

## **A solution-free crystal-mounting platform for native SAD**

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The native SAD phasing method uses the anomalous scattering signals from the S atoms contained in most proteins, the P atoms in nucleic acids, or other light atoms derived from the solution used for crystallization. These signals are very weak and careful data collection is required, which makes this method very difficult. One way to enhance the anomalous signal is to use long-wavelength X-rays; however, these wavelengths are more strongly absorbed by the materials in the pathway. Therefore, a crystal-mounting platform for native SAD data collection that removes solution around the crystals has been developed. This platform includes a novel solution-free mounting tool and an automatic robot, which extracts the surrounding solution, flash-cools the crystal, and inserts the loop into a UniPuck cassette for use in the synchrotron. Eight protein structures (including two new structures) have been successfully solved by the native SAD method from crystals prepared using this platform.

**Keywords:** native SAD, solution-free mounting tool, automation, robots