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Molecular Cancer Therapeutics
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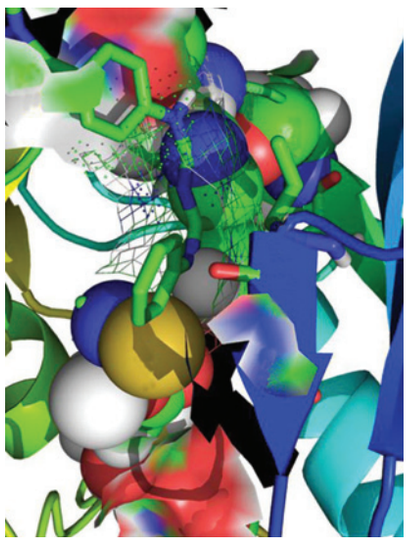
PRECLINICAL DEVELOPMENT

MOLECULAR MEDICINE IN PRACTICE

ABOUT THE COVER

The cover figure depicts a homology model indicating the binding mode of a small molecule inhibitor complex with Axl kinase. The surface represents the active site residues and the spheres depict the hydrophobic and gatekeeper site residue interactions. In addition to the overall conserved structure of the kinase domain, the ATP-binding pockets of Axl and Mer possess features that establish molecular interactions with ATP that are common to other protein kinases. For details, see article by Verma and colleagues on page 1763.



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