***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

No power analysis was used to estimate sample size.

For archaeological samples, we were constrained by the number of objects available for analysis. We analysed three double-buttons from the two main archaeological sites (Havnø and Hornstaad, where the taxonomic determination was uncertain) and one for the Pestera site, where the determination was already available on morphological basis. This information can be found in the main manuscript and in Supplementary Files 1 and 3.

For reference shells, we analysed five freshwater molluscs (one shell for each taxon) and two marine (one shell for each taxon). Using one biological replicate only is customary in the proteomics analysis of shell matrices. The analysis of five shells within a single clade (unionoids) is exceptional (typically, only one taxon is analysed per clade). This information is available in the main manuscript and in Supplementary Files 2 and 3.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

We use a multi-analytical approach in order to validate our results (for example, the authenticity of the protein sequences from ornaments is assessed by analyzing the extent of amino acid racemization, the frequency of deamidation, and the validation of product ion spectra). We provide sample size, number of replicates (biological and technical), identification of any potentially compromised samples for each of the analytical methods used, and this is described in Supplementary File 3, sections 3.1, 3.2, 3.3, 3.4, 3.5.

We did not exclude any outlier.

Proteomics raw data were deposited in the ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the PRIDE partner repository with the data set identifier PXD011985.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Due to the sample size and the nature of the experiments reported, statistical assessment of the data was not appropriate. For the measurements of stable isotopes and amino acid data we provide mean and standard deviation values (Supplementary File 3, sections 3.3 and 3.4).

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

This information does not apply to our study as we were conducting a qualitative comparison between proteomes from archaeological ornaments of unknown taxonomy and reference shells of known origin.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

We provide source data and R code used to produce Figure 3.