

STRENDA DB –a Web-based Assessment and Storage Tool for Enzymology Data

The STRENDA Commission (STandards for Reporting ENzymology Data, www.beilstein-strenda.org) made up of experts from the enzyme chemistry community and supported by the Beilstein-Institut, has developed the STRENDA Guidelines in tight consultation with the community. The aim is to improve the quality of enzyme function data in the literature. Today, more than 60 biochemical journals already recommend authors to refer to these guidelines when reporting enzyme kinetics data.

To enable scientists to easily prepare data for manuscripts, the STRENDA Commission has developed a web-based portal for the direct electronic submission of data by the authors prior to publication. This portal called STRENDA DB provides an assessment tool with which authors, journals' editors and reviewers can check whether the reporting of experimental data is compliant with the STRENDA guidelines and thus matches the instructions for authors from the journals. The data entered are stored in STRENDA DB and will be made publically accessible after they have been published in a journal. More than 20 biochemical journals recommend their authors to deposit their experimental data in STRENDA DB.

However, as Findability and Accessibility of datasets stored in STRENDA DB are relatively easy to implement, making the data interoperable is still a challenge. There might be multiple ways to address this issue (and I'd be keen to learn more about this) and certainly, a reasonable way is the creation of a standardized data exchange format that allows the seamless transfer of data from the lab bench via tools to databases and back. Here, I will shed very briefly some light on EnzymeML which is a community-developed data exchange format in its first version for enzymology and biocatalysis data that also provides an API for Python and Java libraries to be integrated into both applications and databases.

Type of Poster

A solution

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Session Classification: Poster

Track Classification: Poster