Molecular Cancer Therapeutics

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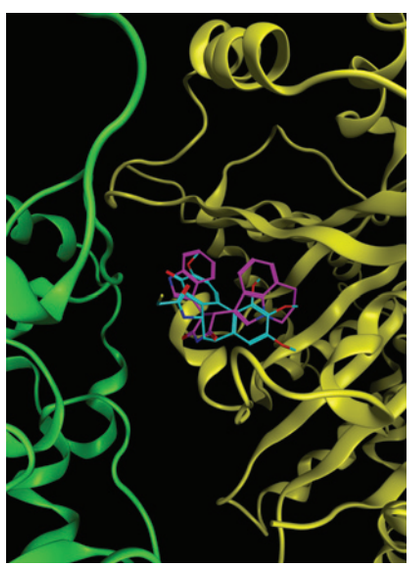
MODELS AND TECHNOLOGIES

ABOUT THE COVER

This is an image of the predicted binding model in which tivantinib (ARQ197) binds to the colchicine binding site of tubulin, calculated by GOLD docking program. Top-scored binding pose of tivantinib (magenta) to tubulin was overlaid on the structure of colchicine (cyan)-tubulin complex. Tivantinib was originally identified as a c-MET inhibitor and is currently under clinical evaluation. However, recent reports suggest that its cytotoxic activity was caused by microtubule dysfunction. Aoyama and colleagues show that tivantinib competitively inhibited binding of colchicine to purified tubulin. For more details, see the article by Aoyama and colleagues on page 2978.



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