



Substantive Editing - Example

The following text was generated using Google's automatic translation, from an abstract originally published in Chinese.

iTRAQ technology is the isotope relative labeling and absolute quantitative technology, mainly used in protein identification and quantitative analysis, combined with tandem mass spectrometry analysis, has become one of the main means of proteomics research. Because of the differences in the expression of parasite proteins at different developmental stages and the unique life history, the selectivity and pathogenicity of the host are quite different, and the iTRAQ technique is applied to the parasite proteomics study, which can effectively find out the differential protein expressed in different stages of parasites and the differential proteins expressed by the host after infection can be analyzed by high precision. This provides a technical support for further exploring the life history of parasites and studying the mechanism of interaction with the host. The rapid diagnosis and treatment of parasitic diseases, to find new drug targets and so on. This paper briefly describes the development of iTRAQ quantitative proteomics and its application in parasitic diseases.

Revision:

iTRAQ (isobaric Tags for Relative and Absolute Quantitation) technology is the isotope relative labeling and absolute quantitative technology, an analytic tool used mainly used in for protein identification and quantitative analysis, combined quantitation. In combination with tandem mass spectrometry analysis, iTRAQ has become one of the main means of a major tool in proteomics research. Because of the Due to differences in the expression of parasite proteins at different developmental stages, and the unique to a life history, the selectivity and pathogenicity of the host are quite different, and the iTRAQ technique that is applied unique to the each parasite proteomics study, which can effectively find out The differential protein expressed in different stages of parasites and the differential proteins expressed by the host after, the host's reaction against parasite infection can vary considerably. When iTRAQ technology is used for the study of parasite proteomics, differences in the expression patterns of parasite's and host's proteins can be identified, and analyzed by with high precision. iTRAQ thus constitutes a valuable tool for further rapid diagnosis, for exploring the parasites' life history of parasites histories, and studying the their mechanism of interaction with the host. The rapid diagnosis and treatment of, and also for analyzing potential drug targets for treating parasitic diseases, to find new drug targets and so on. This paper briefly describes the development of iTRAQ as a tool for quantitative proteomics, and its application in the study of parasitic diseases.

Comment [Query 1]: Text in blue represents text that had to be written de novo by the Editor.

Comment [Query 2]: Text highlighted in yellow represents text that had to be deleted and replaced by new text.

159 words → 77 words were rewritten (48% of the original text had to be replaced)

Edited text:

iTRAQ (isobaric Tags for Relative and Absolute Quantitation) technology is an analytic tool used mainly for protein identification and quantitation. In combination with tandem mass spectrometry analysis, iTRAQ has become a major tool in proteomics research. Due to differences in the expression of parasite proteins at different developmental stages, and to a life history that is unique to each parasite, the host's reaction against parasite infection can vary considerably. When iTRAQ technology is used for the study of parasite proteomics, differences in the expression patterns of parasite's and host's proteins can be identified, and analyzed with high precision. iTRAQ thus constitutes a valuable tool for rapid diagnosis, for exploring parasites' life histories, and their mechanism of interaction with the host, and also for analyzing potential drug targets for treating parasitic diseases. This paper briefly describes the development of iTRAQ as a tool for quantitative proteomics, and its application in the study of parasitic diseases.