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ABOUT THE COVER
The cover image shows the chemical structure of the novel RAF inhibitor BI 882370 and a schematic representation of its binding mode in the ATP pocket derived from the co-crystal structure with wild-type BRAF kinase. Arrows indicate key polar interactions between the inhibitor and the protein. Solvent-exposed parts of both the ligand and the protein residues are indicated as blue spheres. Green circles indicate amino acids with lipophilic side chains and pink circles show amino acids with polar residues. For details, see the article by Waizenegger and colleagues beginning on page 354.

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