

Supporting Information

An alternative to ‘propylene/Leonard linker’ for studying arene interactions in flexible pyrazolo[3,4-*d*]pyrimidine core based models both at molecular and supramolecular level

*Kamlakar Avasthi,^{*a} Amantullah Ansari,^a Ruchir Kant,^b Prakas R. Maulik,^b Krishnan Ravi kumar,^c Partha Chattopadhyay^d and Nirmal D. Adhikary^d*

^aMedicinal and Process Chemistry Division, Central Drug Research Institute, CSIR, Lucknow 226001, India; ^bMolecular and Structural Biology Division, Central Drug Research Institute, CSIR, Lucknow 226001, India; ^cX-Ray crystallography Division, Indian Institute of Chemical Technology, Hyderabad 500007, India, ^dChemistry Division, Indian Institute of Chemical Biology, Kolkata 700032, India.

E-mail address: kavasthi@rediffmail.com

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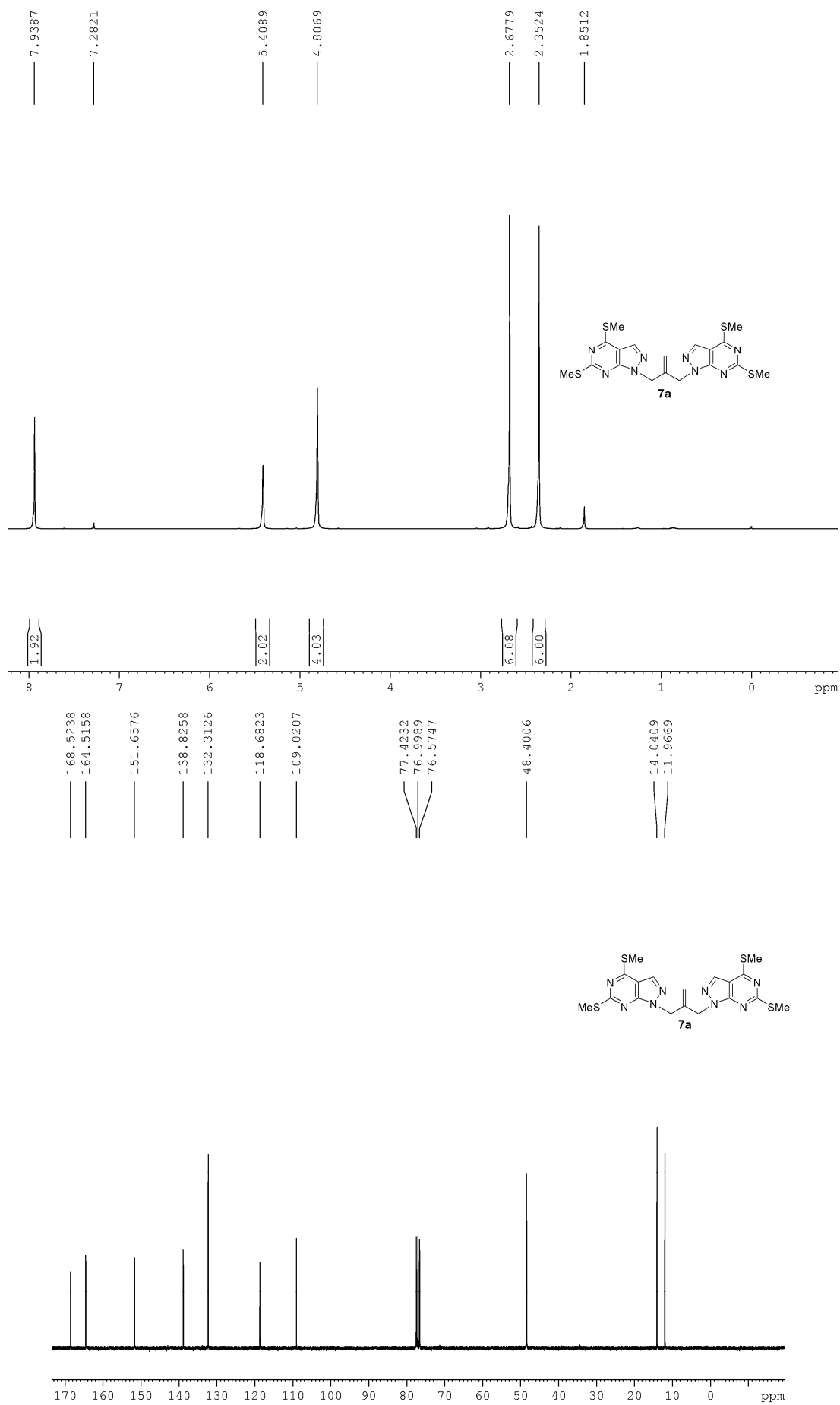


Fig. S1 ¹H and ¹³C NMR Spectra of compound **7a** in CDCl₃

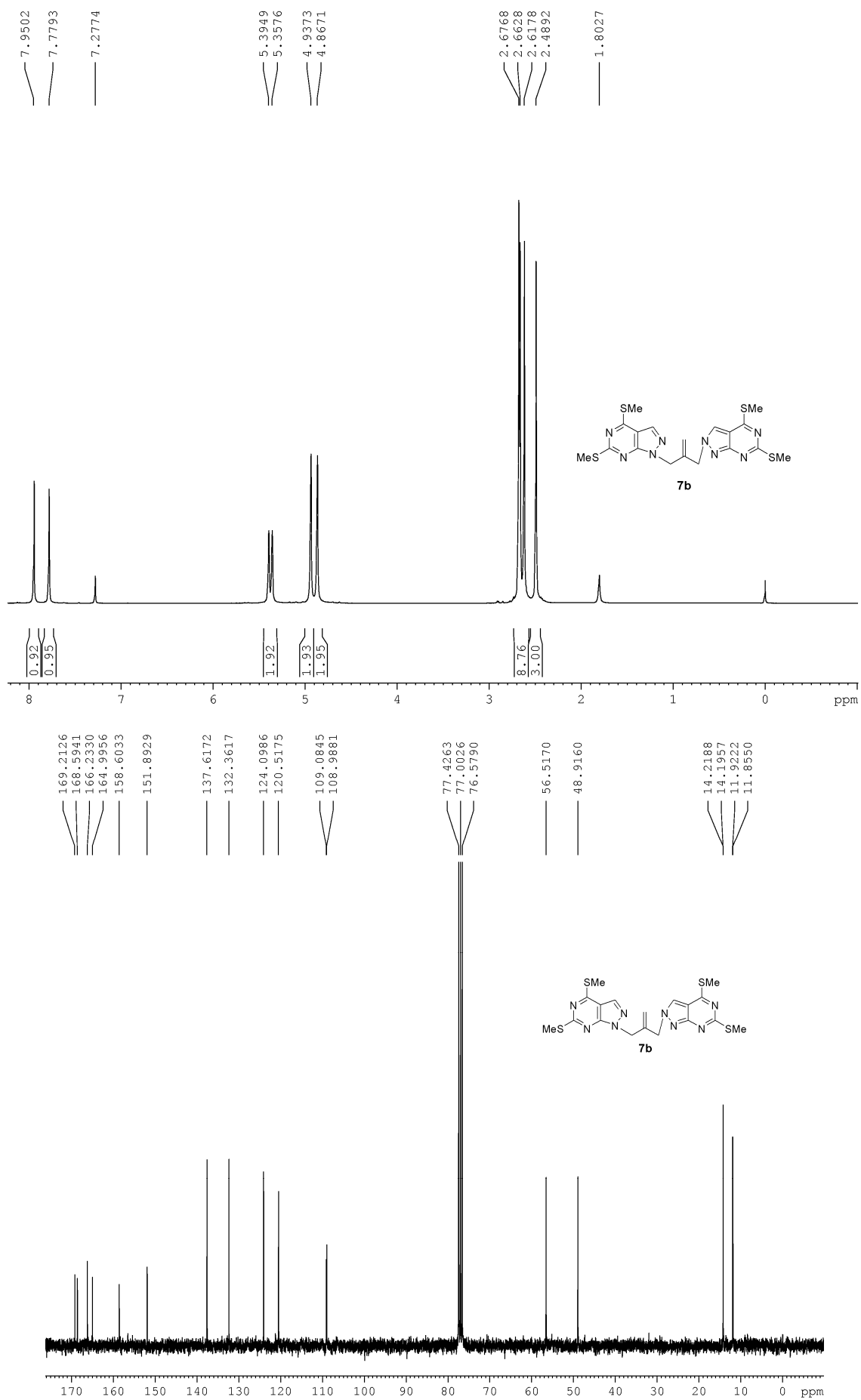


Fig. S2 ¹H and ¹³C NMR Spectra of compound **7b** in CDCl₃

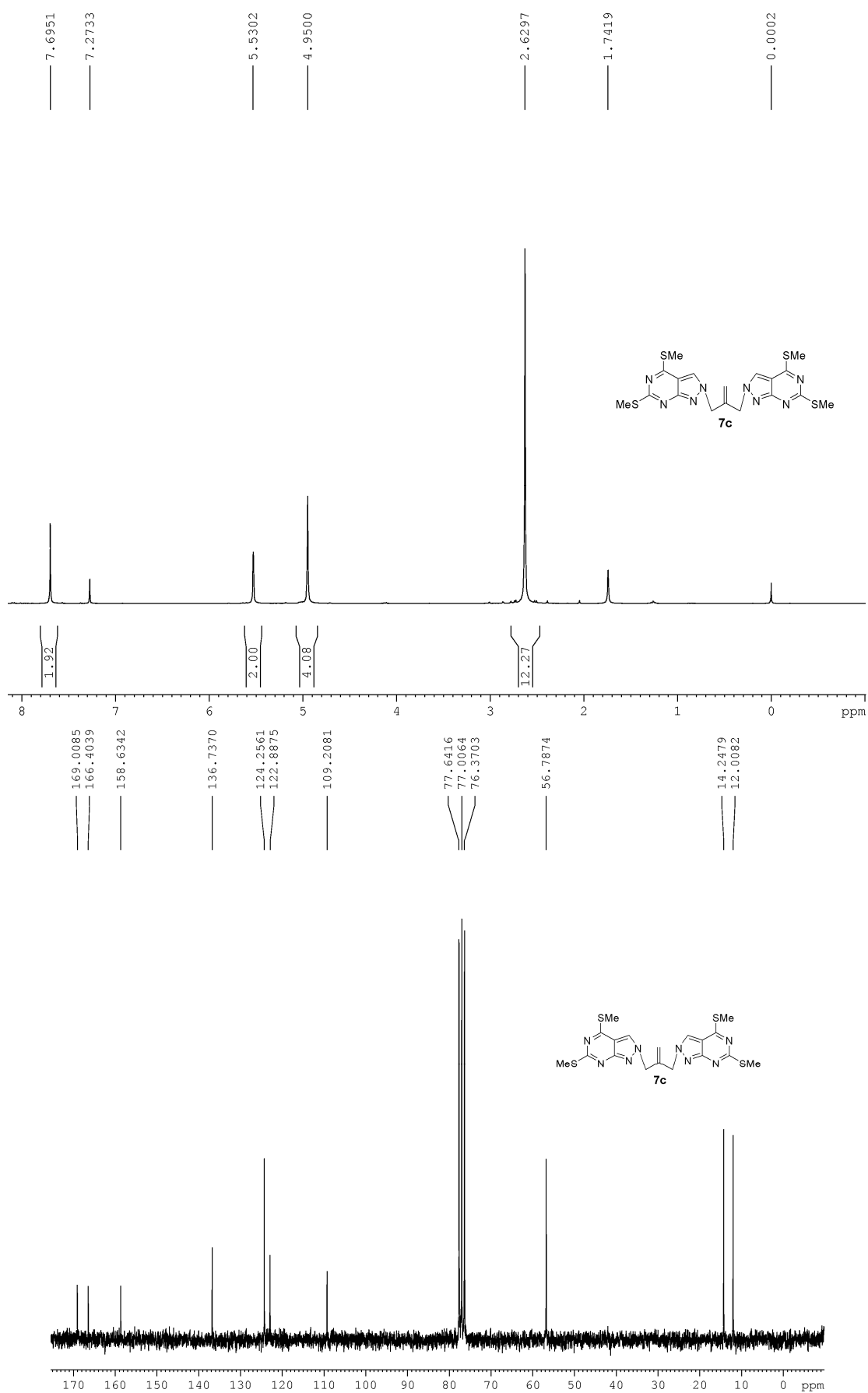


Fig. S3 ¹H and ¹³C NMR Spectra of compound **7c** in CDCl₃

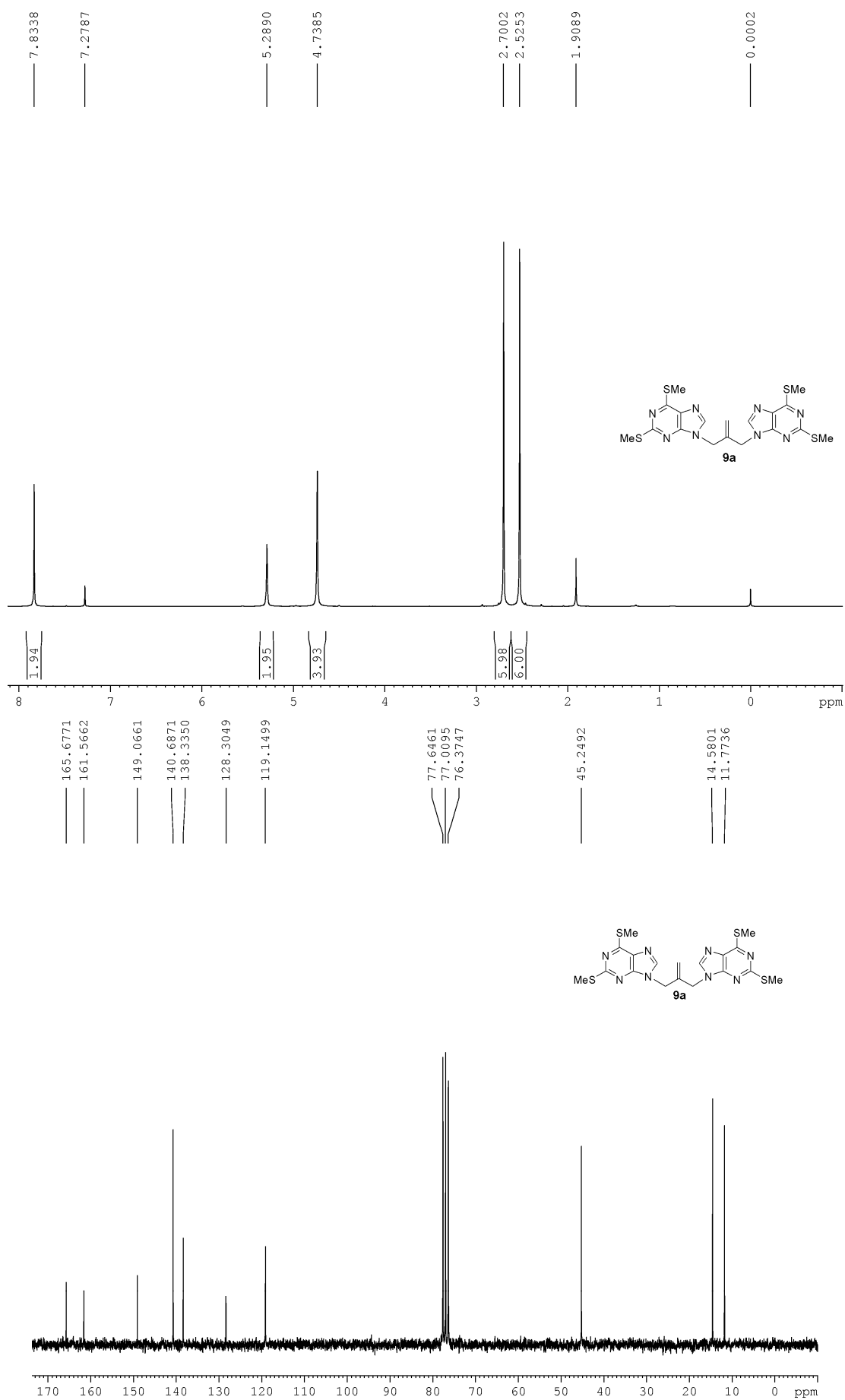


Fig. S4 ¹H and ¹³C NMR Spectra of compound **9a** in CDCl₃

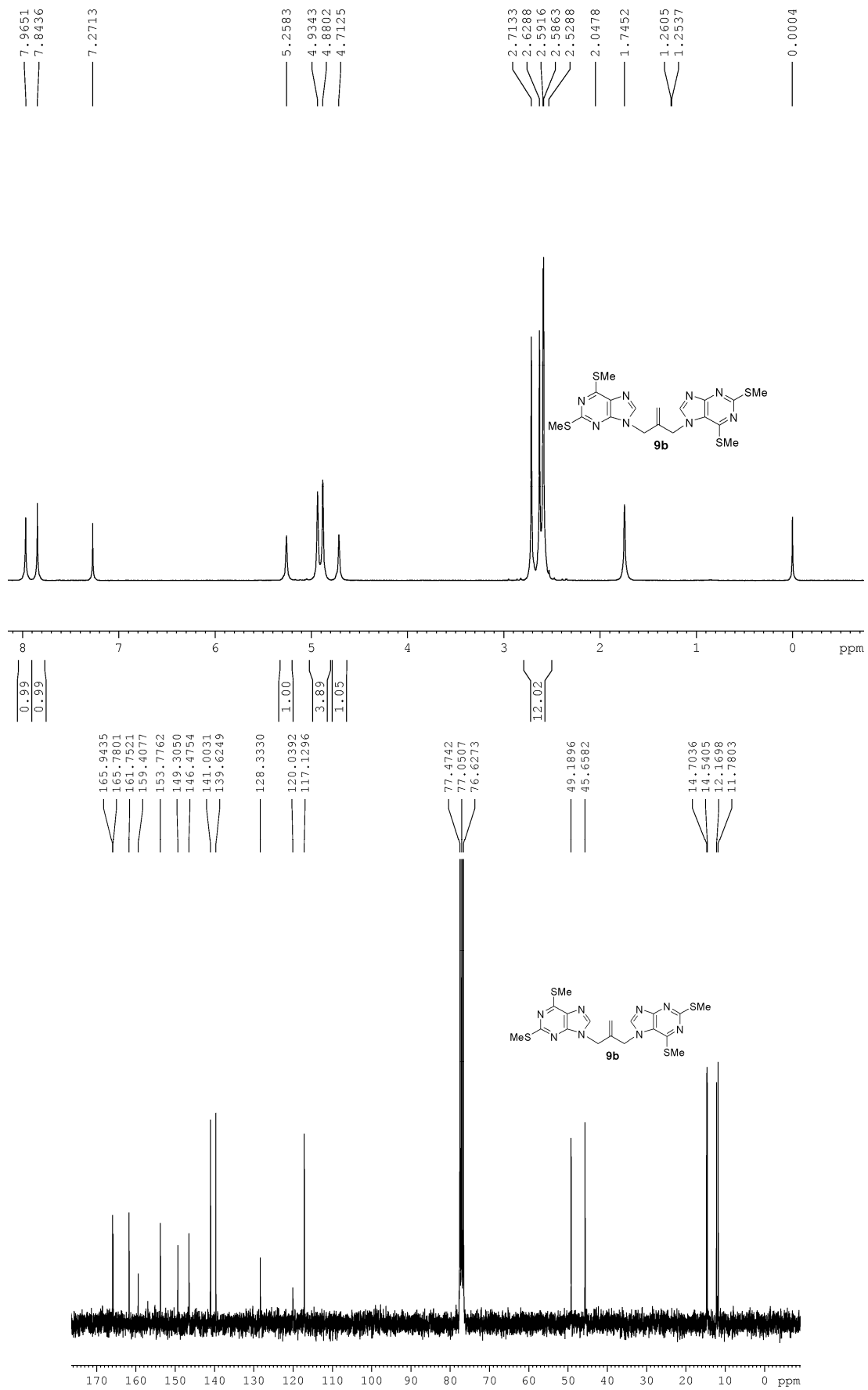


Fig. S5 ¹H and ¹³C NMR Spectra of compound **9b** in CDCl₃



Fig. S6 ¹H and ¹³C NMR Spectra of compound **9c** in CDCl₃

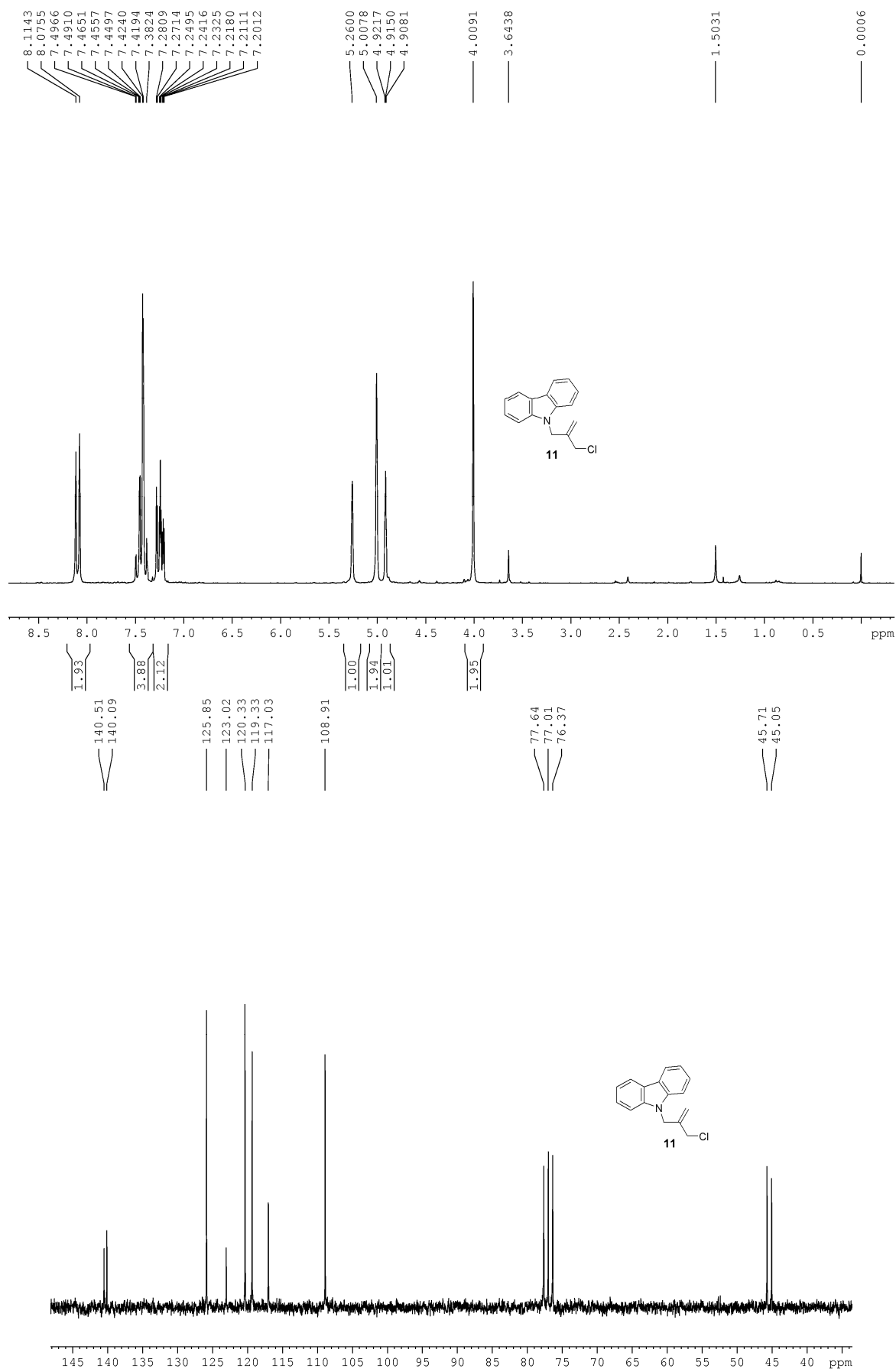


Fig. S7 ¹H and ¹³C NMR Spectra of compound **11** in CDCl₃

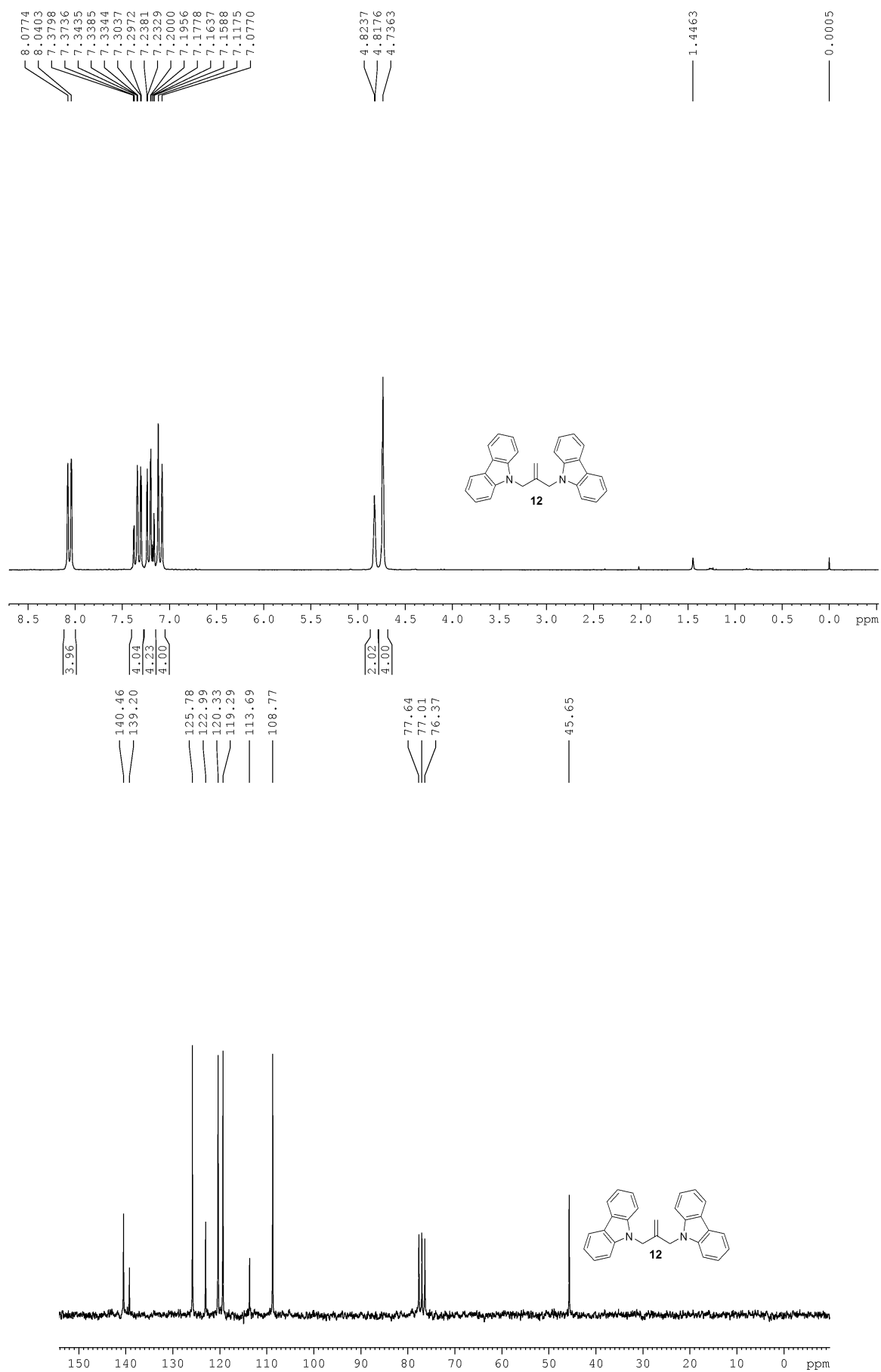


Fig. S8 ¹H and ¹³C NMR Spectra of compound **12** in CDCl₃

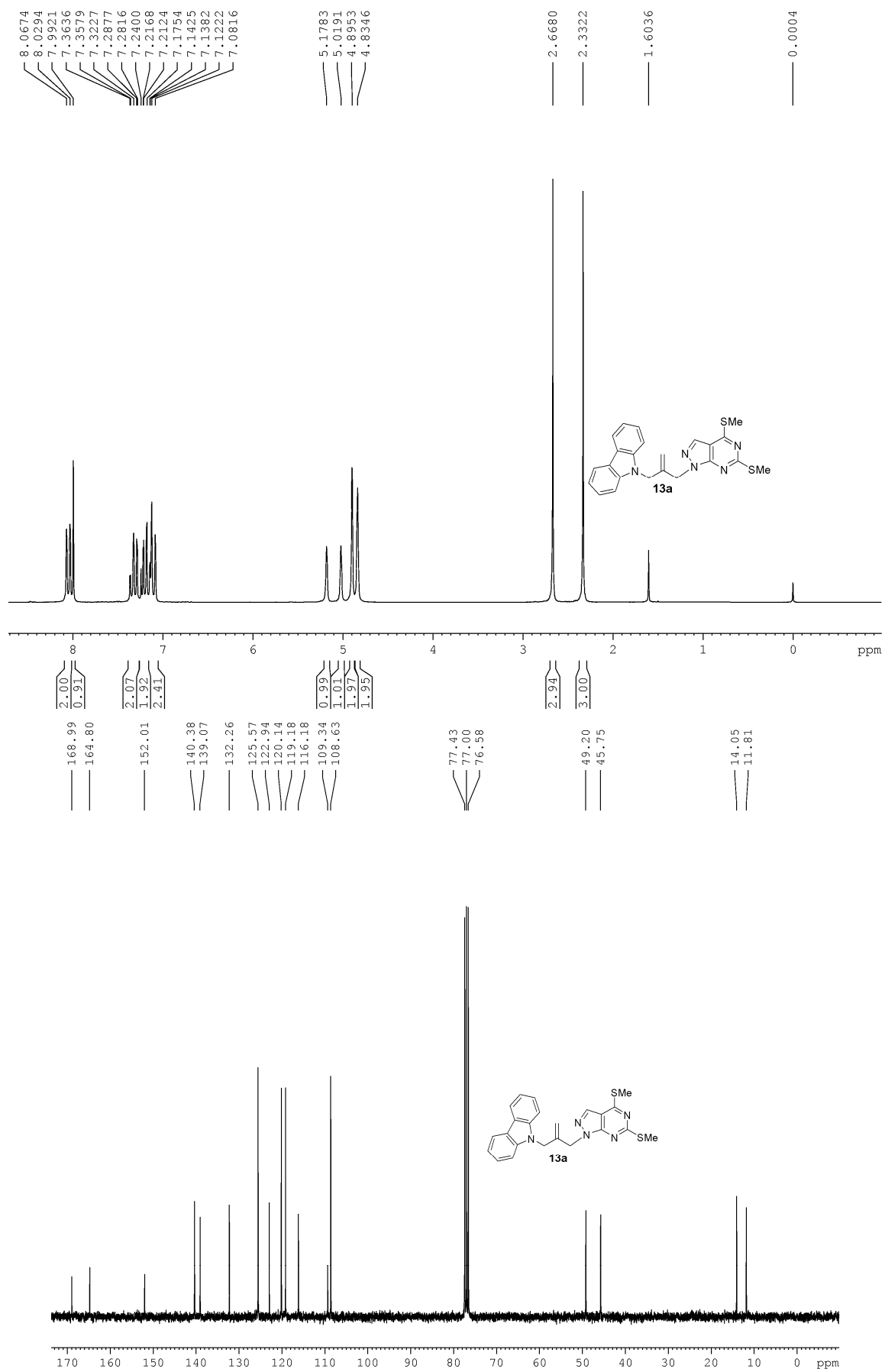


Fig. S9 ¹H and ¹³C NMR Spectra of compound **13a** in CDCl₃

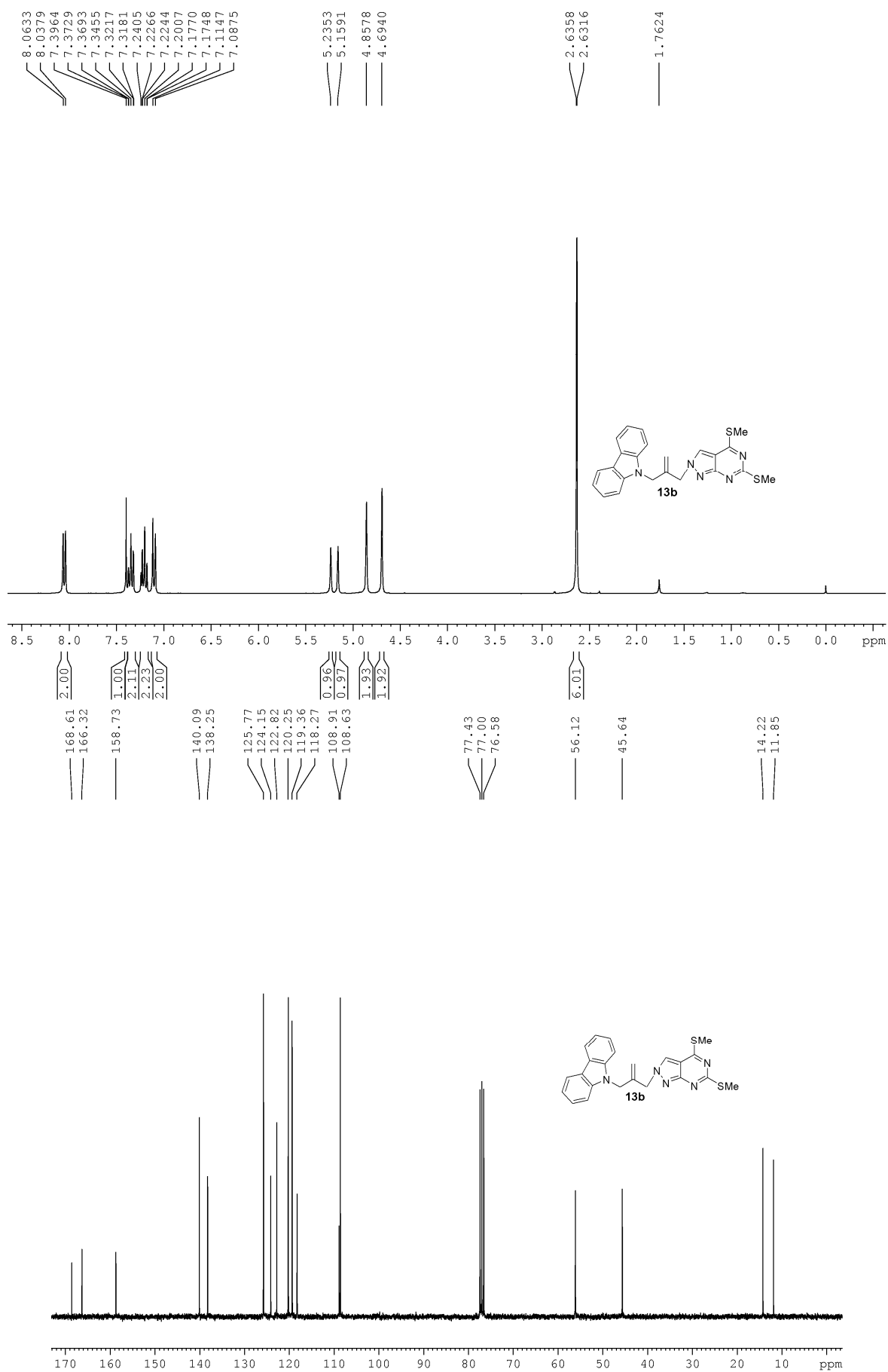


Fig. S10 ¹H and ¹³C NMR Spectra of compound **13b** in CDCl₃

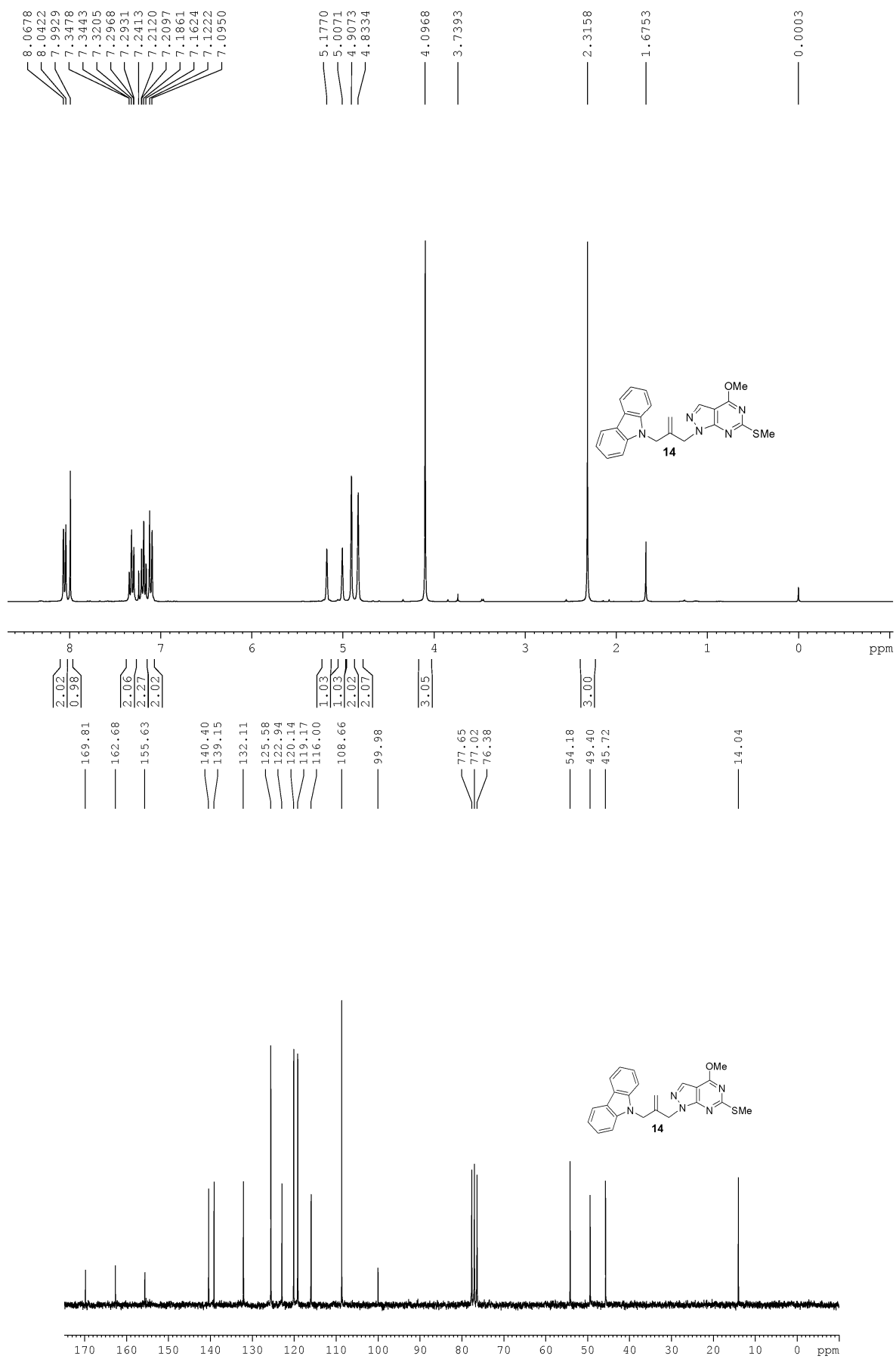


Fig. S11 ¹H and ¹³C NMR Spectra of compound 14 in CDCl₃

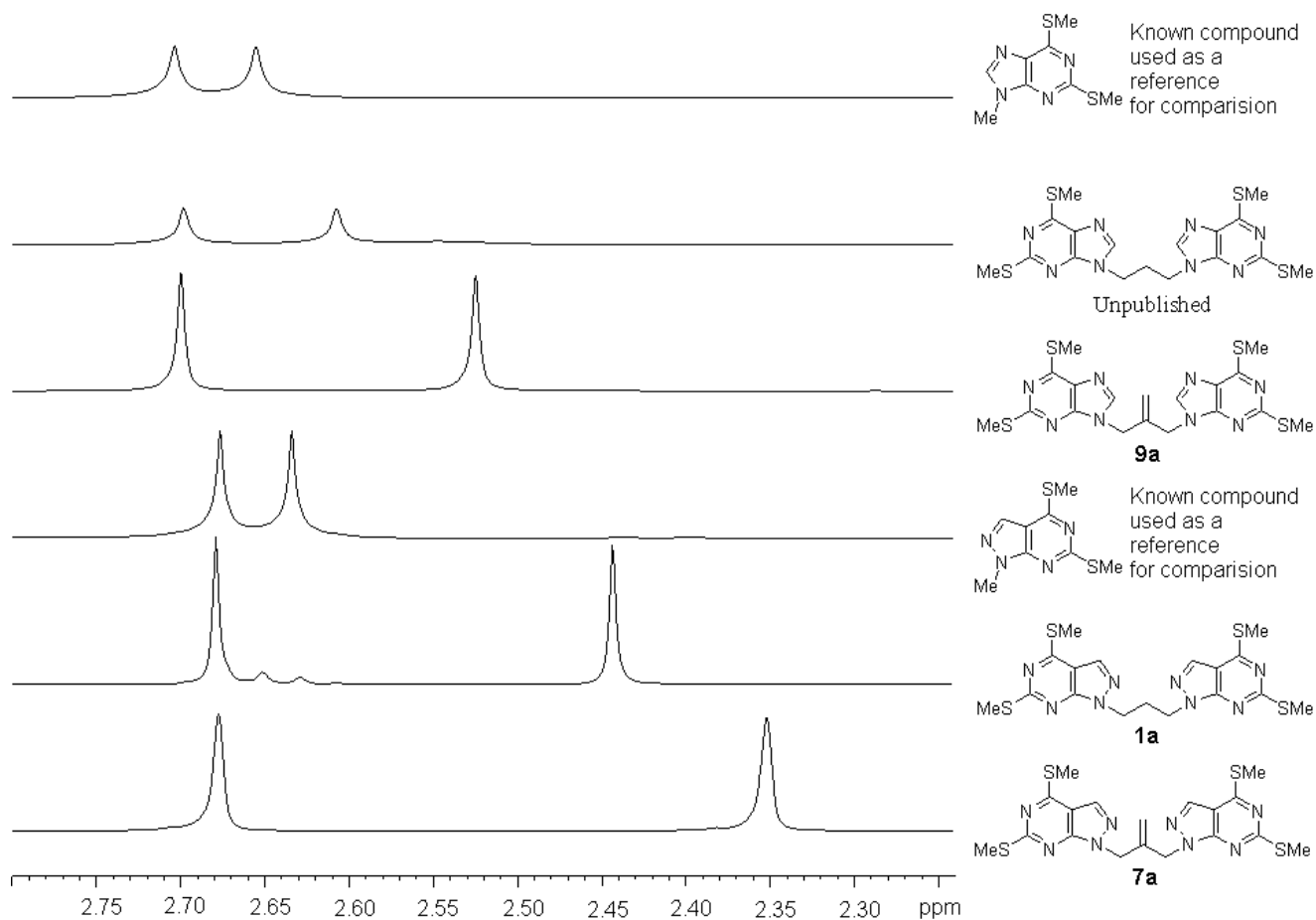
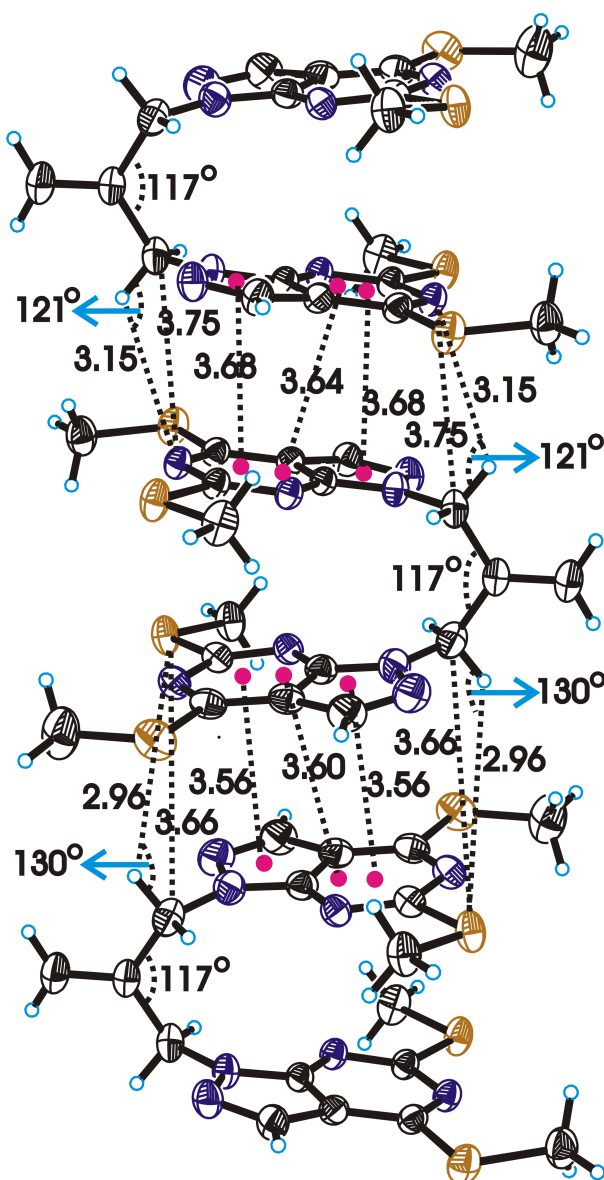
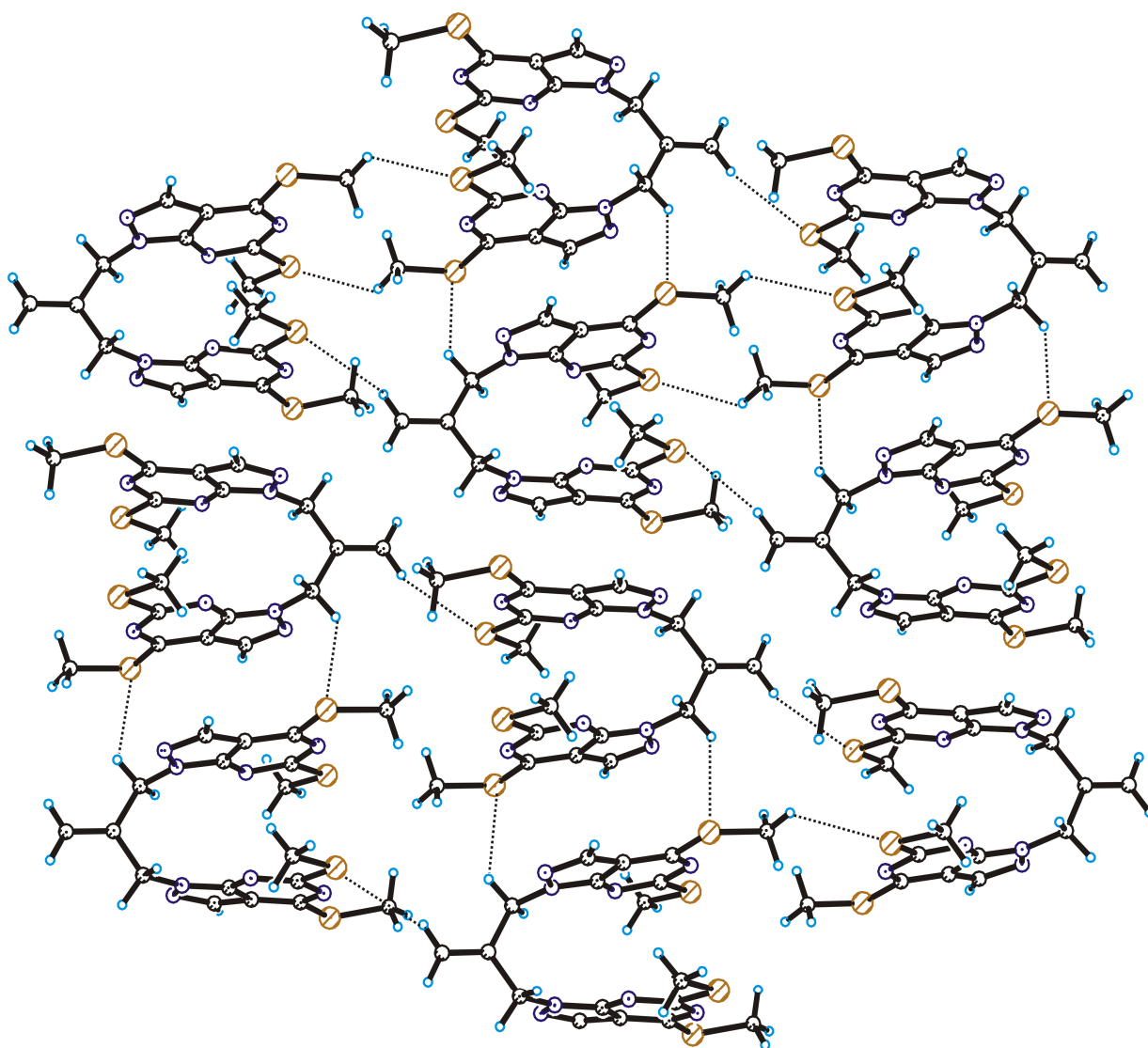


Fig. S12 Stack plot of ^1H NMRs of SMe region of selected compounds



One folded molecule is stacked between two adjacent molecules at each face by different interactions. One side by π - π interactions = Cg(5)...Cg(6) = 3.56 Å; Cg(9)...Cg(9) = 3.64 Å. C-H...S dimern = 2.96 Å, 3.66 Å, 130°. Other side by π - π interactions = Cg(5)...Cg(6) = 3.68 Å; Cg(9)...Cg(9) = 3.64 Å. C-H...N dimern. = 3.15 Å, 3.75 Å, 121°. This pattern keeps on repeating to form an infinite vertical stack. This pattern is different from that of corresponding propylene linker compound.

Fig. S13 Part of the vertical columns of **7a** formed as a result of π - π and C-H...S interactions (at 30% probability level).



CH...S interaction (SCH₃...SCH₃) = 2.97 Å, 3.66 Å, 130°
CH...S interaction (NCH₂...SCH₃) = 2.96 Å, 3.66 Å, 130°

Fig. S14 Network formed by C-H...S interaction in **7a**.

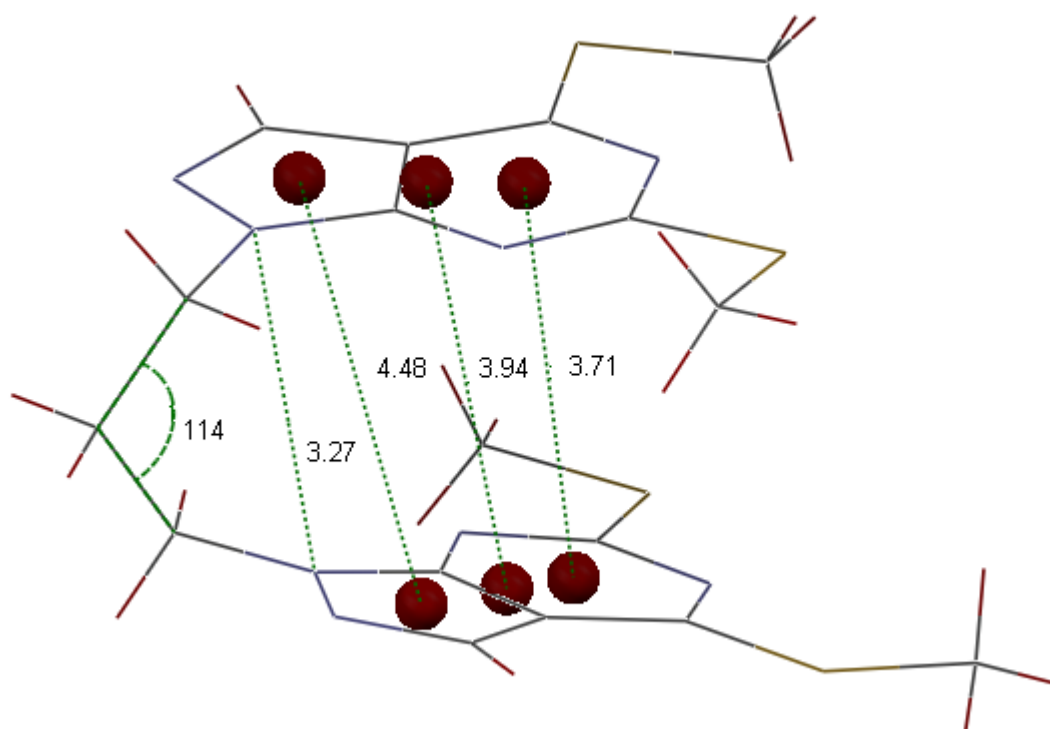
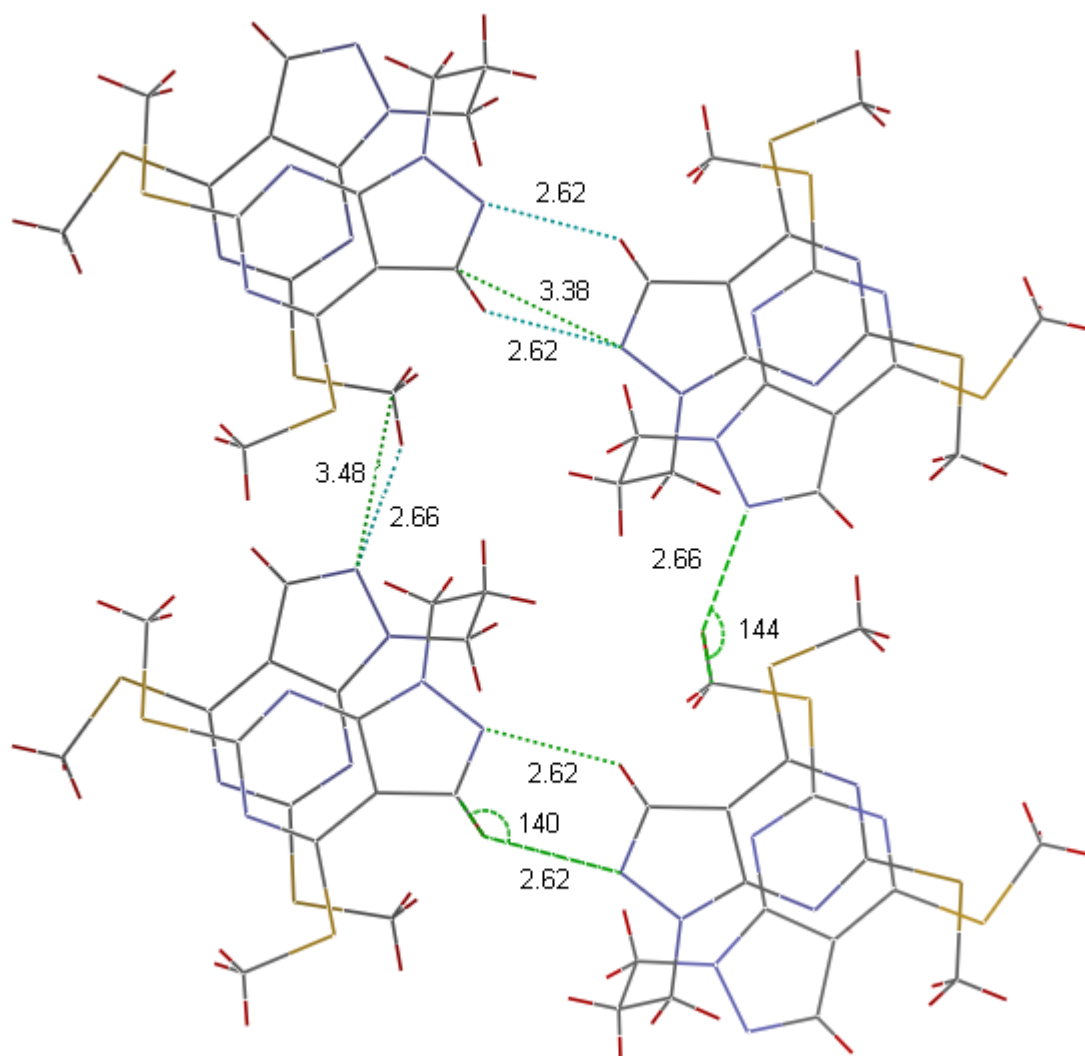
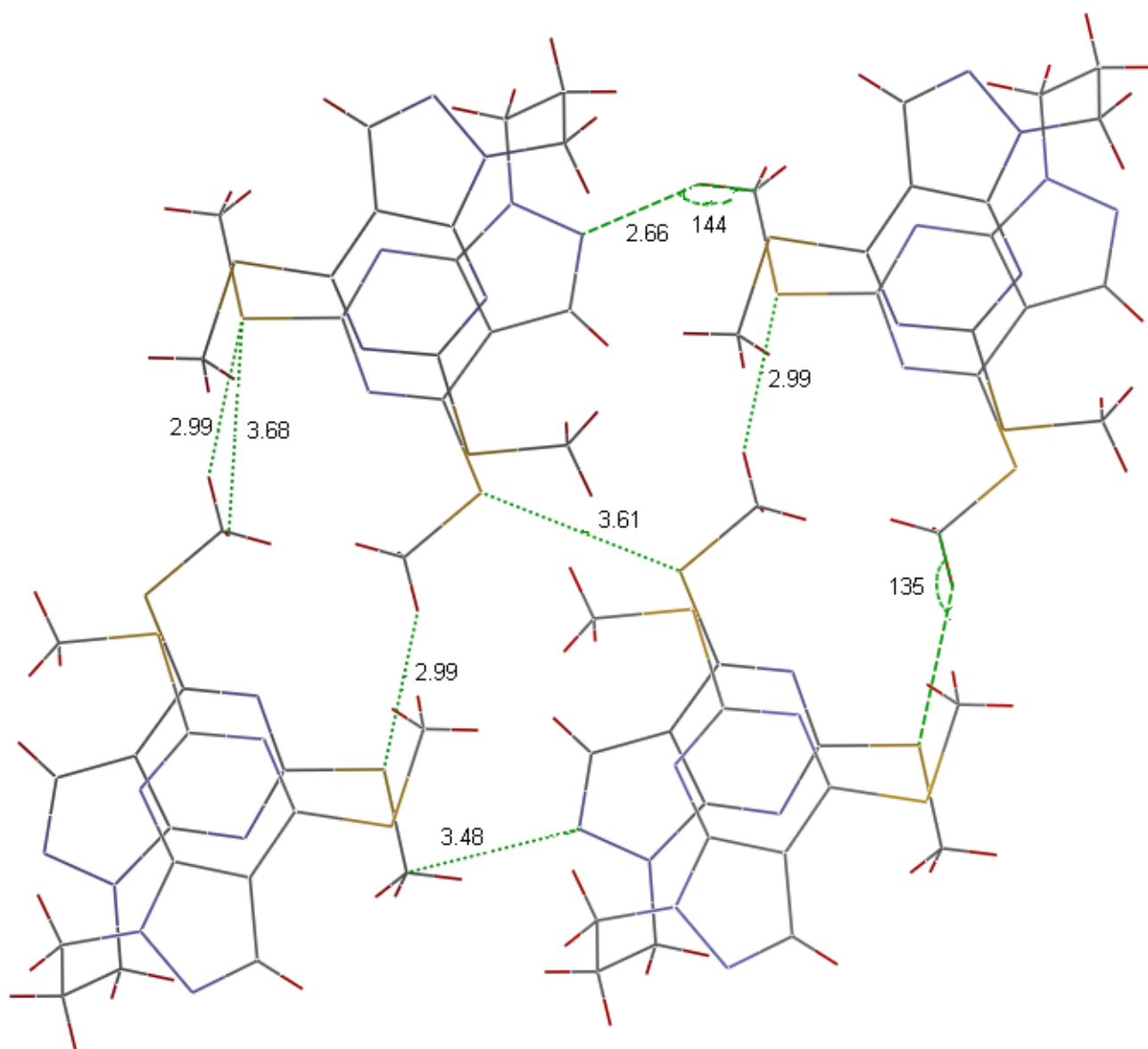


Fig. S15 Important distances and angle of **1a**.



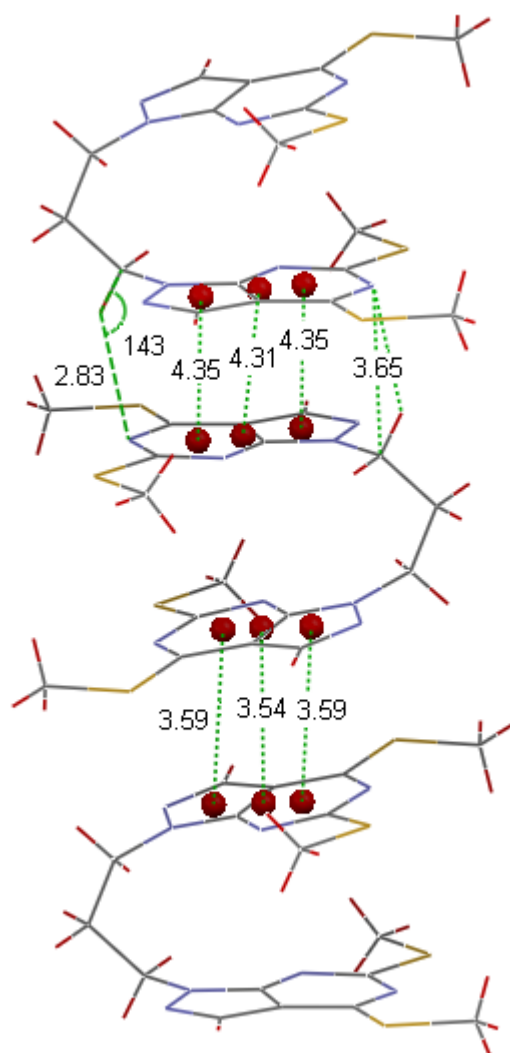
CH...N dimer = 2.62 Å, 3.38 Å, 140°
 CH...N dimer = 2.66 Å, 3.48 Å, 144°

Fig. S16 CH...N interactions in **1a**.



CH...S dimer = 2.99 Å, 3.73 Å, 135°;
 CH...N dimer = 2.66 Å, 3.48 Å, 144°;
 S...S dimer = 3.61 Å .

Fig. S17 CH...S, CH...N and S...S interactions in **1a**.



One folded molecule is stacked between two adjacent molecules at each face by different interactions.
 One side by π - π interactions = Cg(5)...Cg(6) = 3.59 Å & 3.59 Å and Cg(9)...Cg(9) = 3.54 Å;
 Other side by C-H...N dimern. = 2.84 Å, 3.65 Å, 143°.
 Cg(5)...Cg(6) = 4.35 and Cg(9)...Cg(9) = 4.31
 This pattern keeps on repeating to form infinite vertical stack.

Fig. S18 π - π and C-H...N interactions in **1a**.

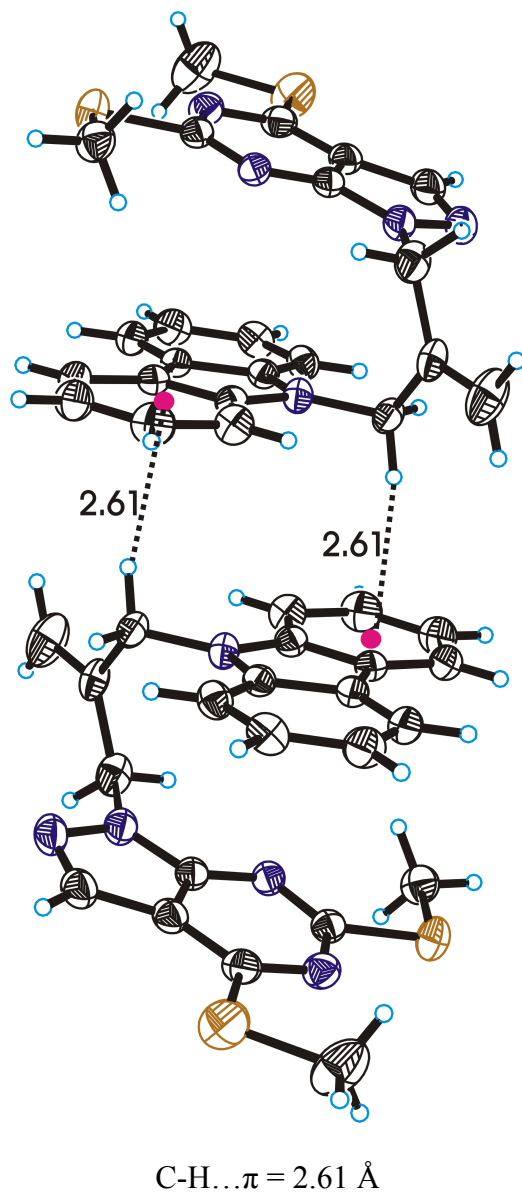
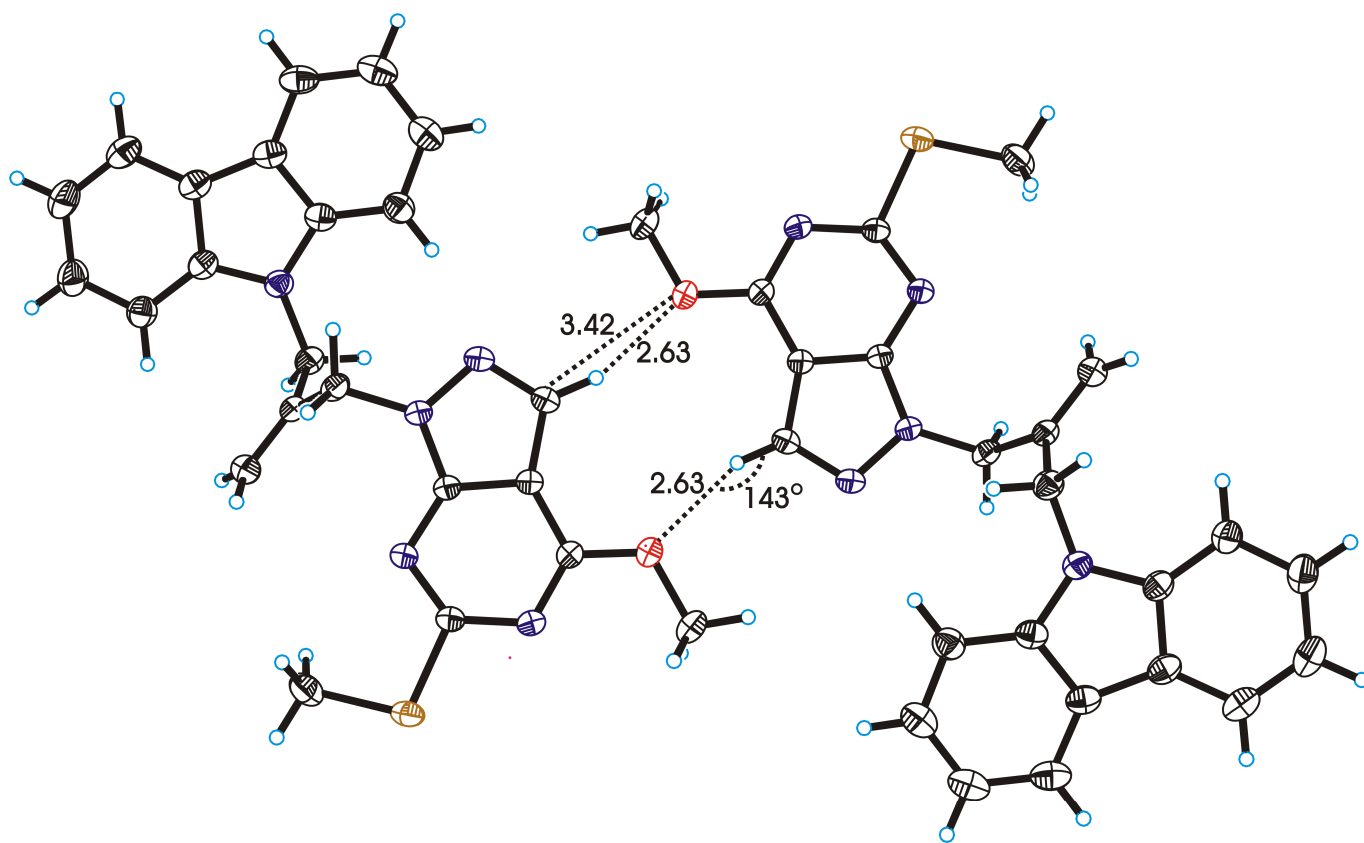


Fig. S19 C-H... π dimerization in **13a** (at 30% probability level).



C-H...O = 2.63 Å, 3.42, 143°

Fig. S20 C-H...O dimerization in **14** (at 30% probability level).