**, A fully automated workstation for the analysis of cell culture media, the C2MAP system measures changes of 95 components in a culture supernatant as culturing progresses using LC-MS/MS, resulting in high-quality reproducible data.

Shimadzu also released the **Micro-ESI 9030 Flowrate Compatible Ionization Interface** compatible and based on the **Nexera Mikros Microflow Liquid Chromatography Mass Spectrometry System**. Covering the complete range from microflow to semi-microflow, this system allows operators to realise high sensitivity, yet with the reliability and ruggedness of HPLC. The LCMS-9030 Q-TOF system is a research grade mass spectrometer designed to deliver high-resolution, accurate-mass detection with fast data acquisition rates, allowing scientists to identify and quantify more compounds with greater confidence.

Shimadzu also announced a major diversion from the instrument based sales approach of all the major instrument manufacturers in launching the **recently developed the Amyloid Mass Spectrometry (MS) Screening Service** — a new simple, low-cost **blood test for the early screening** for Alzheimer's biomarkers of amyloid-positive subjects. This method enables early and accurate detection of amyloid deposition in the brain with an easy-to-acquire blood sample. Unlike conventional methods, Shimadzu's new test is minimally invasive, cost-effective and suitable for large-scale deployment.

It is reportedly the only blood test capable of detecting abnormal amyloid-beta deposition in the brain with 90% accuracy

Thermo Fisher Scientific

Thermo Fisher Scientific headlined with two new high-performance mass spectrometers for protein-based analysis.

The new **Orbitrap Exploris 480** mass spectrometer is designed to combine proven technology, advanced capabilities and intelligence-driven data acquisition techniques to enable researchers to deploy MS for more rigorous, high-throughput protein identification, quantitation and structural characterisation. With a smaller footprint than previous generations, the new system maintains high-resolution, mass accuracy and spectral quality, and includes new features to extend uptime and improve serviceability.

Also, the new Thermo Scientific **Orbitrap Eclipse Tribrid** mass spectrometer reportedly provides scientists in academic, government and biopharmaceutical labs with access to a high-performance Orbitrap Tribrid mass spectrometer featuring flexibility and built-in intelligence. The system incorporates advances that improve sensitivity over previous generations and expand the ability to characterise and quantify complex biomolecules and biological systems.

Both new systems can be combined with the Thermo Scientific FAIMS Pro interface, a differential ion-mobility device, offering labs access to a comprehensive solution that improves selectivity and provides increased productivity across a range of proteomics workflows.

Other new introductions included:

The HR Multi-Attribute Method (MAM) is designed to meet the demand for a single, high-resolution mass spectrometry-based workflow to directly assess the quality of increasingly complex biotherapeutics. The workflow replaces the complicated sequence of lower-resolution methods that have previously prolonged characterisation timelines. The HR MAM is supported by the Chromeleon Chromatography Data System (CDS) software.

New analytical software solutions bring together Compound Discover Software, Mass Frontier Software and mzCloud/mzVault libraries to assist customers identify unknown compounds and compare them to known compounds across multiple databases – whether connected to the cloud or offline. The TraceFinder Software 5.0 update, offers quicker and easier access to important information from both the TSQ Quadrupole and Q Exactive Hybrid Quadrupole-Orbitrap mass spectrometry platforms.

Remote instrument access is also possible by using the Thermo Scientific Almanac web-based application to monitor instrument run status and data acquisition in real time through a browser or mobile device.



Figure 4. Thermo Scientific Orbitrap Eclipse Tribrid

Waters Corporation

The new Waters™ SELECT SERIES Cyclic™ IMS integrates cyclic ion mobility (cIM) technology into a high performance research-grade time-of-flight mass spectrometer. The combination of the new IMS capability with improved mass spectrometry (MS) performance and software, this platform allows leading researchers to expand their scientific discovery potential.

Ion mobility mass spectrometry rapidly obtains information for structural elucidation and enhances system peak capacity. The SELECT SERIES Cyclic IMS replaces the traditional linear ion mobility region with a new compact cyclic ion guide. Ions traverse around the ion guide and with every pass, greater ion mobility resolution is achieved. The new cyclic device provides scalable, high-resolution ion mobility separations and introduces the unique ability to perform ion mobility/ion mobility and IMSn experiments.

The new SYNAPT™ XS is a new flexible, high resolution mass spectrometer for R&D labs focused on discovery applications. By providing flexibility through inlets and acquisition modes, the SYNAPT XS delivers the freedom of analytical choice for any application. The SYNAPT XS is the newest version of the SYNAPT series with its unique T-Wave IMS configuration, which extends the power of high-resolution analysis. IMS capability on the SYNAPT increases the extent and confidence with which a scientist can profile complex mixtures and characterise complex molecules, and dramatically enhances sample definition.

Waters' also featured the BioAccord™ LC-MS System for Biopharmaceuticals for ASMS debut of the unit introduced in March at Pittcon. The BioAccord is designed to expand the access to high-resolution time-of-flight mass spectrometry, including multi attribute monitoring capabilities, to more scientists who are analysing critical quality attributes.

Figure 5. Waters™ SELECT SERIES Cyclic™ IMS



ASMS Closing Event

Thursday's closing event was held at the Georgia Aquarium. The Georgia Aquarium, which took 27 months to complete and opened in 2005, is a public aquarium in Atlanta, Georgia, US. It houses more than a hundred thousand animals and represents several thousand species, all of which reside in 10 million gallons (US) (38,000 m³) of marine and salt water. It was the largest aquarium in the world from its opening in 2005 until 2012, when it was surpassed by Marine Life Park in Singapore.

The Aquarium's notable specimens include whale sharks, beluga whales, California sea lions, bottlenose dolphins, and manta rays and other marine life. In addition to the aquarium access a buffet dinner and a drink was included in the ticket price. The buffet closed at 8:00 pm. to permit attendees to view the aquarium until 9:00 pm.

Future ASMS Dates

Dates and venues for the forthcoming ASMS meetings have been announced as follows:

68th ASMS Conference, 14 - 18 June 2020, Denver, CO

69th ASMS Conference, 6 - 10 June 2021, Philadelphia, PA

70th ASMS Conference, 5 - 9 June 2022, Minneapolis, MN

71st ASMS Conference, 4 - 8 June 2023, Houston, TX

72nd ASMS Conference, 2 - 6 June 2024, Anaheim, CA



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