

Poster Presentation

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CCP4: a resource for macromolecular crystallography

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CCP4 has been serving the software needs of the protein crystallography community for more than 30 years. In this time the CCP4 Suite of software has been refined through contributions from some of the leading developers in the field of protein crystallographic software and the feedback of both expert and novice users. Today it is a highly comprehensive suite, providing tools and packages covering all aspects from data collection through to structure deposition. Here we will present details of the latest release series of the Suite, version 6.4. This release brings updates to many of the key elements in the Suite. The most obvious of these is the integration of the rolling updates mechanism. This is used to distribute timely fixes, update existing programs and introduce new functionality to users of the suite. Recent updates have seen updates to major programs such as phaser and imosflm/mosflm, and the introduction of a major overhaul of the Experimental Phasing pipeline Crank. An overview is given of the operation behind the updates and releases, including the jhbuild system, repositories and testing, the availability of nightly builds, and work towards the next major release of CCP4. This will see the integration of the CCP4MG package, along with preparations for the introduction of the long awaited CCP4i2.

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