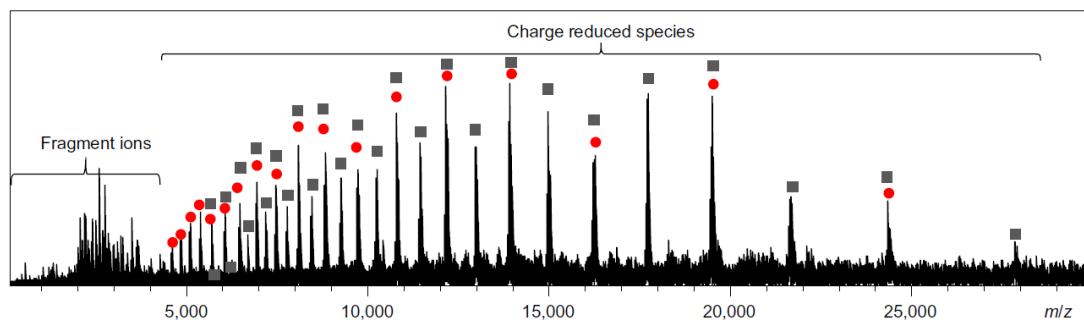


An integrated native mass spectrometry and top-down proteomics method that connects sequence to structure and function of macromolecular complexes

任洪翔

Abstract

Mass spectrometry (MS) has become a powerful tool to quickly and efficiently identify proteins in biological samples. Two sets of experiment for the MS study of a protein complex are native MS and proteomics MS, which are often performed separately because of sample complexity and technical limitation. Proteomics MS allows for the sequence identification of protein complex, while native MS provides structural information. The development of an integrated native MS and top-down proteomics method using Fourier-transform ion cyclotron resonance (FTICR) to analyze macromolecular protein complexes in a single experiment is described in this article. This integration allows the study of large and complex proteins in greater detail, providing insight into the functional dynamics of the system.



S R P	L S D Q E K	R K D I S V R G L A	G V E N V T E L K K	N F N R H L H F L L	V I K D R I N V A T P R	49
D Y Y	F A L A H T V	R D H L V G R W I R	T Q Q H Y G E K D P	K R I Y Y L S L E F I	Y M G R T L Q N T M	99
V N L A E N A C D	E A T Y Q L G L D M	E E L E E I E E D A	G L G N G G L G R L	A A C F L D S M A T	149	
L G L A A Y G I	R Y E F G I F N Q K	I C G G W Q M E E A	D D W L R Y G N P W	E K A R P E F T L P	199	

V S L A E K V I P A	A D L S E Q I S T A	G T E A S G T G N M	K F M L N G A L T T	L G T M D G A N M E M	699	
A E E A G E E N F F	I F G M R V E D V D	I R L D Q R G N I A Q	E Y Y D R I P E L R	Q I L E Q L S L G F	749	
F S P K Q P D L F K	D I V N L L M H H D	I R F K V F A D Y E E	Y V K C Q E R V S A	L Y K N P R E W T R	799	
M V I R N I A T S G	K F S S D R T I A Q	Y A R E I W G V E L P	S R Q R L P A P D E	K I P	842	

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