



SDI Review Form 1.6

Journal Name:	International Journal of Biochemistry Research & Review
Manuscript Number:	Ms_IJBCRR_35595
Title of the Manuscript:	Analysis of isotopic peaks in hydrogen/deuterium exchange mass spectra for precise measurement of isotope average centroid mass of peptides and proteins
Type of the Article	Short communication

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)

PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Compulsory REVISION comments	NO	
Minor REVISION comments	I am suggesting a minor adaption of the title "Analysis of isotopic peaks in hydrogen/deuterium exchange mass spectra for precise measurement of isotope average centroid mass of peptides and proteins" using R software environment for statistical computing and graphics as a tool"	The title of the manuscript has been modified as: "Analysis of isotopic peaks in hydrogen/deuterium exchange mass spectra for precise measurement of isotope average centroid mass of peptides and proteins using R programming language"
Optional/General comments	Lines 191 to 193: Gaussian fitting to determine the exact maxima peak for individual peaks in an isotopic distribution and subsequent calculation of the average centroid mass is found to be appropriate mathematical approach for HDX data analysis.	Lines 191 to 193 have been modified as: Gaussian fitting to determine the exact peak maxima for individual peaks in an isotopic distribution and subsequent calculation of the average centroid mass is mathematically more appropriate approach for HDX data analysis.