

From Bench to Internet: Sharing Proteomics Data and Methods through the Open Access Journal

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Proteomics is a rapidly growing research field with potential consequences for all bioscience. Advances in proteomics technologies, including mass spectrometry coupled with bioinformatics, have enabled us to produce large amounts of data from the entire protein complement of a cell, tissue or organism under different conditions. Now, these advances are presenting us with complex challenges around data management. To promote data sharing in the scientific community, proteomics data and datasets coupled with detailed metadata need to become more FAIR: findable, accessible, interoperable and re-usable. Addressing these challenges and facilitating better proteomics data management require the development of applicable standards based on formal structures and procedures. To this end, the Japanese Proteomics Society (JPrOS) has launched a new data journal – the *Journal of Proteome Data and Methods (JPDM)*.

JPDM is a peer-reviewed, fully open access journal that is published online-only via the J-STAGE platform. *JPDM* publishes four article types: *Data Descriptor*, *Protocol*, *Data Processing Note*, and *Review*. The journal will consist primarily of *Data Descriptor*, which are intended to provide detailed descriptions of data rather than to address hypotheses or to present novel scientific interpretation or insight. They include metadata on the samples analyzed, the sample preparation methods, mass spectrometry measurements and data analysis. We ask authors to complete a dataset summary table to provide basic information on the data and to show why the data described in the *JPDM* article is of value to the greater scientific community. These requirements make datasets more easily searchable and thus more useful to others.

JPDM collaborates closely with the Japan Proteome Standard Repository/Database (jPOST), one of the partner repositories in the ProteomeXchange Consortium (PX). When data producers deposit their datasets in jPOST and publish detailed metadata in *JPDM*, the journal sends feedback to the PX repository. *JPDM* thus adds value to proteome datasets by providing detailed metadata. As *Data Descriptor* contain only the metadata and the important aspects of its generation, authors can still publish research based on their data in other journals.

In addition to *Data Descriptor*, *JPDM* provides a forum for articles highlighting and sharing experimental approaches (*Protocol*) and computational tools (*Data Processing Note*) that may have never left the lab or normally go unnoticed in published research. *Review* present novel or unique overviews of recent or important developments in proteomics.

JPDM aims to accelerate the visibility of all kinds of data, protocols and tools in the field of proteomics, making them easier to find, access, inter-operate and re-use. We hope you will join us in making the journal a success by submitting your vital work to *JPDM*.

Editor-in-Chief, Journal of Proteome Data and Methods

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