

Introduction to the Standards for Reporting Enzymology Data as Proposed by the STRENDA Commission

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This journal follows the recommendations of the STRENDA (Standards for Reporting Enzymology Data) Commission of the Beilstein-Institut for the reporting of kinetic and equilibrium binding data. Detailed guidelines can be found at (<http://www.strenda.org/documents.html>). All reports of kinetic and binding data must include a description of the identity of the catalytic or binding entity (enzyme, protein, nucleic acid or other molecule). This information should include the origin or source of the molecule, its purity, composition, and other characteristics such as post-translational modifications, mutations, and any modifications made to facilitate expression or purification. The assay methods and exact experimental conditions of the assay must be fully described if it is a new assay or provided as a reference to previously published work, with or without modifications. The temperature, pH and pressure (if other than atmospheric) of the assay **must** always be included, even if previously published. In instances where catalytic activity or binding cannot be detected, an estimate of the limit of detection based on the sensitivity and error analysis of the assay should be provided. Ambiguous terms such as “not detectable” should be avoided. A description of the software used for data analysis should be included along with calculated errors for all parameters.

First-order and second-order rate constants should be reported in units of s^{-1} and $M^{-1} \cdot s^{-1}$, respectively. Equilibrium binding constants should normally be reported as dissociation constants with units of concentration (M, mM, μ M, nM). The values k_{cat} , k_{cat}/K_M and K_M from steady-state enzyme kinetics should be reported in units of s^{-1} , $M^{-1} \cdot s^{-1}$ and concentration (mM, μ M, nM), respectively. The steady-state specific activity of an enzyme should normally be reported as a k_{cat} . If there is considerable uncertainty in the molar concentration of the catalyst, the specific activity should be reported as a V_{max} (nmol, μ mol) of product formed per amount of protein per unit time (e.g. μ mol \cdot mg $^{-1}$ \cdot s $^{-1}$).

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