

Supplementary information

Title: Synthesis, biological evaluation and molecular modeling studies of phthalazin-1(2H)-one derivatives as novel cholinesterase inhibitors

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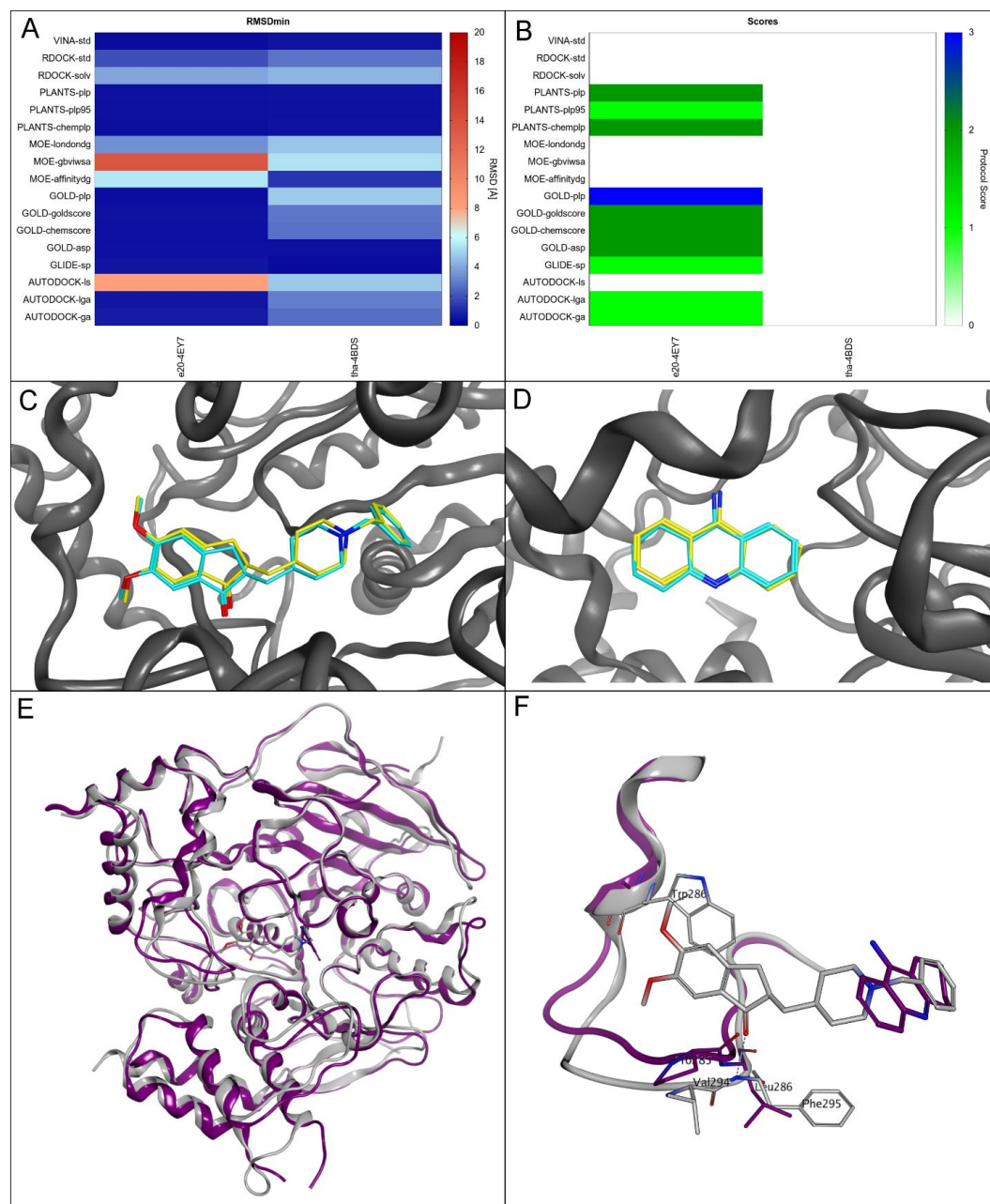
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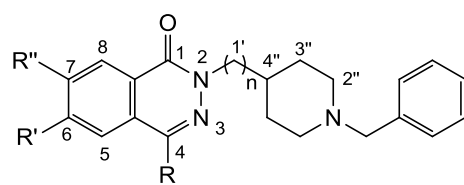
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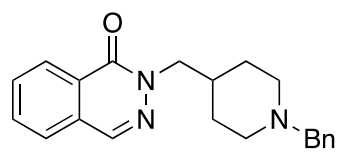


SI Figure 1. In panel A and B, the $RMSD_{min}$ and SCORE heat maps resulted from the Docking benchmark performed with Dockbench are shown. In A, the colour of the map corresponds to the minimum RMSD value obtained by the corresponding docking protocol (y-axis) and protein structure (x-axis). Similarly, in B the final score is presented using a white (weak performance) to blue (best performance) palette as colour scheme. In Panel C and D, the conformation resulted by the selected docking protocol (cyan) is superposed to the experimentally derived one (yellow) for donepezil and tacrine, respectively. In E, the superposition of the human AChE (PDB ID: 4EY7; light grey) and BuChE (PDB ID: 4BDS; violet) is reported using the ribbon representation. In panel F, the same superposition that in panel E is shown, but focusing only into the binding site, where the main differences were found (explicit residue sidechain). The donepezil and tacrine molecules as well as the residue sidechains were shown and colored according the complex they belong (AChE, light grey; BuChE, violet).

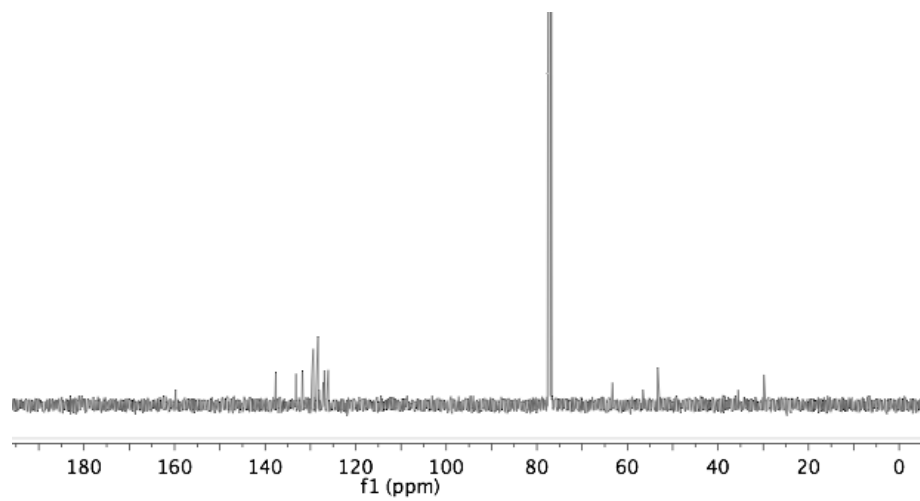
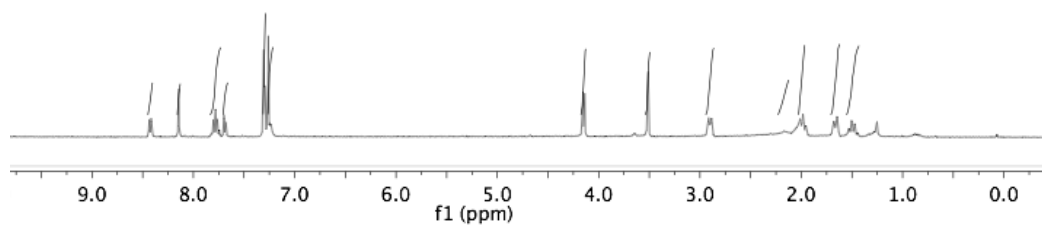


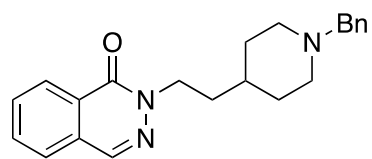
1a-j R = H, *p*-Tol, CH₃; R' = H, OCH₃;
 R'' = H, OCH₃; n = 1,2,3

SI Figure 2. General structure and atom numbering of target compounds

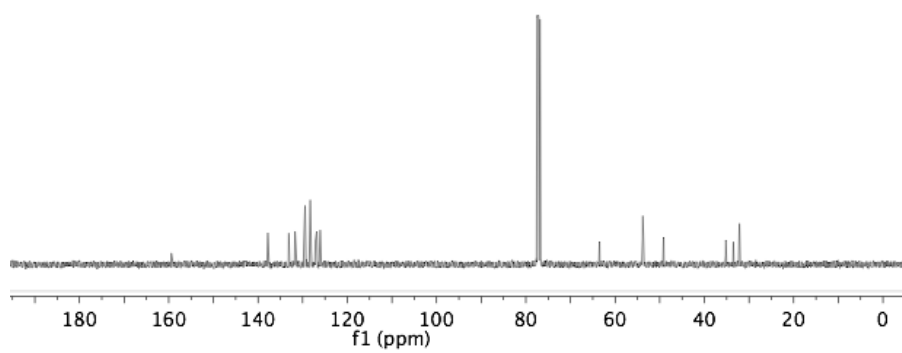
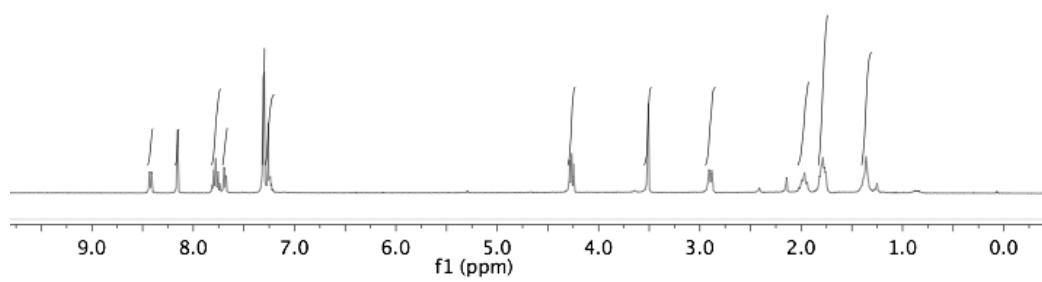


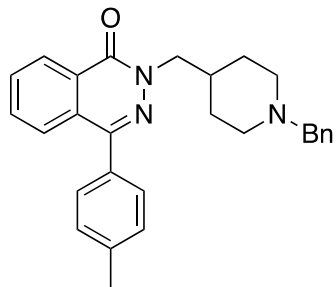
1a



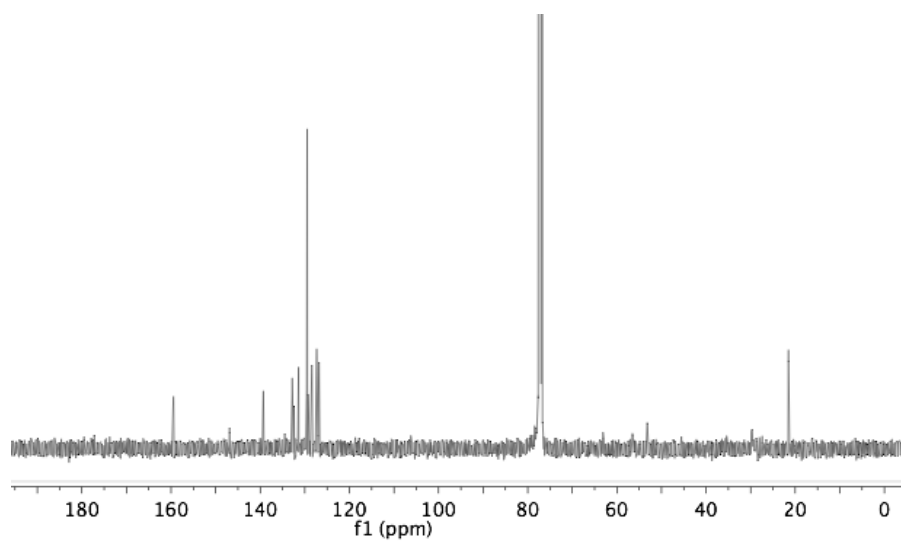
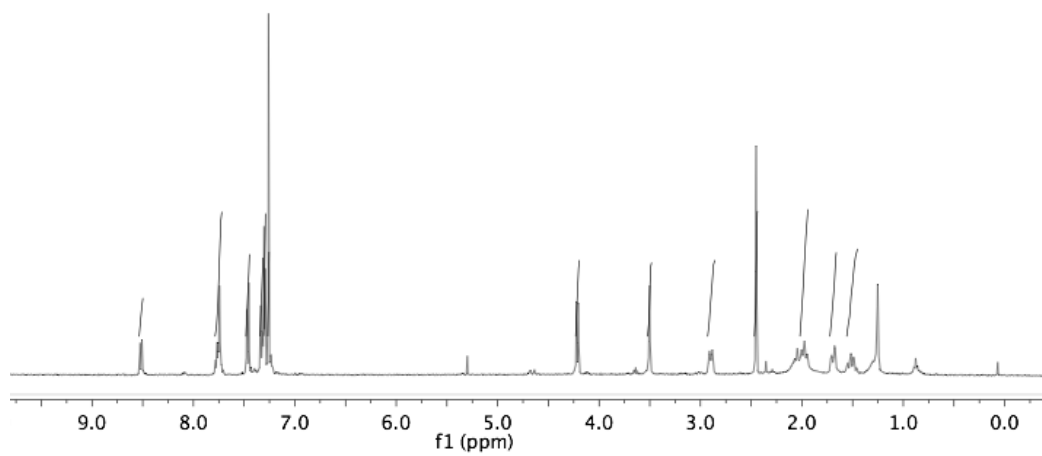


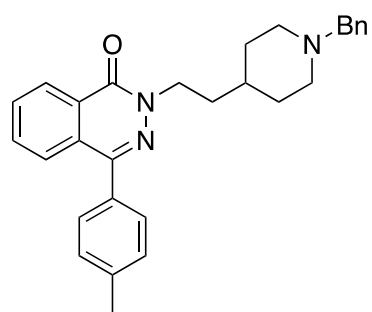
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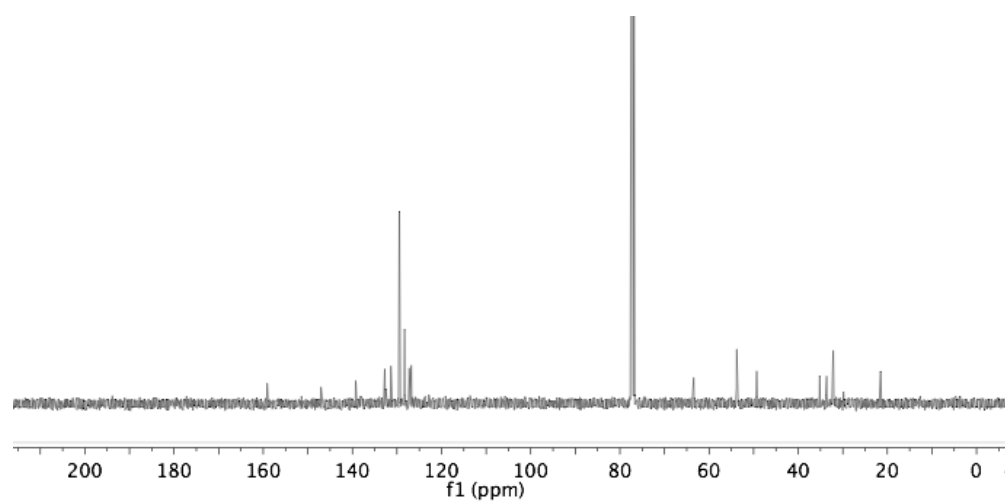
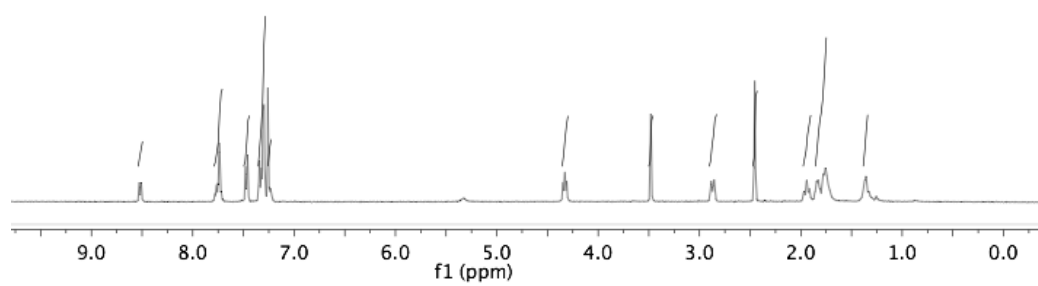


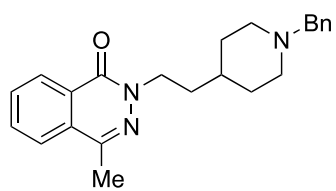
1c



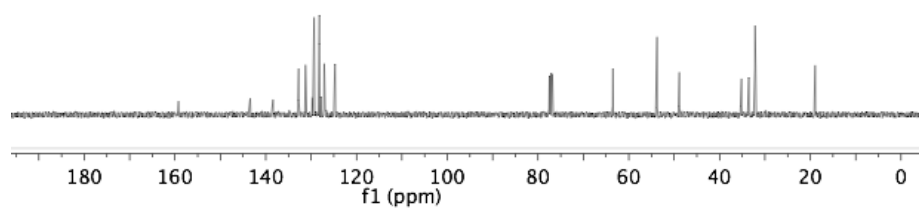
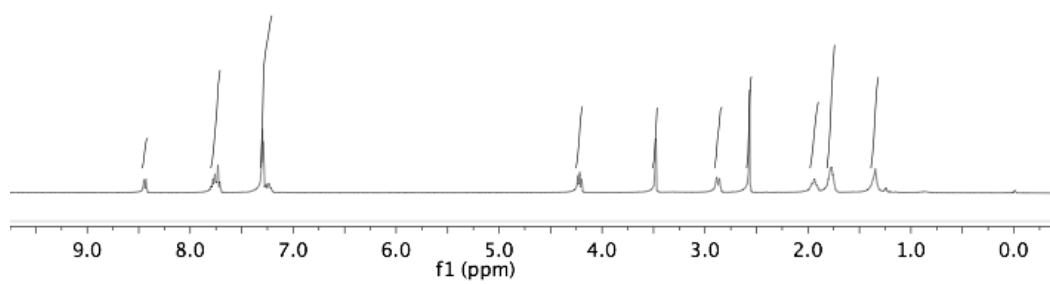


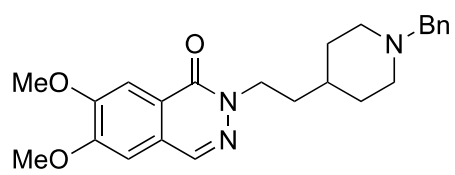
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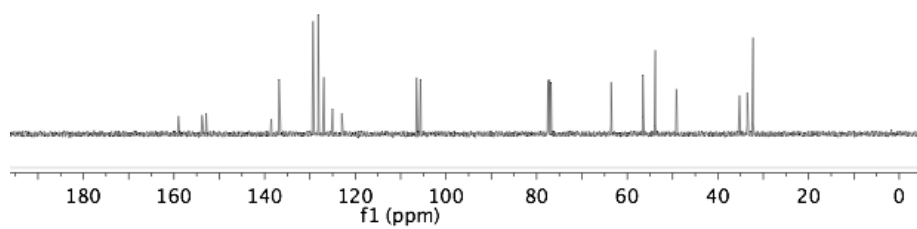
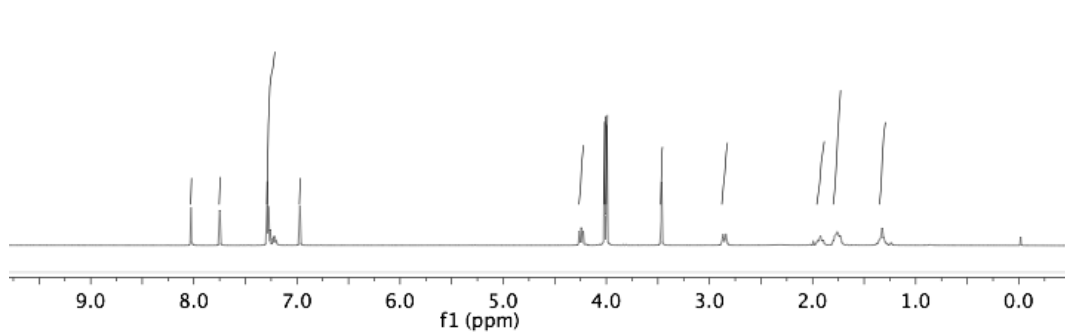


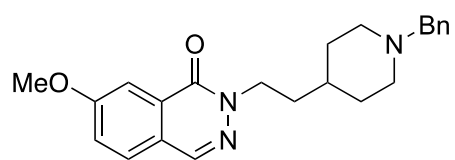
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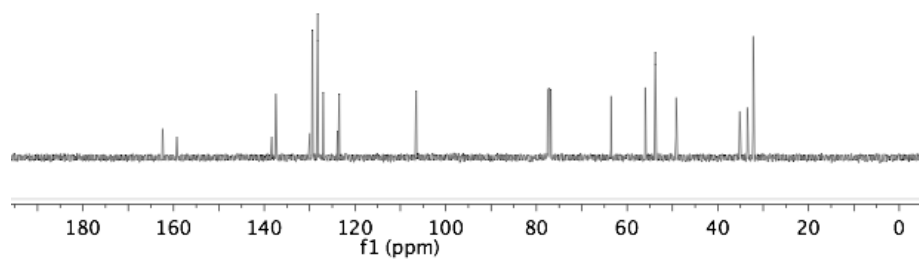
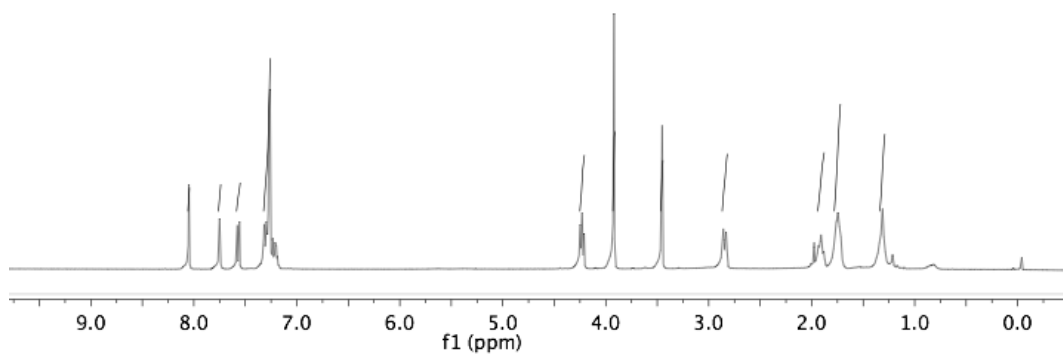


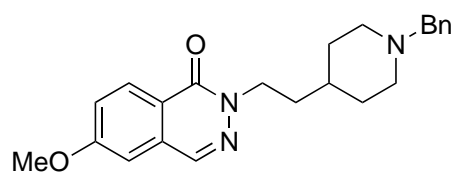
1f



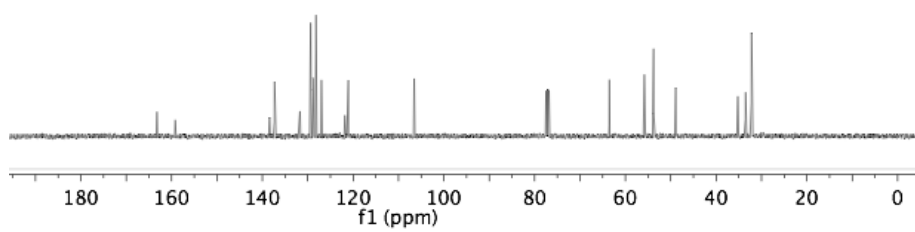
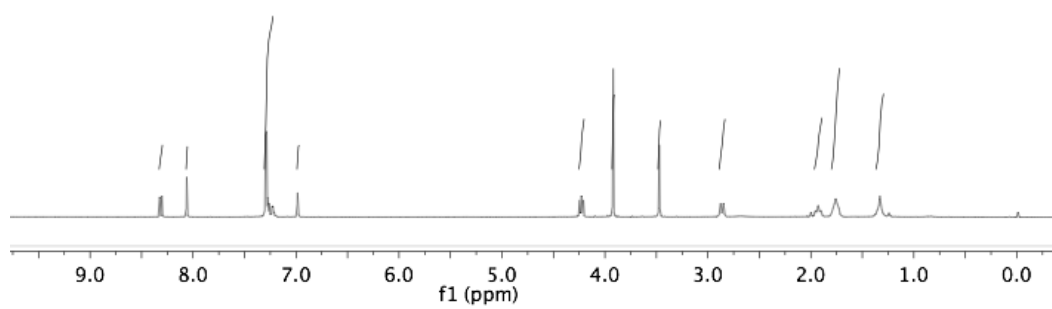


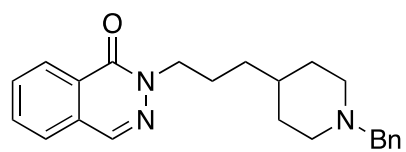
1g



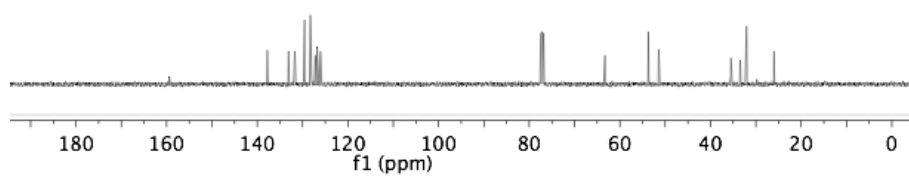
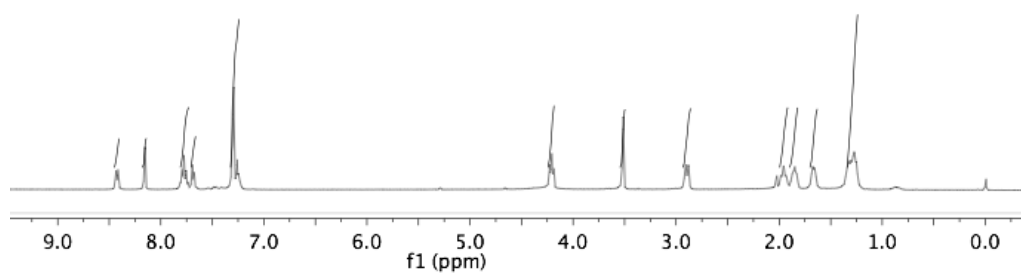


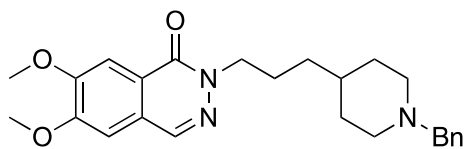
1h





1i





1j

