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check that references are properly cited. especially in the case of older papers, it is important to make sure that all references are included and to justify the inclusion of old references from secondary literature. for the sake of transparency, it is recommended that older references are cited using the system for information on scientific literature (sigle) [27]. depending on the format of the paper, the reference list could be included in the text body of the manuscript or an appendix. references must be easily accessible, easy to cite, and free of improper formatting. include titles and keywords of relevant databases (e.g. embase, scopus, pubmed). the title should also include a general description of the study, such as the experimental settings, treatments, and biological context. describe the methods used for the experiments and provide adequate details about the materials and the apparatus, including source, breed, and preparation. for animal research, indicate whether the studies were conducted under license, and whether relevant protocols were approved by an institutional animal care and use committee. whenever possible, describe the level of behavioral training and housing conditions of subjects used in the experiments. post-processing experimental data requires special attention to data types. unstructured data sets are usually visualized first by pca (see below) and can then be incorporated into a clustering analysis as a second step. for structured data (e.g. mass spectra), data processing typically involves peak list generation followed by compound identification using different library-based search engines [14]. however, as the number of new compounds increases, the time needed for search and identification decreases dramatically. electronic libraries are fast, easy to use, and reliable [4] ; however, verification of the compounds' structures should preferably be done on the original spectra, unless there is information about the spectra in the supplementary material. in such cases, the specific library used to identify the compound is provided in the data tables. it is critical that spectra be appropriately identified by compound; if a compound is not identified, the identification should be

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accompanied by relevant spectra, peak lists, and related information.

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information science is an interdisciplinary field of research and practice in which the science of information-seeking, use, and management plays an important role. scientific information includes not only the published scientific literature but also other publications available to the public in libraries, the professional press, and broadcast media. library science is the branch of science concerned with the efficient operation of libraries as information centers. this course is designed to familiarize students with both the theories and applications of information science. topics include the importance of a research library, the public library, and the information profession; the design, acquisition, cataloging, and organization of libraries and other information resources; the circulation of printed material; and libraries in the information age. ethical and legal issues in the management of information resources are also covered. courses will be delivered in both the school of information studies, university of london, and the school of history, philosophy and religious studies, university of london. students are expected to attend lectures in their department of choice. this course introduces the basic concepts and terms relevant to many types of macromolecular structure-function relationships. we introduce students to structural and mechanistic concepts via an intuitive approach, and then develop examples of these concepts using several well-characterized proteins in their native state. in this way, students will be made aware of the richness of existing information about proteins and the need to be able to find and synthesize useful information. students will use ideas from a variety of fields in their development of models of proteins, and will become familiar with the various representations of proteins, such as drawing, electronic drawing, and 3d modeling. at the same time, they will be introduced to the general concepts in biochemistry and biophysics, including protein structure and enzymology and their applications. this course is intended to encourage thoughtful, formal thinking about protein structure and function, and will help ensure that students are aware of concepts, terminology, and analyses relating to all biological macromolecules. in addition, through a variety of hands-on practical laboratory exercises, students will be introduced to biochemical methods of analysis and protein characterization.

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