

The article “Palaeoproteomic identification of a whale bone tool from Bronze Age Heiloo, the Netherlands” is very well written and makes a significant contribution by expanding the previously unavailable COL1A1 and COL1A2 reference sequences for six baleen whale species and will certainly be useful for future studies.

I have a few minor suggestions to further enhance the quality of the article:

The aim of this study is indeed the proteomic study of the specimen under investigation, but I think some more information on the context can be useful to better understand and contextualise. For example, were any animal bones found in this site? of which animals? other bone artefacts?

Figure 2: Consider adding markers on the figure to indicate where the samples were taken for proteomic analysis. Specify how the samples were collected and what was analysed (powder or fragment).

ZooMS Protocol: Specify how long the samples were left in acid.

Since the samples are from a single artefact, it might be useful to include the ZooMS spectra obtained from the analyses (even with both protocols, cold acid and AMBIC), to show the spectrum quality, the preservation of the sample, and how this changes based on the protocol in terms of obtaining taxonomic information.

Why was a destructive sampling method chosen over a less invasive one?

SPIN: Are there differences in the specificity of the determination within the SPIN framework considering the different protocols used?

“The extraction blank was matched to *Bos* sp. by the SPIN script, but it has been excluded from Table 2 as 84% of the peptide spectral matches in the blank were derived from the trypsin used for digestion. The blank intensity signal can therefore be regarded as background noise.” How do you explain this? Is it normal for the blank to be matched with *Bos*? Elaborate on this point to better support and validate the other results obtained.