Hydrogen Deuterium Exchange Mass Spectrometry And Its

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Hydrogen/Deuterium Exchange (HDX): Structural Mass Spectrometry Understanding Hydrogen Deuterium Exchange (HDX) LC-MS Workflow for Biopharmaceuticals ~~Advances in Hydrogen-Deuterium Exchange Mass Spectrometry That Can Improve Studies of Biosimilars..~~ Hydrogen Deuterium Exchange (HDX) at the Univ. of Texas | Behind the Science *Thermo Scientific HDX LC-MS workflow animation* ~~Structural Insights from Hydrogen-Deuterium Exchange Mass Spectrometry (HDX)~~ *Protein movement and dynamics by Hydrogen Deuterium Exchange Mass Spectrometry (HDX MS)* WEBINAR | Hydrogen Deuterium Exchange Coupled with Cyclic Ion Mobility for Higher Quality Analyses How hydrogen exchange mass spectrometry can help investigate protein higher order structure ~~HDX technology for protein conformation studies~~ ~~Time-resolved ElectroSpray Ionization Hydrogen-deuterium Exchange Mass Spectrometry for Studying Pro~~ Deuterium-depleted water as anti-aging approach? Dr. Thomas Cowan and James Strole //RAADfest

How to make deuterium depleted water - Ultrasonic cavitation

014- Deuterium- Why This Unknown Molecule Could Be the Key to Health, Energy and Longevity with... How To Make Deuterium Depleted Water DDW *Deuterium and Health with Dr. Laszlo Boros, Dr. Que Collins, and Dr. Anne Cooper.* ~~HDX for understanding a protein's higher order structure and function | Behind the Science~~ *Hydrogen Class 11 Chemistry | One Shot | CBSE NEET JEE*

Dr. Jack Kruse / Nourish Vermont 2017*UNACADEMY FRAUD (NAMO SIR CHEATING) HDX 2 Gallon Sprayer - Thoughts and Setup* Hydrogen or deuterium exchange Analyzing Viruses using Hydrogen Deuterium Exchange Mass Spectrometry *Biopharm Higher Order Structure \u0026 Conformation Stability Analysis with HDX* nanoACQUITY UPLC for Hydrogen Deuterium Exchange Facilitating Drug Discovery with HDX-Mass Spectrometry

Deuterium Exchange in Aromatic Systems

Facilitating Drug Discovery with HDX-Mass Spectrometry**Studying cofactors with HDX-MS at the Univ. of Alabama | Behind the Science Hydrogen Deuterium Exchange Mass Spectrometry**

Researchers in the United States have demonstrated that the viral spike protein used by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to infect host cells adopts an open conformation ...

Study identifies SARS-CoV-2 spike conformation exposing potential new therapeutic targets

Graham Cooks, "The ß-cleavage Reaction in Ethers", Organic Mass Spectrometry 3, 127 (1970 ... "Molecular Beam Study of Hydrogen-Deuterium Exchange on Low and High Miller Index Platinum Single Crystal ...

Publications: 1970 - 1979

21 Biological Mass Spectrometry and Proteomics ... Through x-ray structure determination and Markov transient and Deuterium exchange analyses, we identified the allosteric binding site and revealed ...

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Journal of the American Society for Mass Spectrometry

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Analytical Chemistry 2018

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Molecular Biology and Biochemistry

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Hydrogen exchange mass spectrometry is widely recognized for its ability to probe the structure and dynamics of proteins. The application of this technique is becoming widespread due to its versatility for providing structural information about challenging biological macromolecules such as antibodies, flexible proteins and glycoproteins. Although the technique has been around for 25 years, this is the first definitive book devoted entirely to the topic. Hydrogen Exchange Mass Spectrometry of Proteins: Fundamentals, Methods and Applications brings into one comprehensive volume the theory, instrumentation and applications of Hydrogen Exchange Mass Spectrometry (HX-MS) - a technique relevant to bioanalytical chemistry, protein science and pharmaceuticals. The book provides a solid foundation in the basics of the technique and data interpretation to inform readers of current research in the method, and provides illustrative examples of its use in bio- and pharmaceutical chemistry and biophysics In-depth chapters on the fundamental theory of hydrogen exchange, and tutorial chapters on measurement and data analysis provide the essential background for those ready to adopt HX-MS. Expert users may advance their current understanding through chapters on methods including membrane protein analysis, alternative proteases, millisecond hydrogen exchange, top-down mass spectrometry, histidine exchange and method validation. All readers can explore the diversity of HX-MS applications in areas such as ligand binding, membrane proteins, drug discovery, therapeutic protein formulation, biocomparability, and intrinsically disordered proteins.

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Hydrogen deuterium exchange mass spectrometry has emerged as an important technique to probe protein structure and conformational dynamics. The rate of exchange of hydrogen with deuterium by the peptide backbone is dependent on the solvent accessibility, extent of hydrogen bonding in secondary structural elements and protein dynamics. The extent and the rate of deuterium incorporation are affected by changes in protein structure, interaction with ligand, protein-protein interaction and environmental factors such as pH and temperature. These conformational changes can be global and/or local. The increase in the mass is used to localize the deuterium incorporation after pepsin digestion of the protein and analysis by electrospray ionization mass spectrometry. In this dissertation traditional HDX-MS and a new deuterium trapping assay were used to probe the interaction sites between E. coli cysteine desulfurase SufS and acceptor protein SufE. SufS and SufE form an important part of the SUF pathway, essential for the biosynthesis of Fe-S clusters under oxidative stress and iron depletion conditions. In addition, SufE is known to stimulate SufS cysteine desulfurase activity, but the mechanism is unknown. The HDX-MS results show that the regions affected by the SufS-SufE interaction are dependent on the catalytic intermediate states of the two proteins. HDX-MS was also used to probe the conformational changes resulting upon persulfuration of SufS of Cys364 in the active site. The persulfuration of SufS not only affected regions in the active site cavity, but also had other conformational changes in more distal regions. Based on our findings a model for the interaction SufS and SufE was proposed. A mechanism for the enhancement of SufS cysteine desulfurase activity upon interaction with SufE was also postulated. In all this work demonstrates that hydrogen deuterium exchange mass spectrometry and the deuterium trapping methodology optimized for this system can be easily and effectively used to study the protein-protein interactions and the accompanying changes in structural dynamics for other proteins. Deuterium trapping was demonstrated to be fast, sensitive and reliable method to deduce the changes in solvent accessibility between two or more states of a protein. Both techniques can easily be applied to large number of protein complexes to determine the regions of interaction as well as gain mechanistic information not available through traditional methods such as X-ray crystallography and NMR.

Proteins are biological macromolecules responsible for the majority of all physiological processes. In order to properly function proteins are required to adopt highly ordered structures. These structural aspects may be found within a single protein or arise from multi-protein complexes. Here hydrogen/deuterium exchange mass spectrometry (HDX-MS) is employed as a tool to determine the extent of protein higher order structure. Exposure to D2O-based solvent causes the heavier isotope to exchange with amide hydrogens in the polypeptide backbone. This exchange is mainly dependent on protein conformation because the presence of stable hydrogen-bonded secondary structure will impede the incorporation of deuterium when compared to regions that are unstructured. In this work HDX-MS is used to study denaturant-induced unfolding of oxidized and reduced cytochrome c as well as ATP binding to the subunit of FOF1-ATP synthase. This work also lays the foundation to use this technique to study larger, more complex systems.