

Supplementary Table S1. List of currently available, common HX MS software.

Software name	What it does?	Refs.
HD Desktop	Derived from “The Deuterator” software by the same group. Integrated platform for both analysis and visualization of HX MS data. Provides efficient and manageable workflow for HX MS data. http://deuterator.florida.scripps.edu/	[1,2]
HDExaminer	Commercial solution, supporting various MS data formats including high-resolution MS data. http://www.massspec.com/HDExaminer.html	[3-5]
HXExpress	Semi-automatic data analysis that generates deuterium uptake and peak width plots and improves the speed of analyzing HX MS data. http://www.hxms.com/HXExpress	[6]
Hydra / Mass Spec Studio	Semi-automated software, less processing time for HX MS data. Accommodates MS/MS and supports alternative data collection. Allows for better localization of deuterium after MS/MS fragmentation. https://github.com/dschriem/MassSpecStudio	[7]
HeXicon	Workflow for automatic deuteration distribution estimation with increased sequence coverage. It allows insight into possible bimodal exchange rather than just average deuteration for each time point. http://hci.iwr.uni-heidelberg.de/MIP/Software/hexicon.php	[8,9]
DynamX	Commercial software with simultaneous visualization of raw MS data, identified peptides, deuterium uptake graphs and comparability plots. Multi-functional user interface. Integrates with ion mobility separation. http://www.waters.com/waters/nav.htm?cid=10168585	[10]
HDX Analyzer	HDX analyzer integrates the graphic visualization and statistical analysis to enable the effective evaluation of hydrogen exchange data. This software analyzes data from a wide range of instruments. http://people.tamu.edu/~syuan/hdxanalyzer/	[11]
ExMS	Processes high-resolution MS data, verifies peptide assignment, extracts deuterium incorporation information. Checkpoints during processing allow for manual intervention in processing routines. http://HX2.med.upenn.edu/download.html	[12]
HDX Finder	Web based tool, utilizes mzML and mzXML formatted data files, works with high-resolution data and creates multiple graphical outputs. https://hdxanalyzer.kumc.edu/	[13]
MS Tools	Web based application for visualization and presentation of HX MS data. http://ms.biomed.cas.cz/MSTools/ ; USA Mirror: http://www.hxms.com/mstools/	[14]
AUTOHD	Computer program that takes in a list of mass spectra, defines isotopic clusters and identifies them using a list of candidates peptides generated from enzymatic fragmentation or dissociation. http://www.ms-utils.org/autohd.html	[15]

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