DIY, Modular Automation Platform Built from Affordable Components for Directed Evolution and Molecular Biology, Toward Closed-Loop Workflows

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Many experiments in materials science and chemical/biological engineering rely on iterative, trial-and-error workflows: preparing many samples under slightly different conditions, running measurements, and repeating this cycle over long periods to optimize function and performance. In practice, these workflows often involve routine liquid handling and sample transfers that must be executed consistently to ensure reproducibility. However, performing such repetitive procedures manually is time-consuming, physically demanding, and prone to human error and day-to-day variability.

In this study, we use directed evolution as a concrete testbed for iterative molecular discovery workflows, where functional peptides and proteins are obtained through repeated selection cycles that must be executed reproducibly over long periods. This repetitive manual work not only places a significant burden on researchers but also introduces risks of human error and inconsistency. To overcome these challenges, we built a do-it-yourself (DIY) laboratory automation system by integrating an open-source liquid handling robot (Opentrons, OT-2) with a six-axis robotic arm (uFactory, xArm). Notably, this system was assembled in-house using commercially available components, aiming to balance accessibility and affordability without relying on expensive, highly customized solutions.

With this DIY system, we automated major steps in a directed evolution workflow, including in vitro transcription and translation, nucleic acid purification, binding selection, washing, and elution processes. A full run operated for ~11 hours with ~1 hour of human involvement mainly for initial sample preparation. Through a series of test experiments against four protein targets, the system successfully identified peptides that bind to three out of the four targets; the only negative result was BSA, consistent with its well-known promiscuous binding.

Crucially, the six-axis arm complements OT-2 by automating physical sample logistics between devices, enabling a more end-to-end workflow than liquid handling alone. The arm-integrated peripherals include temperature control, automated cap opening/closing, and magnetic-bead capture modules, enabling robust handling of tube-based workflows. A particularly noteworthy achievement is that our system selected binding peptides for targets that had previously resisted identification through manual experiments by skilled researchers, highlighting its potential to reduce manual labor while improving reproducibility and success rates.

All operations are executed from structured protocol files with automatic logging of step parameters and sample states, improving traceability and reproducibility. Building on these results, we are expanding the platform toward general molecular biology and iterative experimental loops by integrating additional instruments—thermal cycling, gel electrophoresis with automated readout, and nucleic acid quantification with data ingestion. To keep the platform modular, we are implementing standardized interfaces (Model Context Protocol, MCP) that separate workflow execution from device control and measurement readout, thereby supporting the development of closed-loop experimental workflows. Beyond directed evolution, the same architecture is applicable to iterative experimental loops common in materials discovery, where repeatable sample preparation, purification, and measurement cycles are critical.

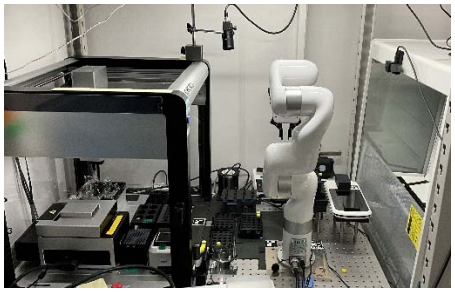

Fig. 1: Overview of the DIY laboratory automation platform.

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