
Subject: Viewing 3D confs with protein

Posted by [chemtv](#) on Mon, 09 Mar 2026 16:54:46 GMT

[View Forum Message](#) <> [Reply to Message](#)

Thanks for all the new capabilities. After an external docking... I have figured out how to "Append" a reference xray ligand and a very small active site selection (as SDFs). My question is: After I set the active site to be shown with another structure that works fine... but if I choose a molecule in the middle of the table, I can't get to the graphics window to rotate the view without it changing the ligand I'm trying to examine. Is there a special key to press to prevent the cursor from selecting neighboring molecules? If not I suppose I can set the "Horizontal Structure Count" to 1? Is that the only solution? Maybe I am just trying to look at too many structures anyway :roll:

Thanks,
Greg
