

## **Speeding up the last mile of structure solution with PDB-REDO**

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### **Abstract**

PDB-REDO is an automated pipeline for the optimisation of crystallographic structure models. It has a 13-year track record of model improvement for both PDB entries and work-in-progress models from practicing crystallographers. PDB-REDO combines model refinement in REFMAC with state-of-the-art model (re)building tools and extensive validation routines. These are tied together with robust decision-making algorithms.

Here we showcase the latest developments that use the power of systematically adding knowledge from known structures to speed up the process of moving from a 'solved' structure to a high-quality structure model. We also discuss PDB-REDO features that cater specifically to high-throughput applications and drug discovery in an industrial setting.