

“Trust but verify” attitude in structural biology

Mariusz Jaskólski

Department of Crystallography, Faculty of Chemistry, A. Mickiewicz University

A number of reports have warned that a growing fraction of biomedical research cannot be reproduced. Structural biology, traditionally viewed as the gold standard in life science, is not without sin as problematic models end up from time to time in the Protein Data Bank (PDB), contaminating the literature and often frustrating other efforts, such as structure-based drug design. The errors are most frequent at the sensitive macro-/small-molecule interface and are manifested by suboptimal/unsatisfactory/or wrong modeling of ligands in the electron density maps. We have analyzed several classes of medicinally important PDB models (including β -lactamases and SARS-CoV-2 proteins) and found errors of various severity, as well as serious ripple effects in the scientific literature. In many cases the models could be significantly corrected and redeposited in the PDB. We always contacted the original authors, with reaction ranging from hostility to fruitful cooperation. The open questions include better quality control, treatment of the new deposits, and retraction of the invalidated papers.