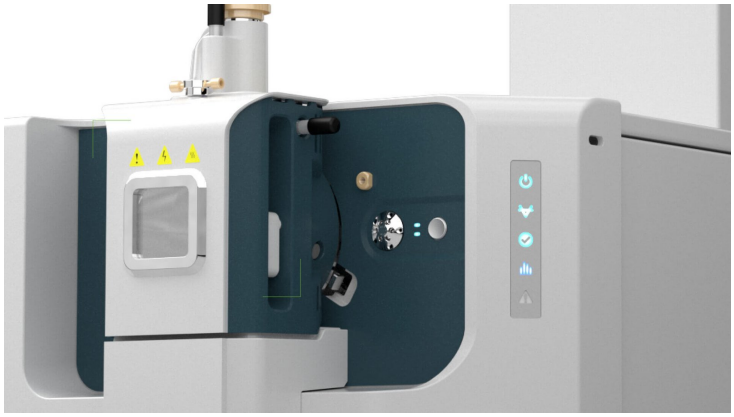
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SCIEX, Evosep to provide robust, high-throughput proteomics workflows

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The companies hope to broaden the collaboration to more applications and instrument platforms



SCIEX and Evosep have announced an agreement to co-market products together to improve robust, high-throughput proteomics workflows for precision medicine.

SCIEX and Evosep plan to use the ZenoTOF 7600 system and the Evosep One to engage with several joint customers to better allow them to develop and validate proteomics-based assays.

Mass spectrometry (MS)-based proteomics has become a central technology in biological research and it is now promising to become equally powerful for precision medicine and large scale multi-omics studies.

Proteomics was challenged by the speed and robustness necessary for precision medicine and biomarker discovery, but with recent advances in sample preparation, chromatography, and mass spectrometry, accurate proteome quantitation in high throughput mode for thousands of samples is now possible.

Dr Jose Castro-Perez, Senior Director of Accurate Mass Product Management at SCIEX said, “The ZenoTOF 7600 system with its enhanced speed of acquisition and sensitivity improvements can detect and quantify up to 40% more proteins than our previous systems and EAD fragmentation delivers new capabilities for post-translational modifications – an important but challenging area in biomarker research. The Evosep One adds even more sensitivity and higher throughput to be the perfect match for translational proteomics on a very large scale.”