

A new field, palaeoproteomics—the study of ancient proteins—has been receiving more attention, leading to proposed guidelines that will establish a foundation for research.

Proteins have the ability to preserve ten times longer than DNA and has the ability to offer scientists a look into the past. Palaeoproteomics can be used to study everything from extinct species, to our ancestors' diets, to the evolution of diseases. Scientists can now use trace amounts of archaeological proteins to reconstruct the relationships of extinct megafauna, track the spread of dairying in prehistory, and characterize immune responses in people who died thousands of years ago.

The study of these ancient proteins has expanded the field exceptionally, however, palaeoproteomics is facing many of the same challenges that the field of ancient DNA was once confronted with—specifically, a lack of consistency in data reporting standards, authentication measures, and procedures taken to avoid contamination. To avoid false claims from lab contamination and misinterpreted data, this guide, published in *Nature Ecology & Evolution*, aims to support good practices in the field and produce more accurate and consistent results.

The team charged with creating the new guide includes international researchers from many of the top universities and institutes currently operating in palaeoproteomics, including the Max Planck Institute for the Science of Human History, the Max Planck Institute for Evolutionary Anthropology, the University of Copenhagen, the University of York, the University of Turin, the University of Oklahoma and the University of Zürich/ETH

Zürich.

However, it must be noted that these authors do not intend to create rigid, unbendable rules, or to overturn existing standards, but rather to consolidate and strengthen the field's best practices.

Even though palaeoproteomics is a relatively new field of study, that means there is so much to explore and uncover.

“Palaeoproteomics holds enormous potential to dramatically expand archaeological, palaeontological and evolutionary research,” explains co-lead author Jessica Hendy, of the Max Planck Institute for the Science of Human History.

“It is crucial that the discipline hold itself to high standards in order to ensure that it is able to meet this potential.”

For more information on palaeoproteomics and the new guidelines, [click here](#).

Protein analysis (young or old) is common in several fields of study. However, one of the biggest challenges that seem to face protein chemists when performing protein LC separations is protein adsorption—proteins adhering to the surface of an UHPLC/HPLC column components such as frits and hardware. This can lead to decreased protein sensitivity, recovery issues, and high LC column backpressure.

If protein adsorption is affecting your protein LC separation, then it might be time to try a column cleaning procedure in your HPLC protein purification protocol or peptide purification reversed phase HPLC method.

However, the best way to eliminate protein adsorption all together is using biocompatible UHPLC/HPLC column hardware—bioZen LC columns. bioZen consists of a new titanium infused biocompatible hardware and frit that eliminates unwanted secondary interactions that can cause carryover or recovery inconsistency.

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