

Supplementary Material for

**Synthesis and evaluation of hybrid molecules targeting
the vinca domain of tubulin**

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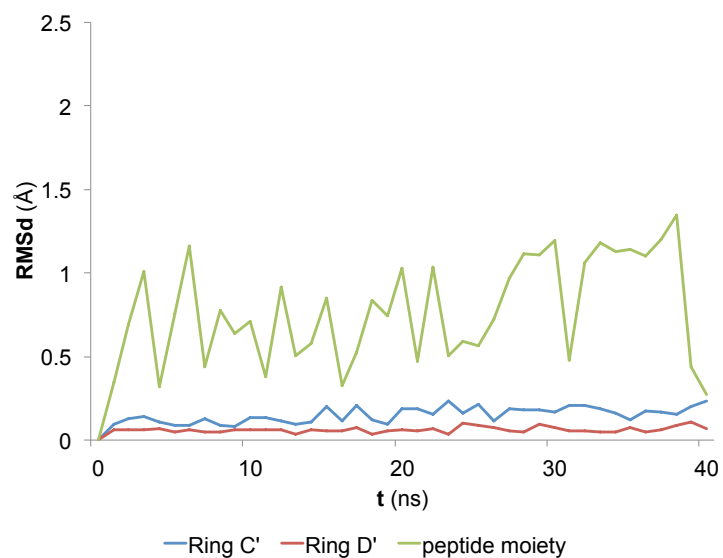
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Additional data of molecular modelling experiments	S2
¹ H and ¹³ C spectra for all new compounds	S6

(a)



(b)

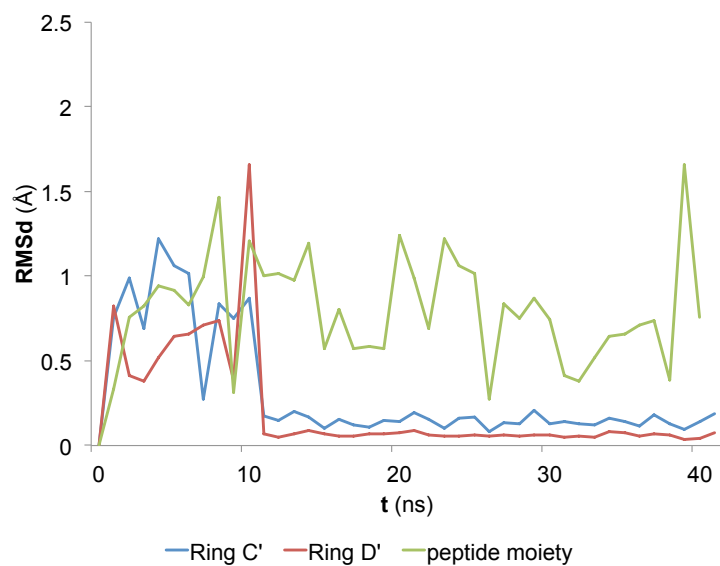


Figure S1. Time evolution of the root-mean-square deviation (RMSd, Å) of **25** (a) and **22** (b) along the unrestrained MD simulation in a box of explicit solvent at 300 K.

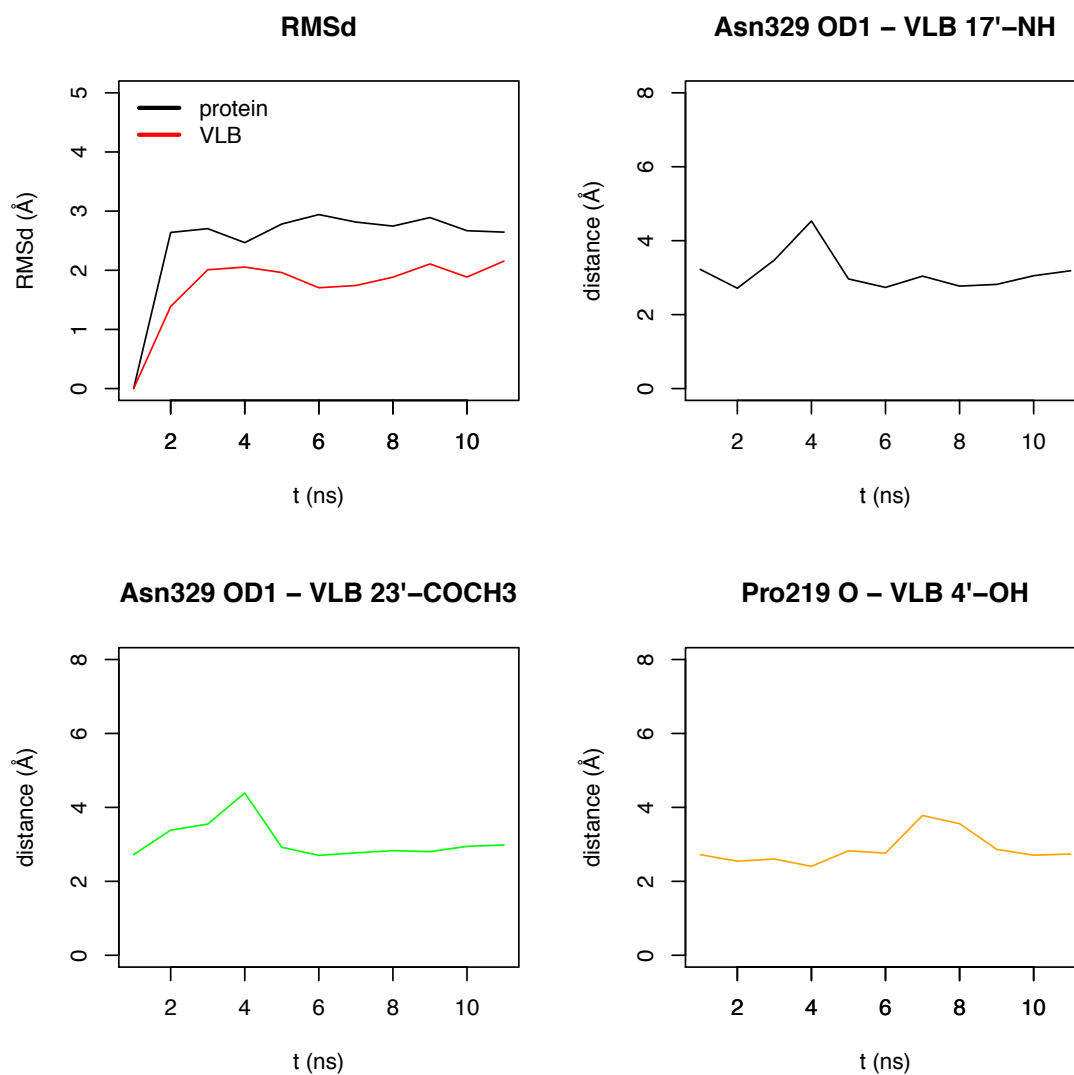


Figure S2. Time evolution of the root-mean-square deviation (RMSd, Å) and key distances (Å) corresponding to the main interactions observed for **1** within the vinca-binding domain along the unrestrained MD simulation in a box of explicit solvent at 300 K.

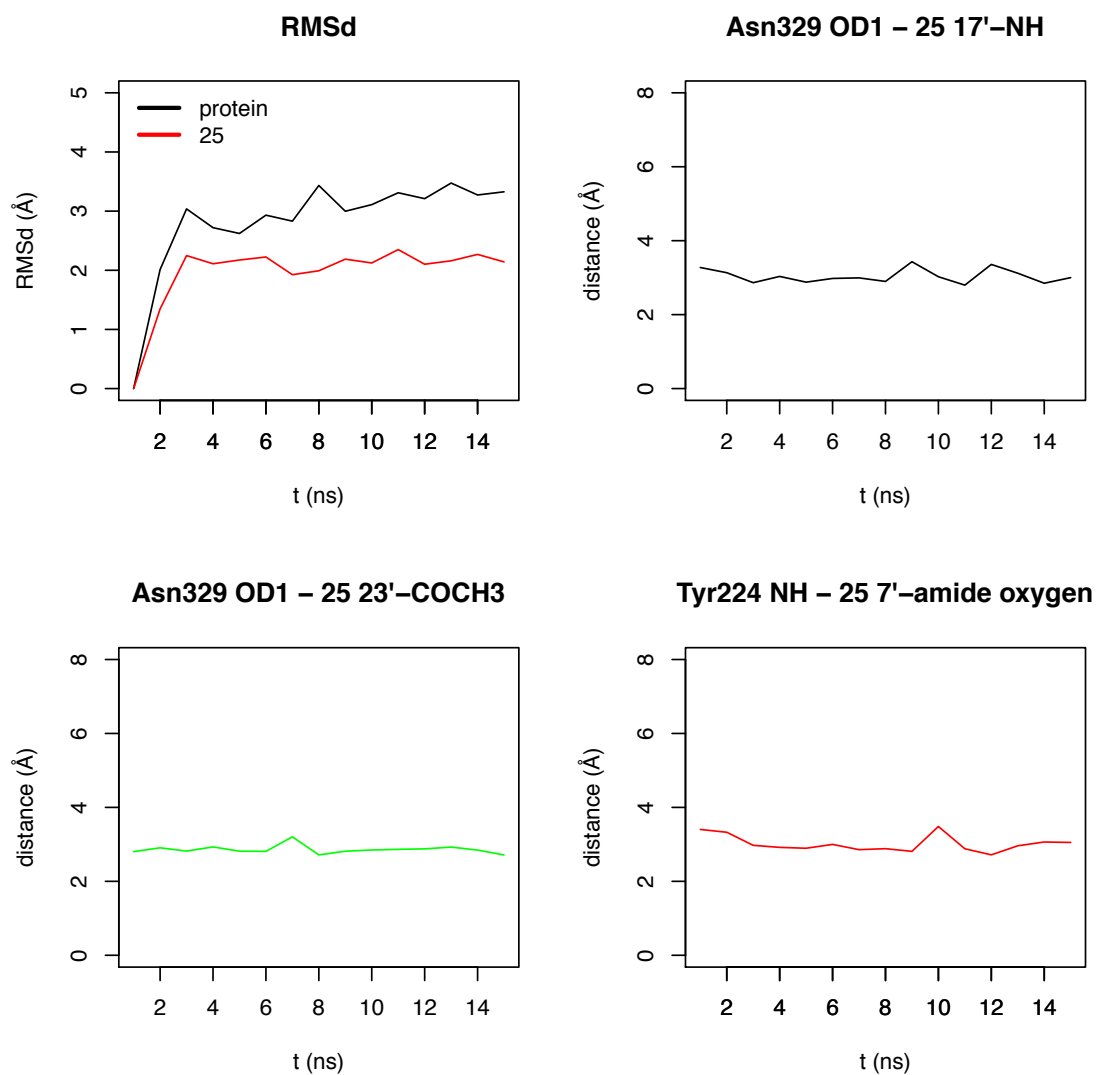


Figure S3. Time evolution of the root-mean-square deviation (RMSd, Å) and key distances (Å) corresponding to the main interactions observed for **25** within the vinca-binding domain along the unrestrained MD simulation in a box of explicit solvent at 300 K.

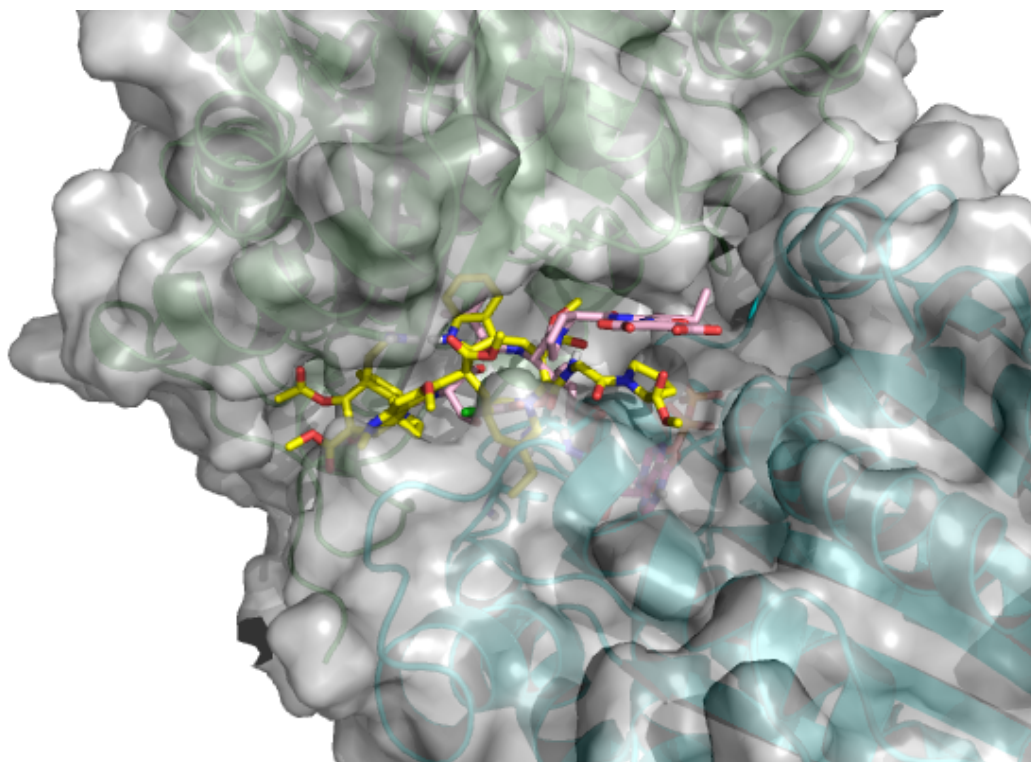
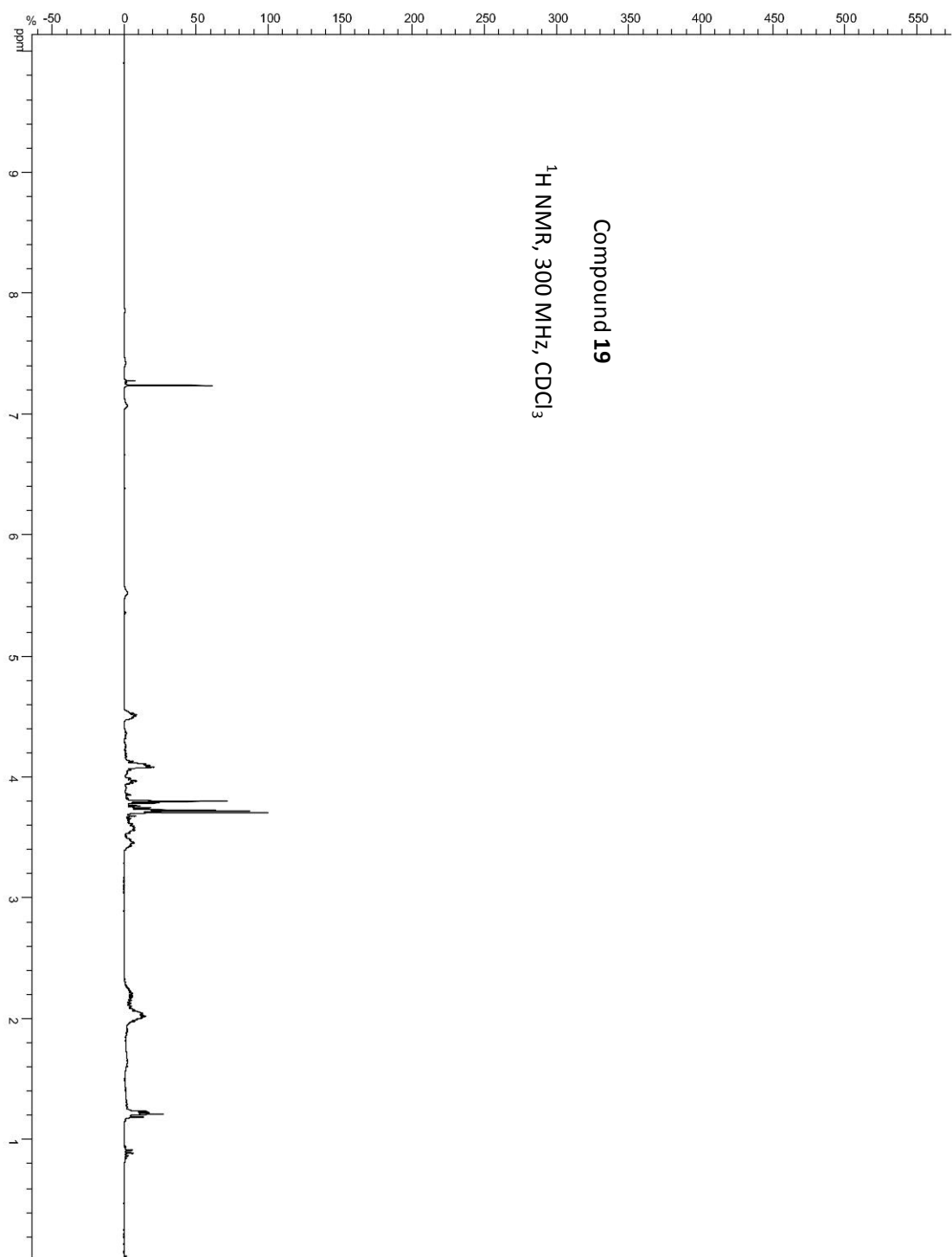
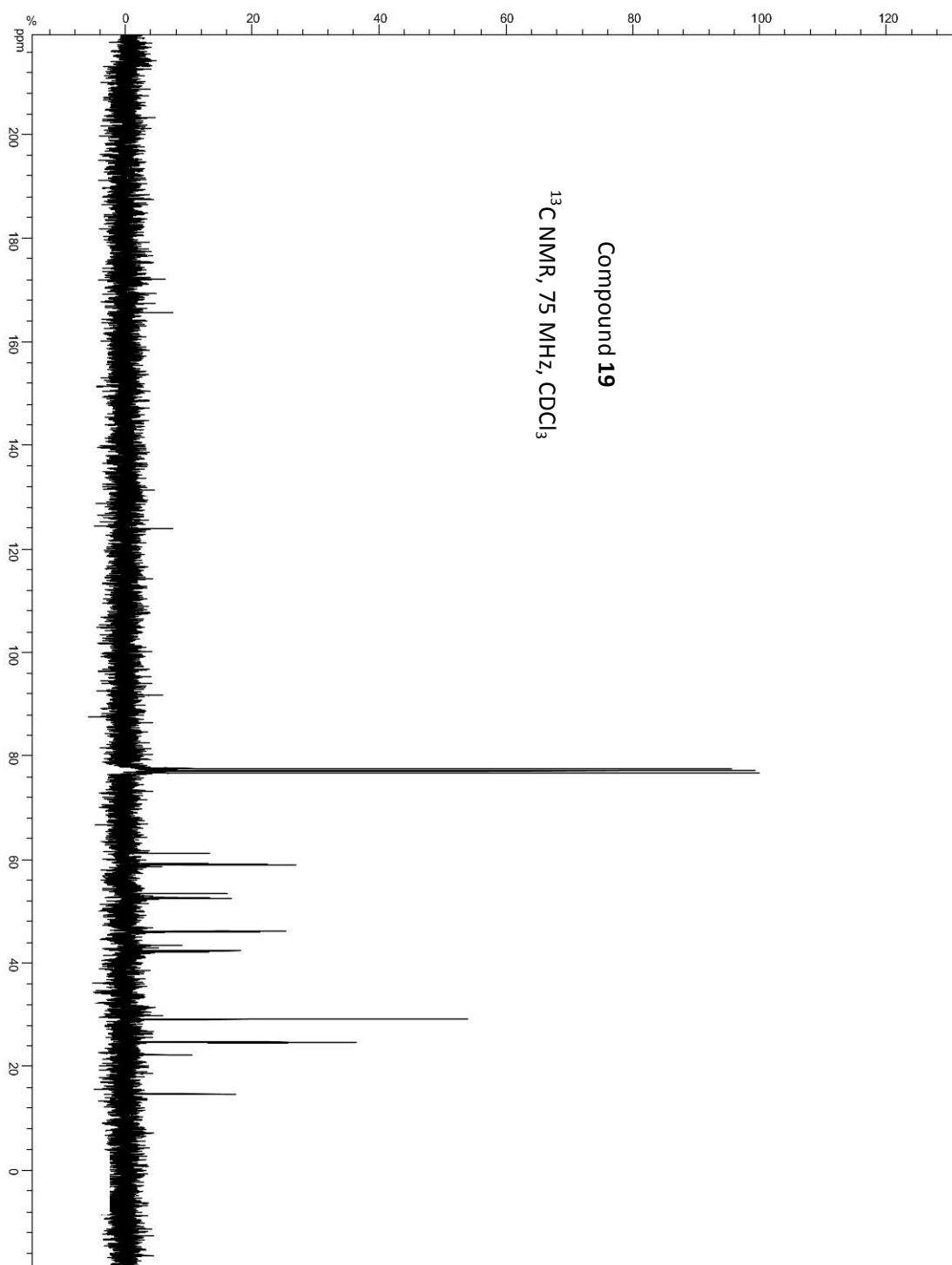
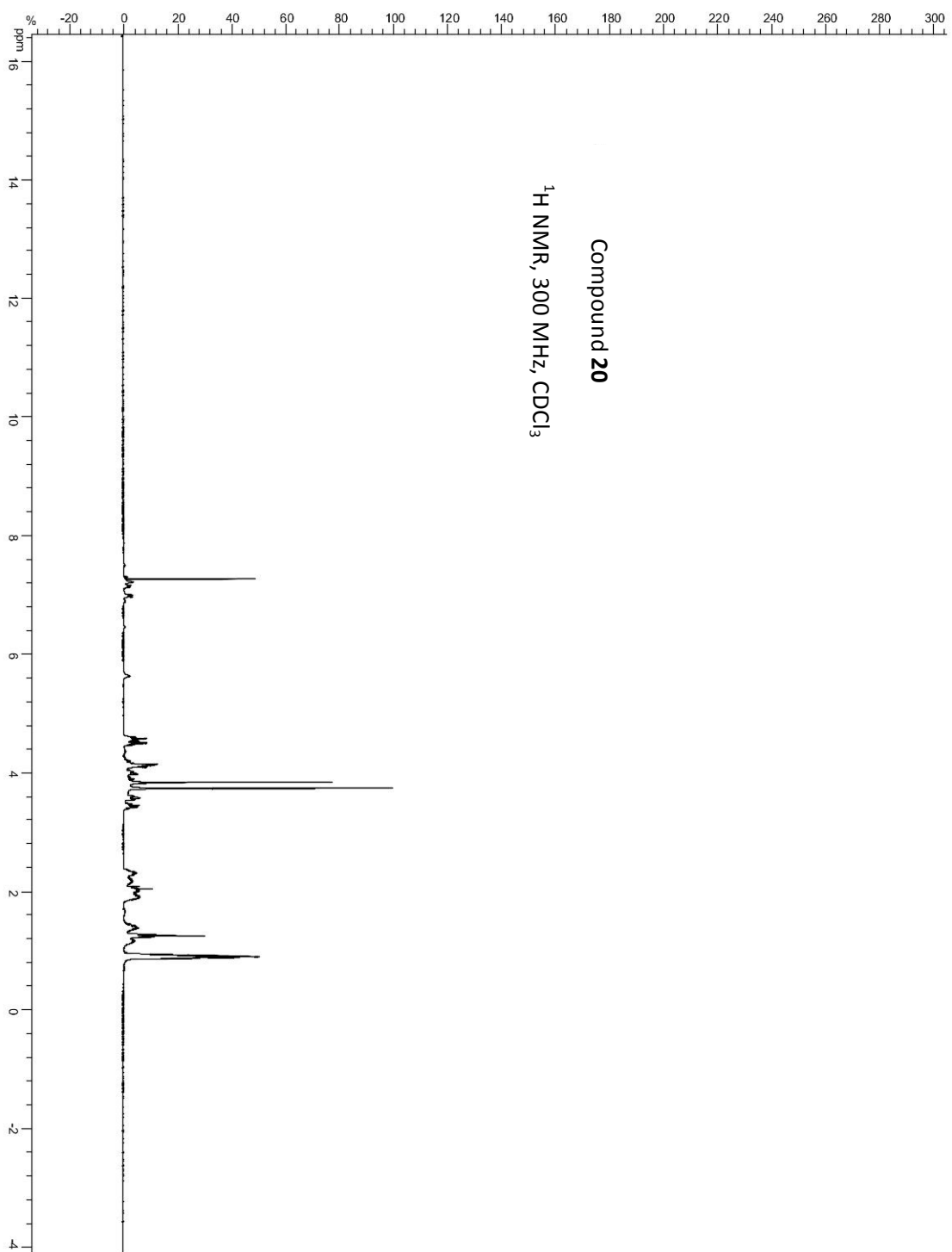
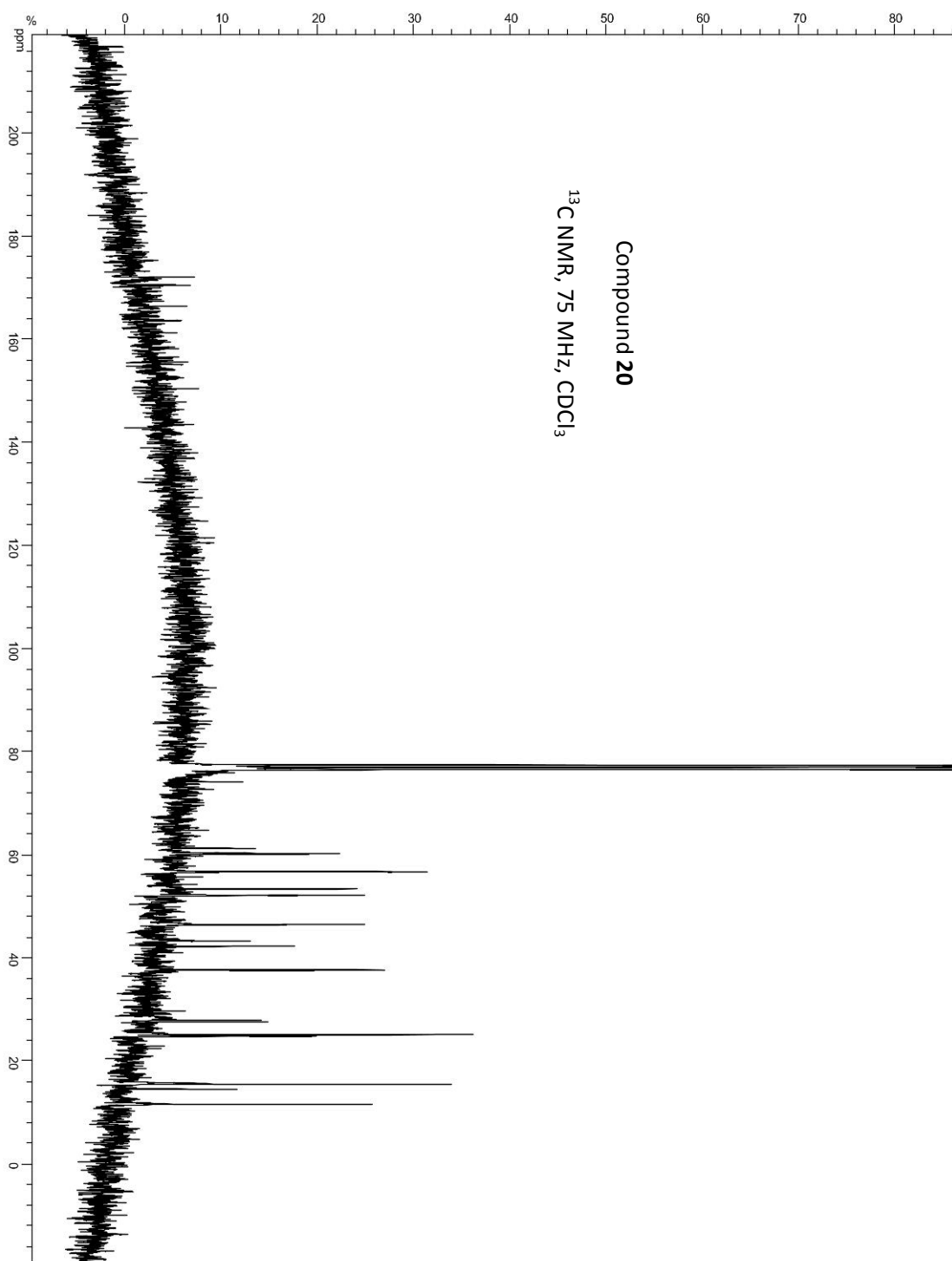


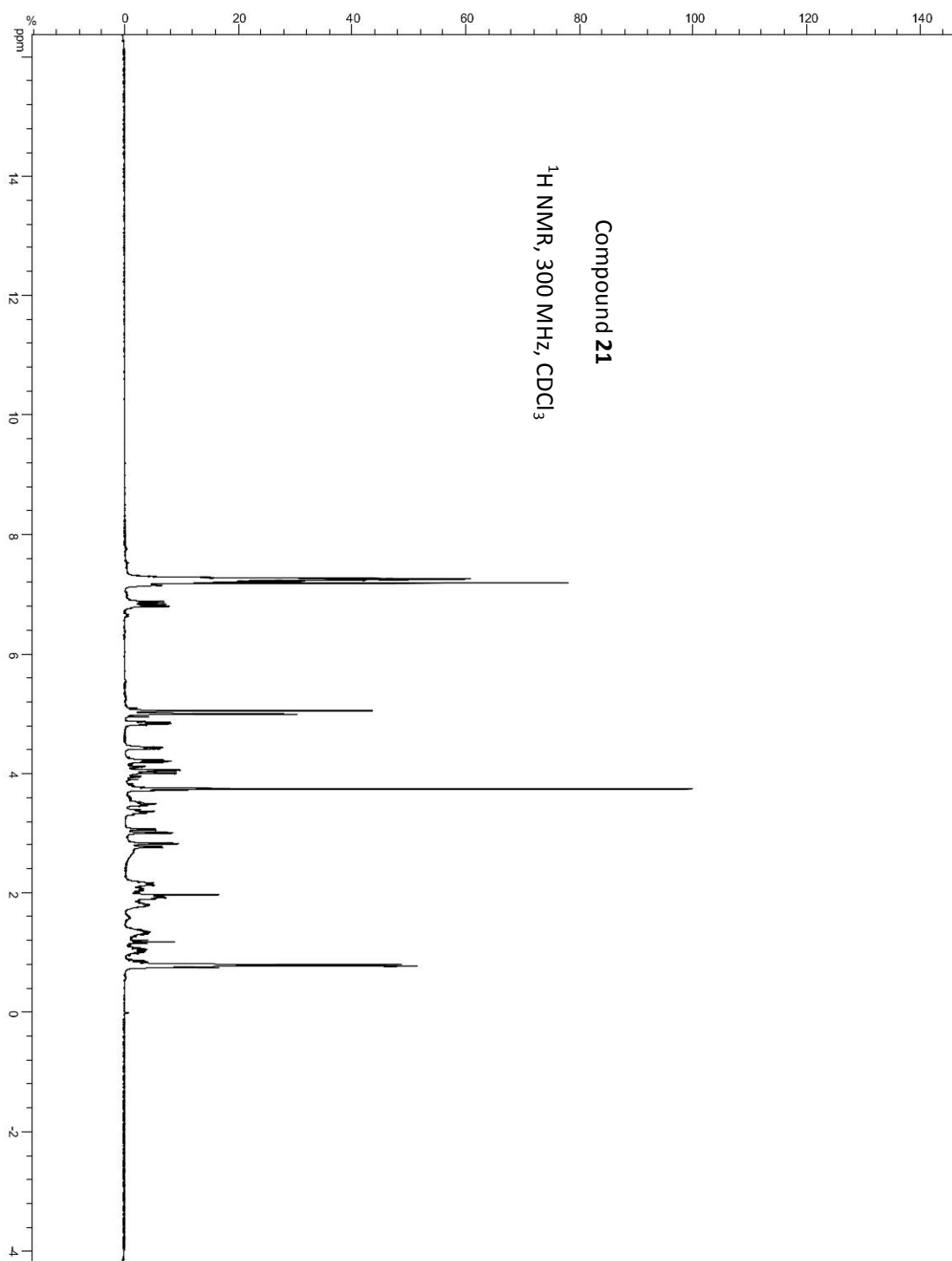
Figure S4. View of the inter-dimer interface showing bound **25** (sticks, C atoms in yellow) in a representative conformation and overlaid **4** (sticks, C atoms in pink) for reference after a best-fit superposition of the protein, which appears enveloped within a semitransparent surface. Cartoon representations of β_1 - and α_2 -tubulin are coloured cyan and green, respectively.

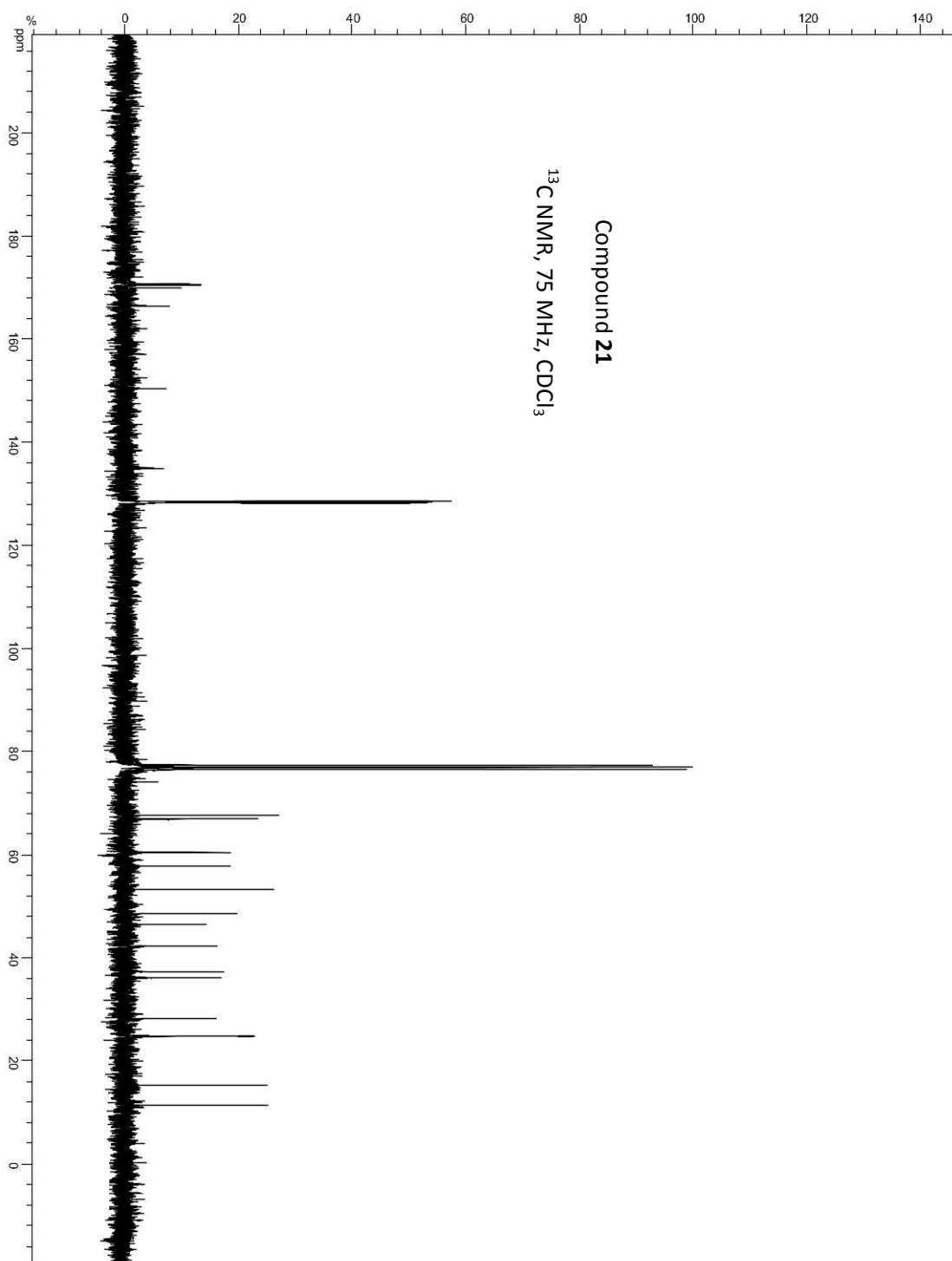


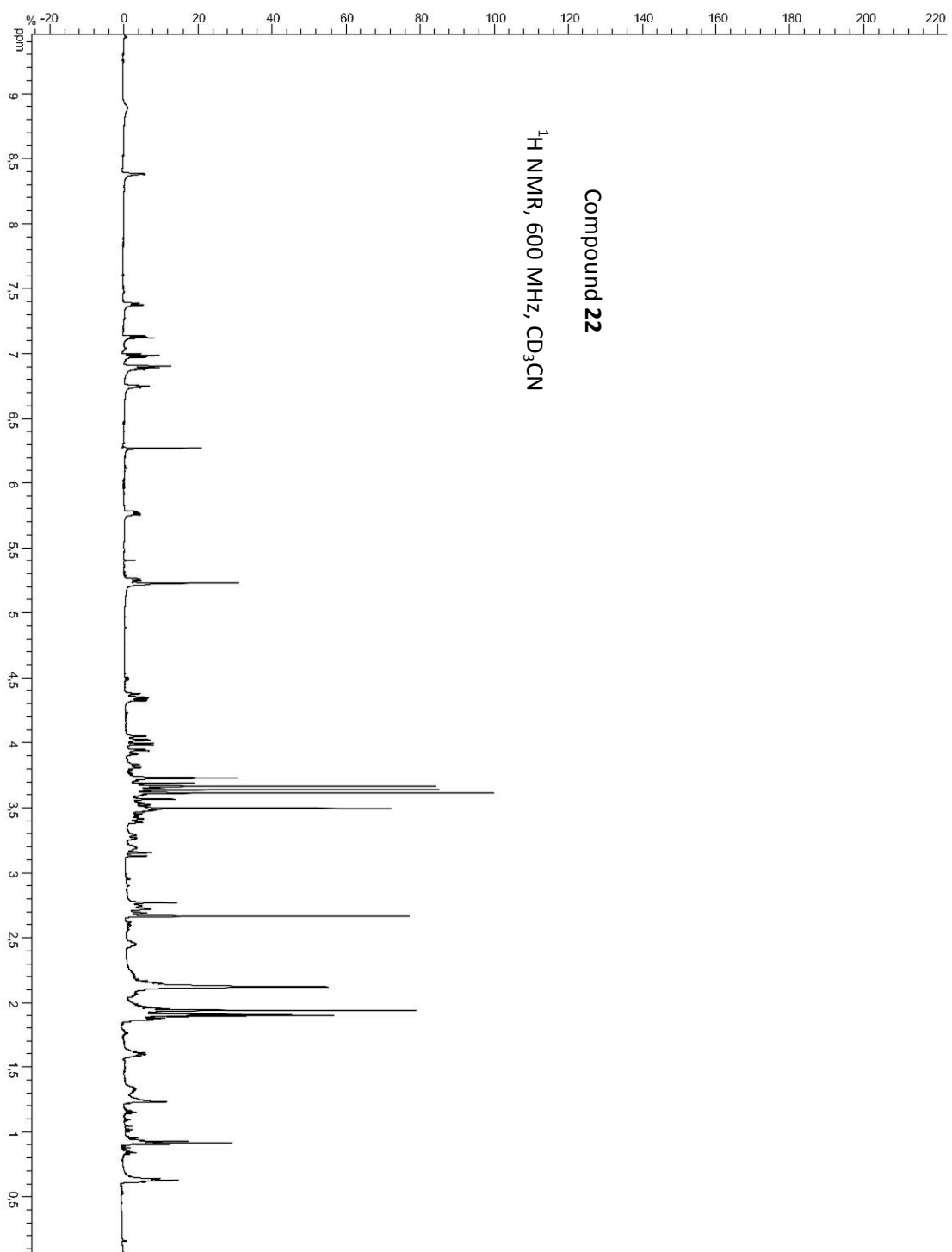


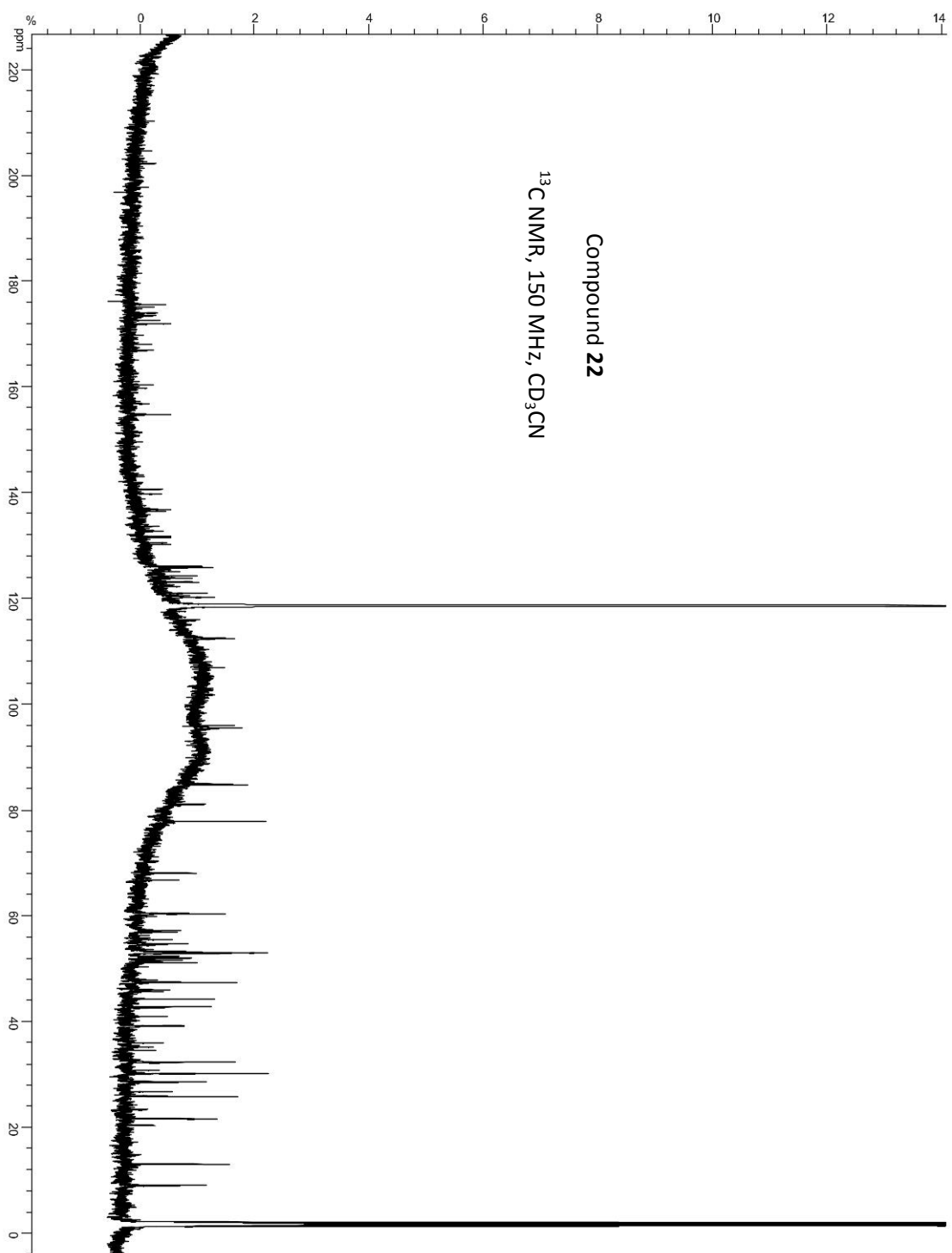


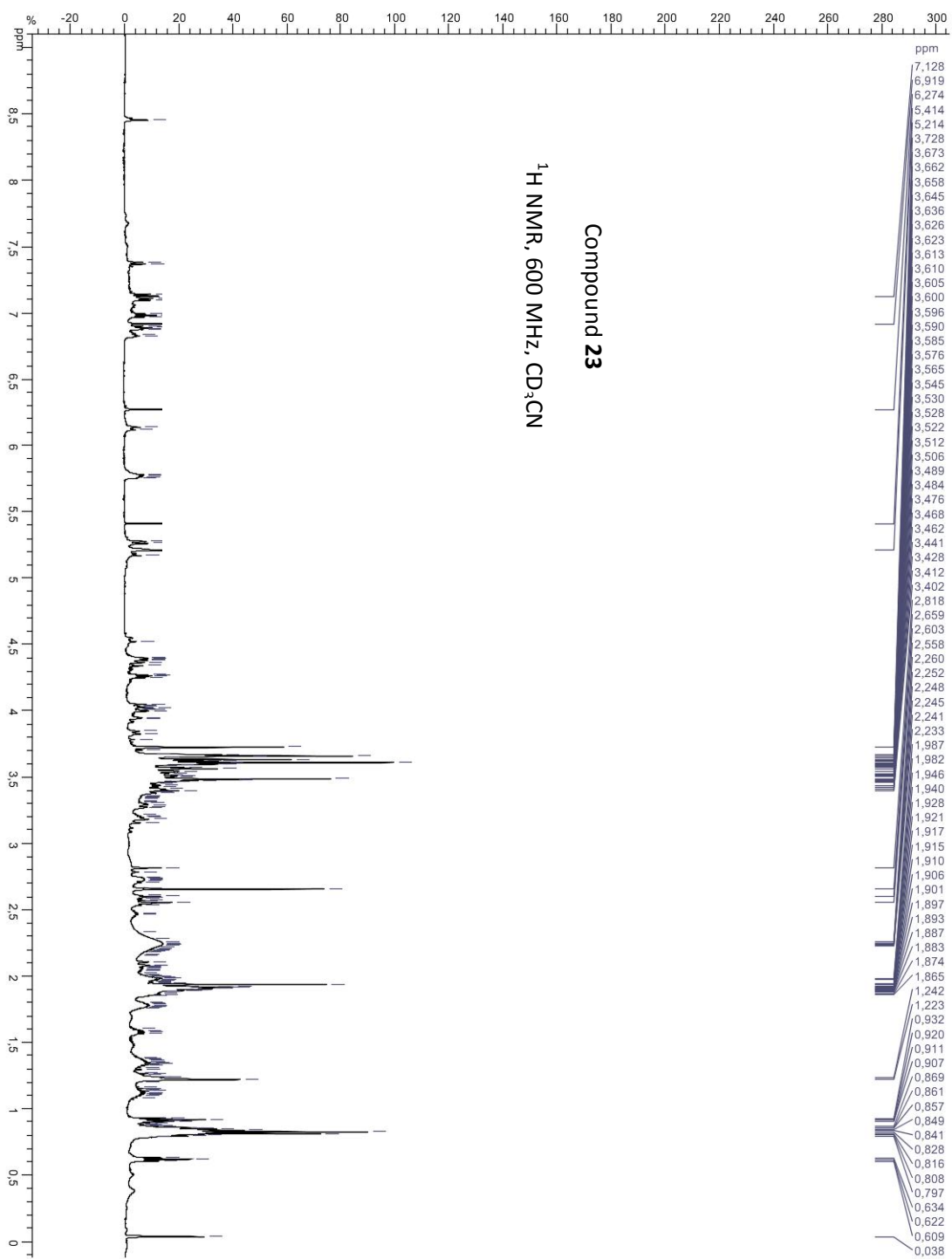


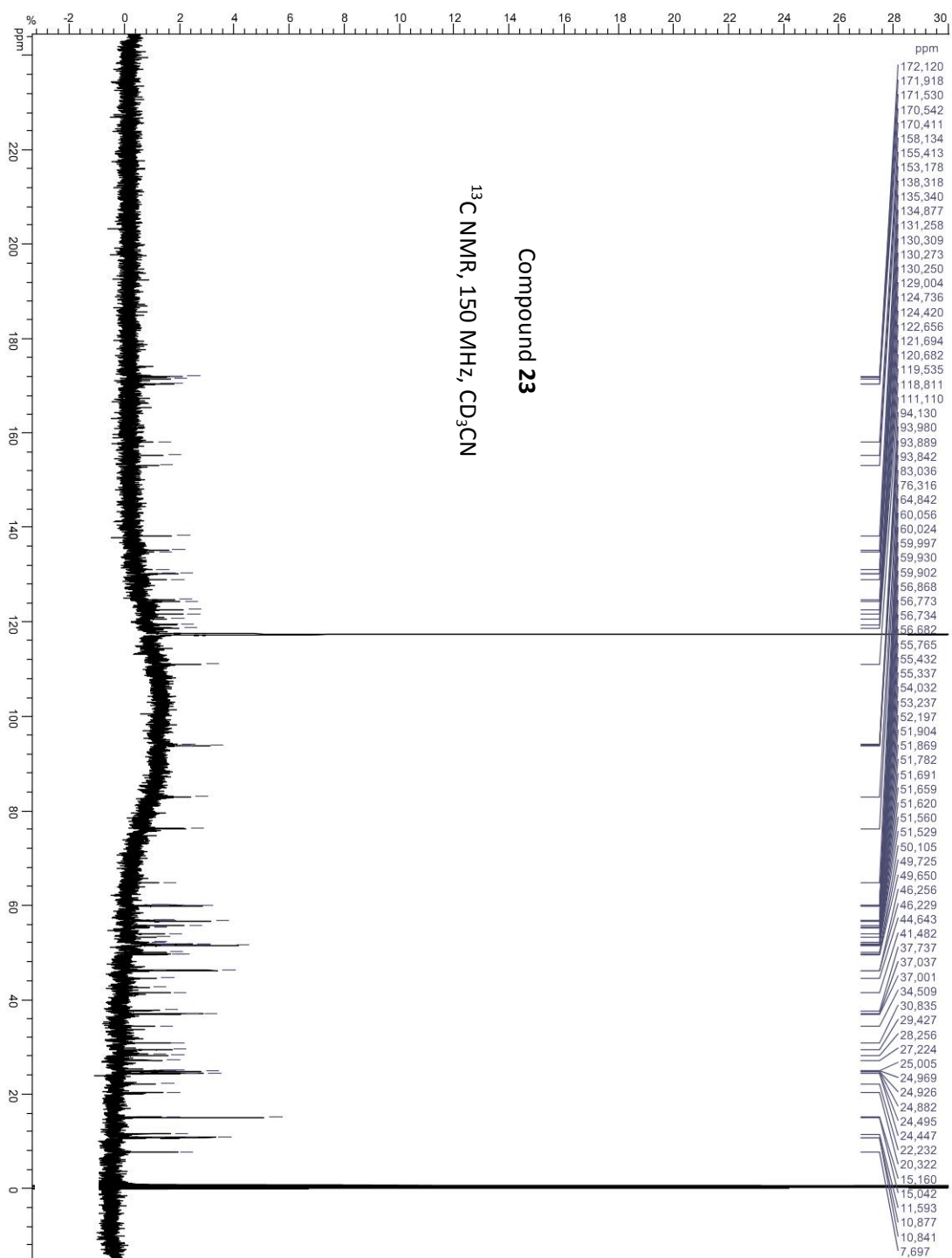












Compound **24**
 ^1H NMR, 600 MHz, CDCl_3

