

TWO DECADES OF ORBITRAP MASS SPECTROMETRY AS A MAINSTREAM TECHNOLOGY FOR HIGH-RESOLUTION ACCURATE MASS ANALYSIS

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Originating from the ideal (and thus never realized) Kingdon trap, the Orbitrap™ analyzer entered mainstream mass spectrometry 20 years ago, five years after the first peer-reviewed publication. In the very first serial instrument, this analyzer was utilized as a detector for ions processed by LTQ Linear Ion Trap MSn Mass Spectrometer and its high sensitivity was enabled by a novel external ion storage device known as the C-trap.

Since then, Orbitrap mass spectrometry applications have expanded continuously through integration with additional capabilities such as quantitative analysis, new fragmentation methods, various ion sources, imaging, and ion mobility.

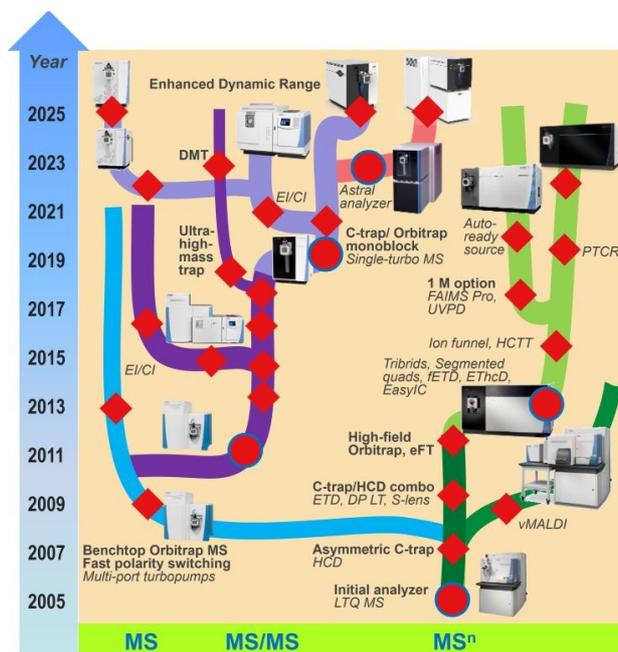
These capabilities have been developed over the lifetimes of five major families of Orbitrap-based instruments, enabling many new modes of operation through parallelization of detection and ion processing and intricate coordination of different ion-optical devices. New methodologies of data-independent, targeted, top-down, and native MS analysis have also been introduced.

The roadmap for future instrument innovations is overviewed, highlighting major paths of advancement including new instrument designs (particularly in conjunction with improved ion scheduling and utilization), analytical modalities, acquisition and fragmentation methods, and innovations in signal processing.

In conclusion, an optimistic outlook on the future of Orbitrap technology is presented, highlighting its compelling potential as a high-resolution platform for not only high-end -omic applications but also for screening, trace contaminants, and targeted analysis via LC/MS and GC/MS.

Thanks/Acknowledgement

I would like to express my deepest gratitude to all colleagues who have contributed to the success of Orbitrap mass spectrometry, each of whom has invested a part of their talent, soul, and professional life to its development.



Development of Orbitrap mass spectrometry