

## Cover Picture

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**The cover picture shows** a compound bound to thrombin, as determined by automated protein–ligand crystallography. The picture illustrates how a diffraction pattern can be automatically analysed to reveal the binding mode of a compound given a 2D chemical structure and a known 3D structure for the protein. The compound shown was developed by means of fragment-based drug discovery, in which the binding of small, low-affinity molecules is determined by crystallography. This approach to drug discovery is enabled by the automation of protein–ligand crystallography. For details, see the full paper by W. T. M. Mooij et al. on p. 827 ff.

