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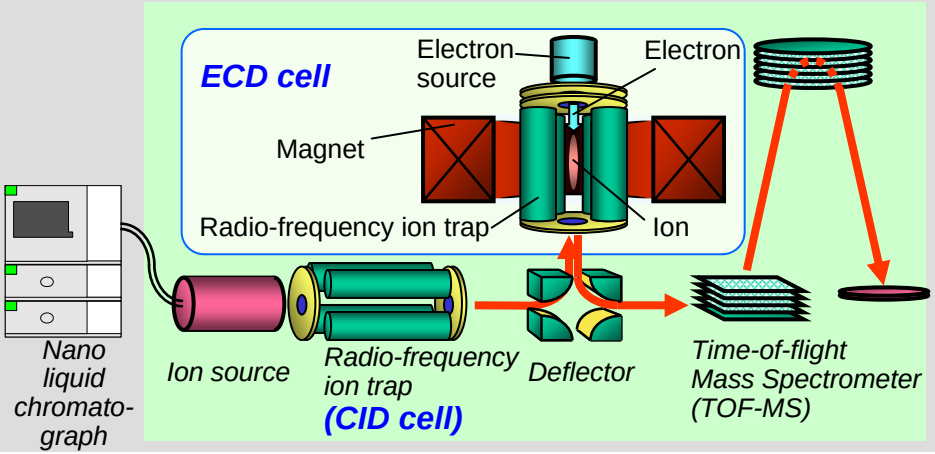
New mass spectrometry technique to enhance protein identification accuracy - for the elucidation of disease mechanisms and pharmaceutical development -

Radio-frequency ion trap TOF mass spectrometer



Comparison of dissociation methods

	CID	ECD
Amino-acid sequence	Non-dissociable sites present	Non-dissociable sites present (complementary to CID)
Modification site	Often lost: inappropriate for disease related proteins	Robustly preserved: advantageous for disease related proteins
Analysis speed (when connected to LC)	High	Low → High (This research)

Hitachi, Ltd. has developed technology to enhance the accuracy of protein identification. Technical difficulties in applying electron-capture dissociation (ECD), a method of dissociating gas-phase ions originating from sample protein molecules, to a high-throughput liquid-chromatograph mass-spectrometer (LC-MS), were overcome for the first time to enable enhanced accuracy in the analysis of proteins. The two key techniques are the new ECD cell capable of obtaining data within a few seconds, and an intelligent real-time data evaluation technique for fast switching between ECD and collision-induced dissociation (CID), the conventional method for dissociation in an LC-MS. ECD is conducted whenever data from the CID is found to be insufficient for identifying a protein, thus enabling identification of proteins which cannot be identified by CID alone. These new techniques are expected to enhance the accurate analysis of disease-related proteins to accelerate the elucidation of disease mechanisms and facilitate the development of new pharmaceutical drugs.

The results of this research will be presented at the 54th MSSJ Annual Conference on Mass Spectrometry, to be held from 17th - 19th May in Osaka, Japan, and the 54th ASMS Conference on Mass Spectrometry, to be held from 28th May - 1st June 2006, in Seattle, U.S.A.

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MSSJ: Mass Spectrometry Society of Japan ASMS: American Society for Mass Spectrometry