

Towards β -Selectivity in Functional Estrogen Receptor Antagonists

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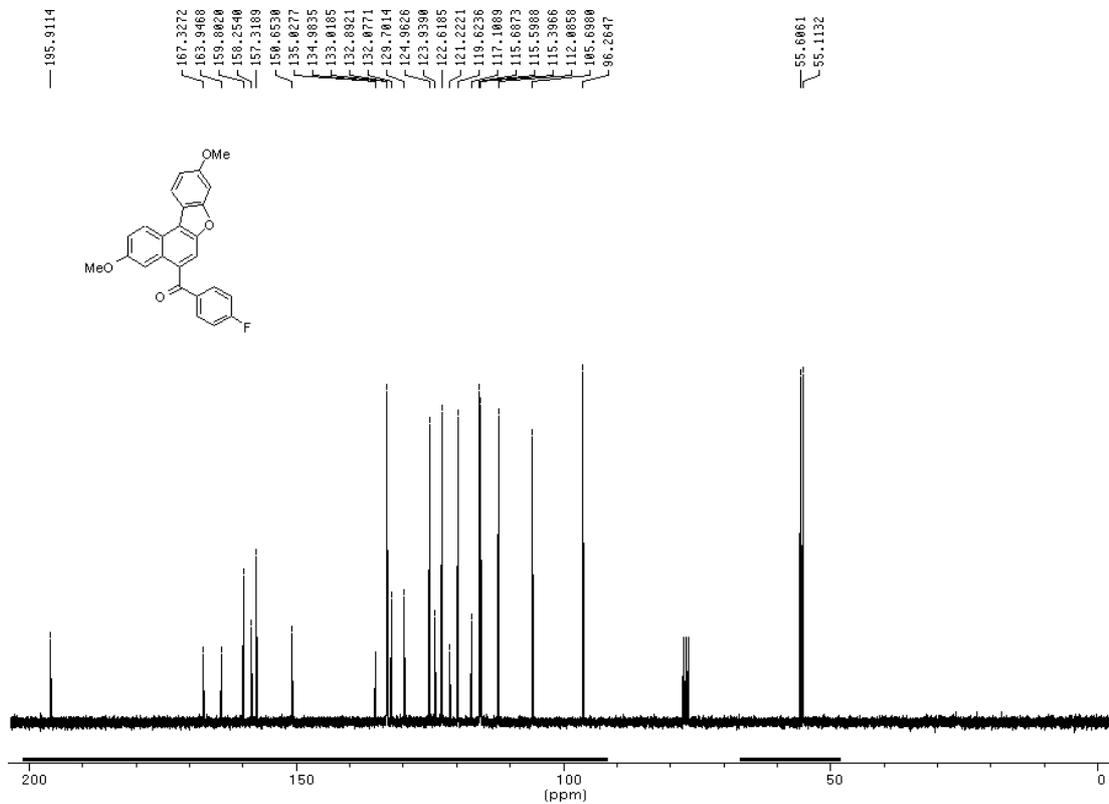
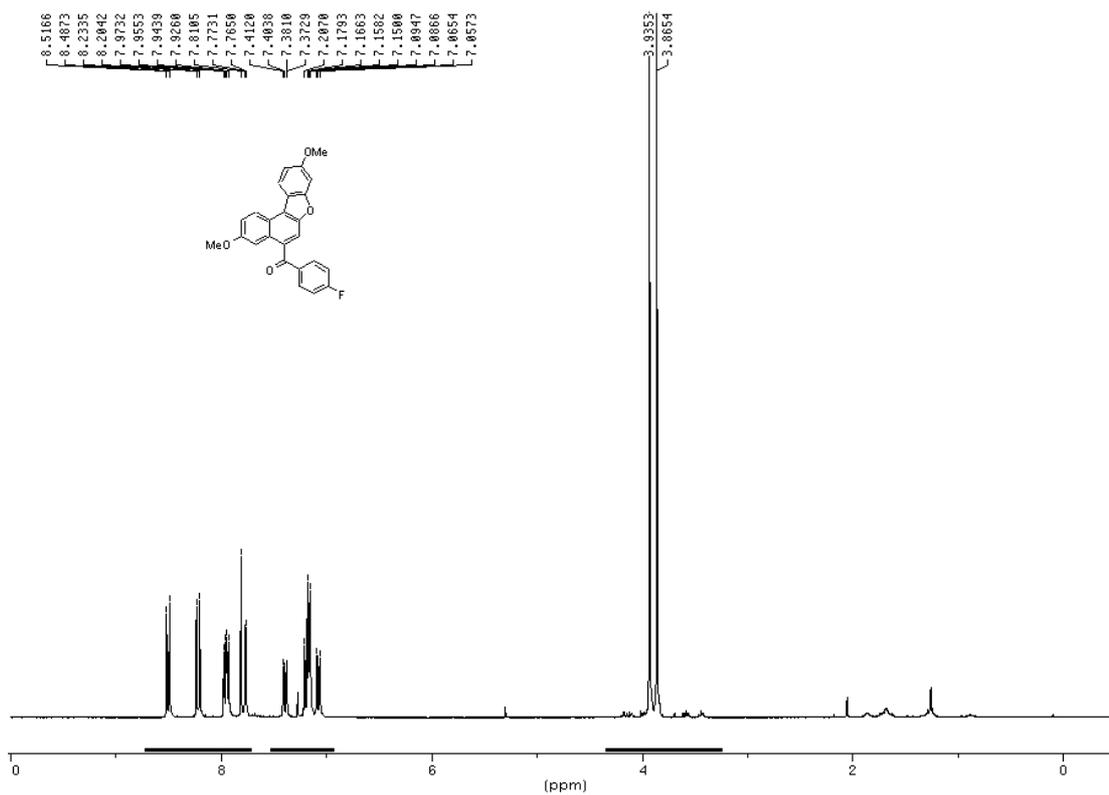
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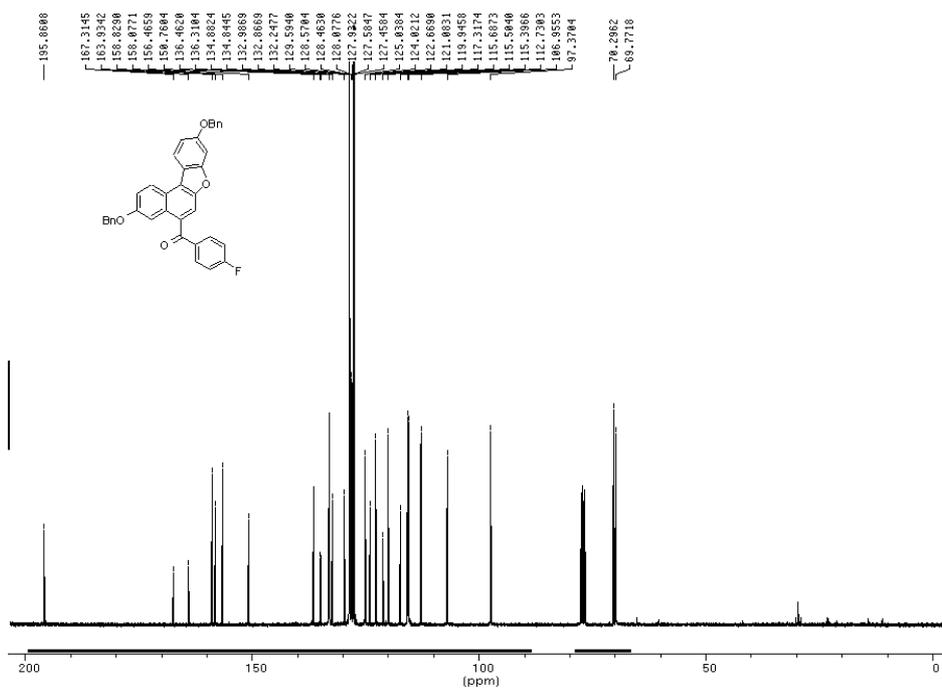
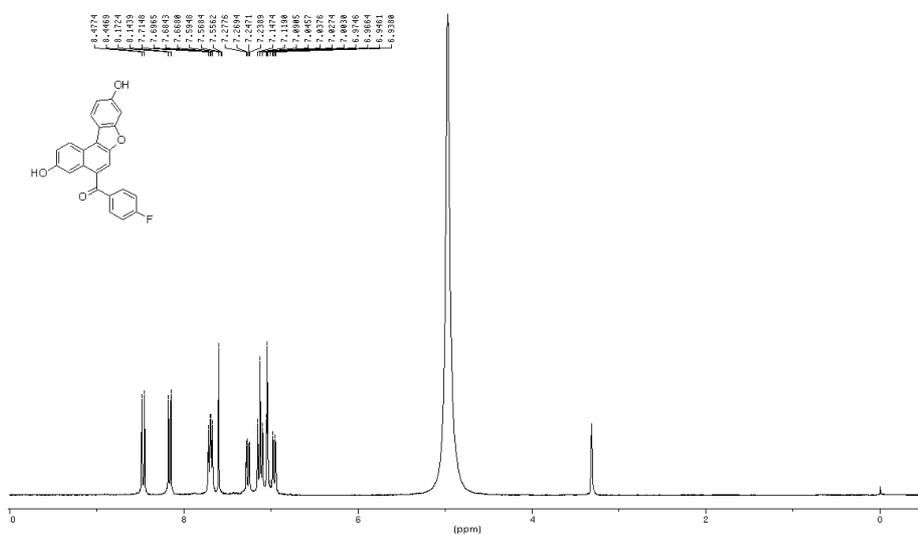
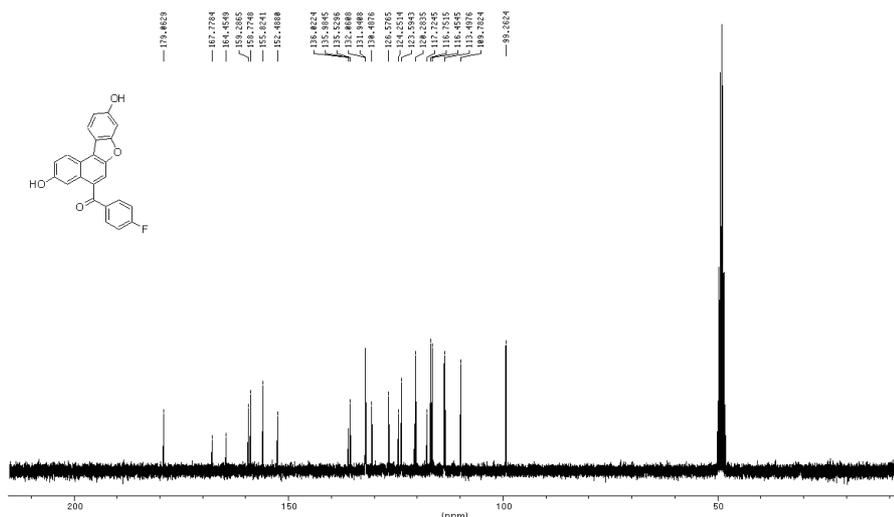
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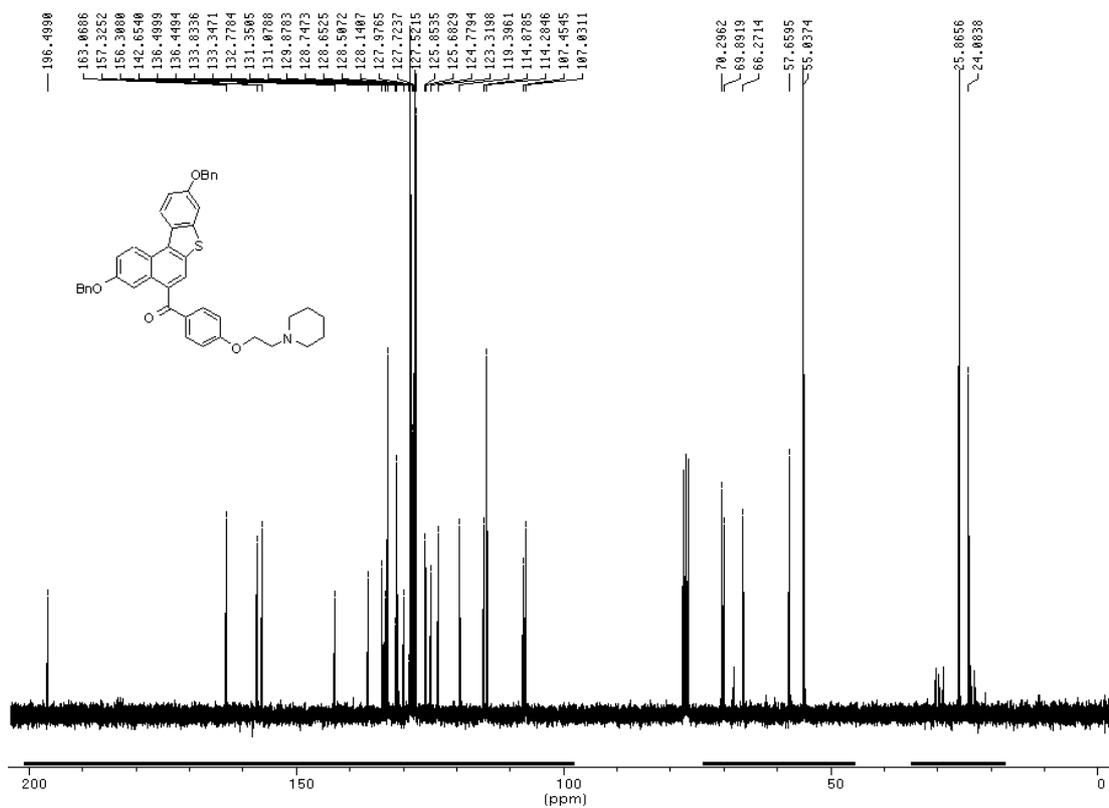
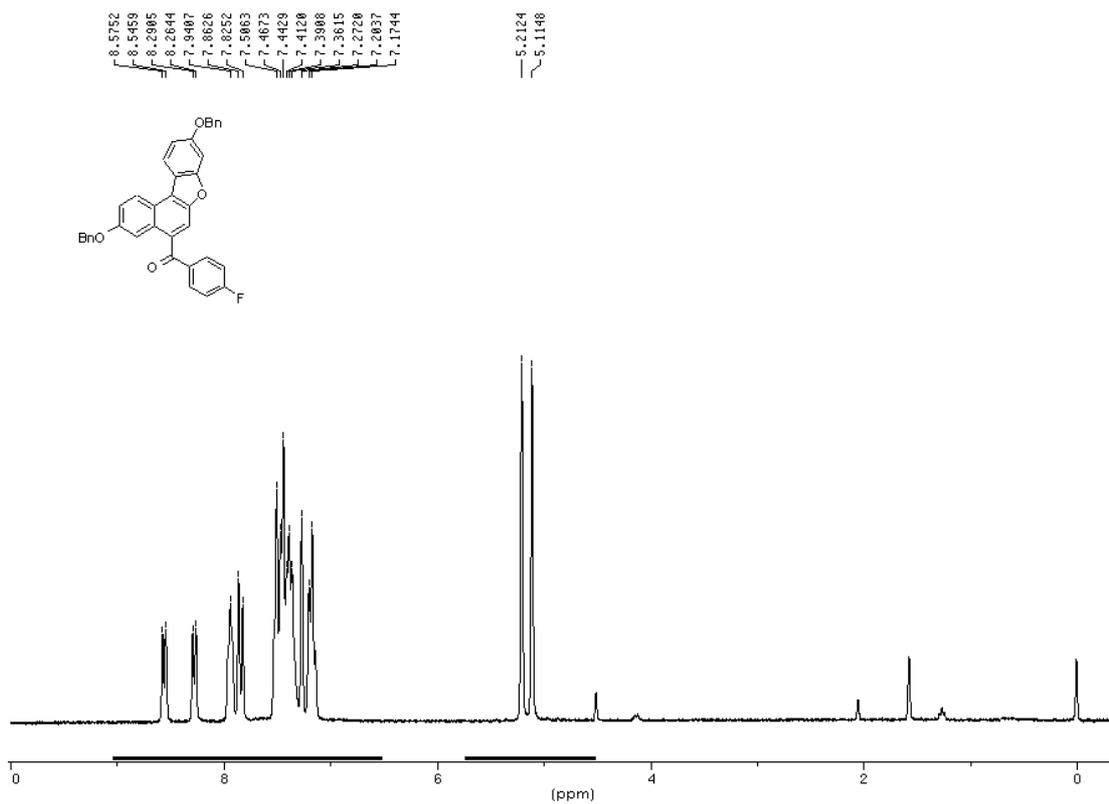
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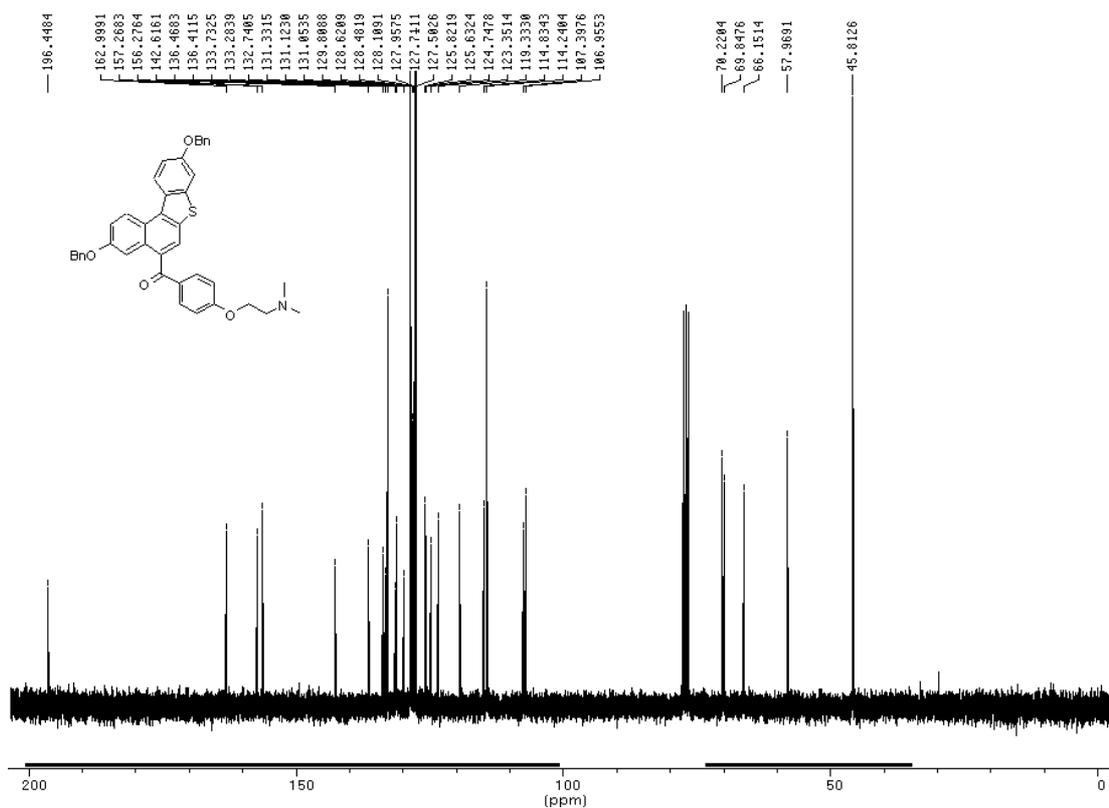
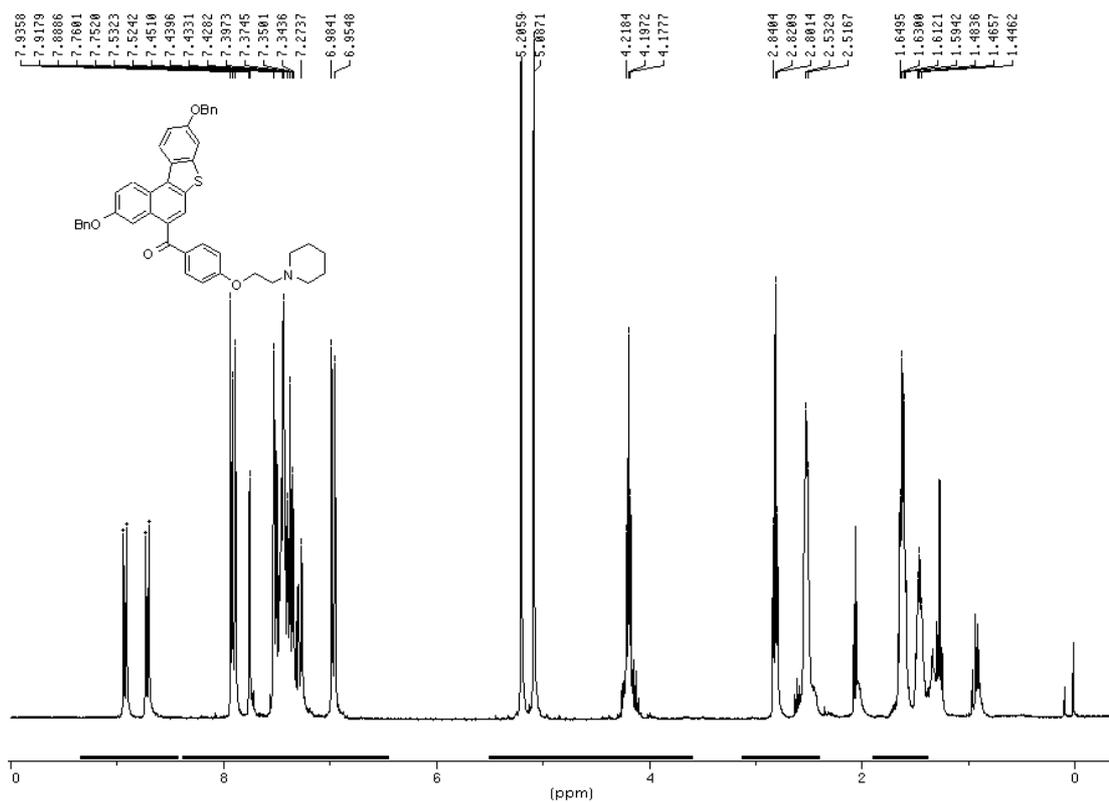
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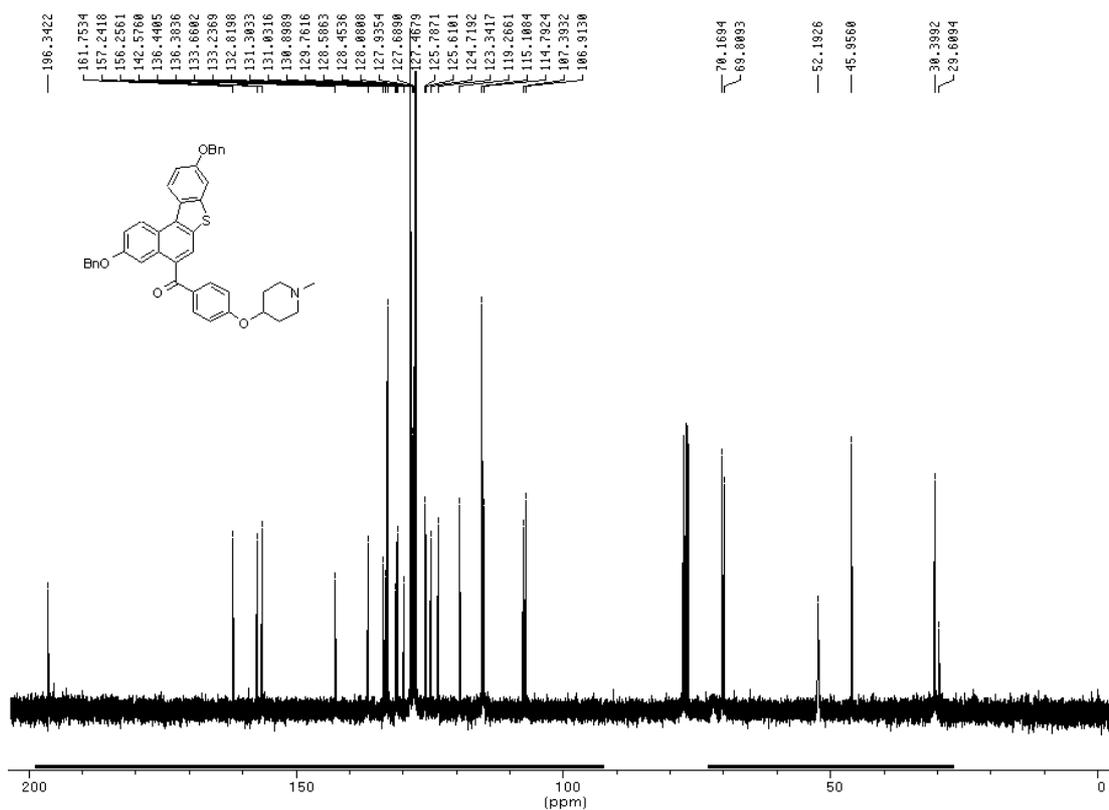
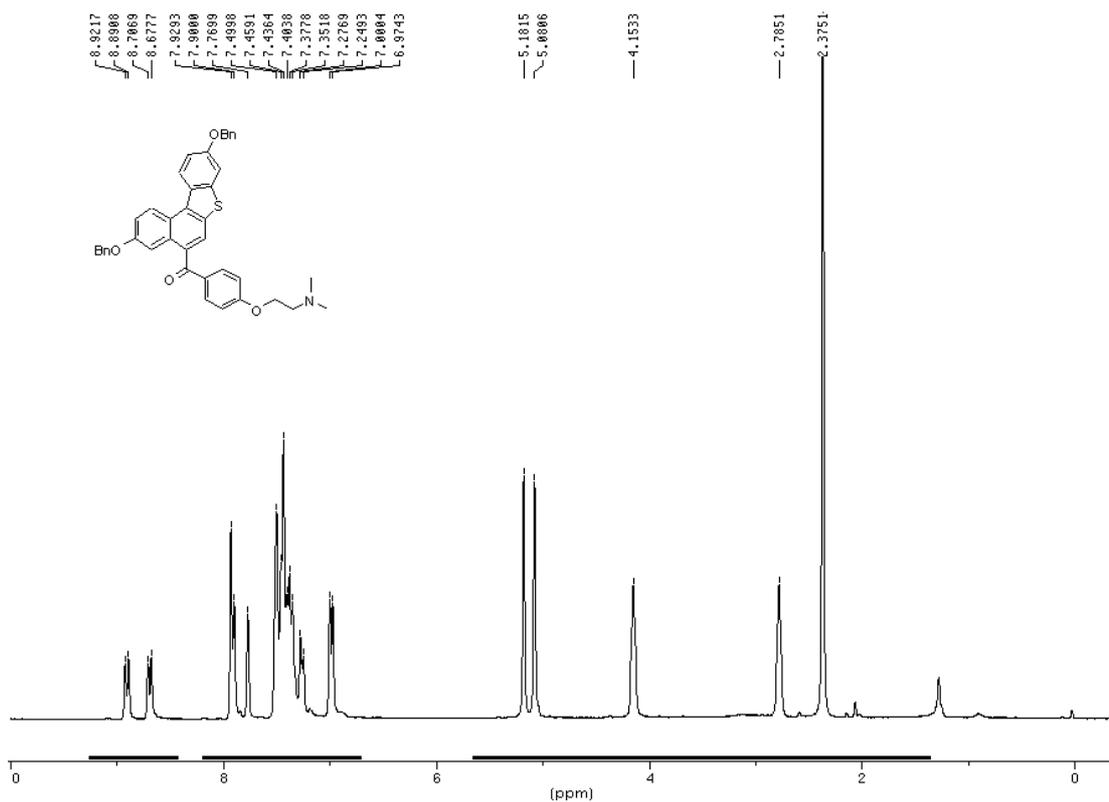
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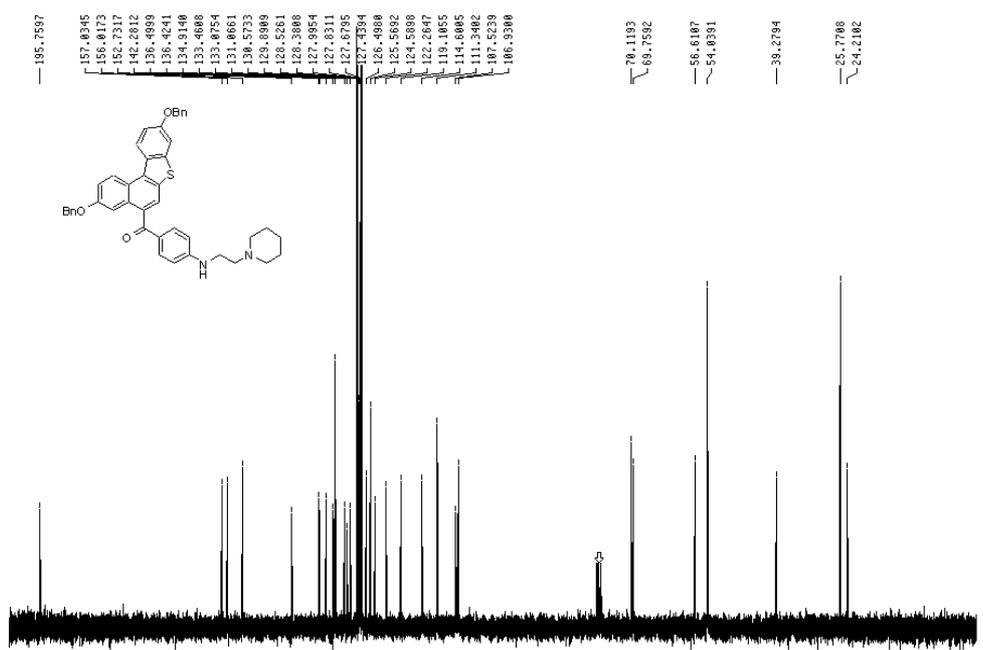
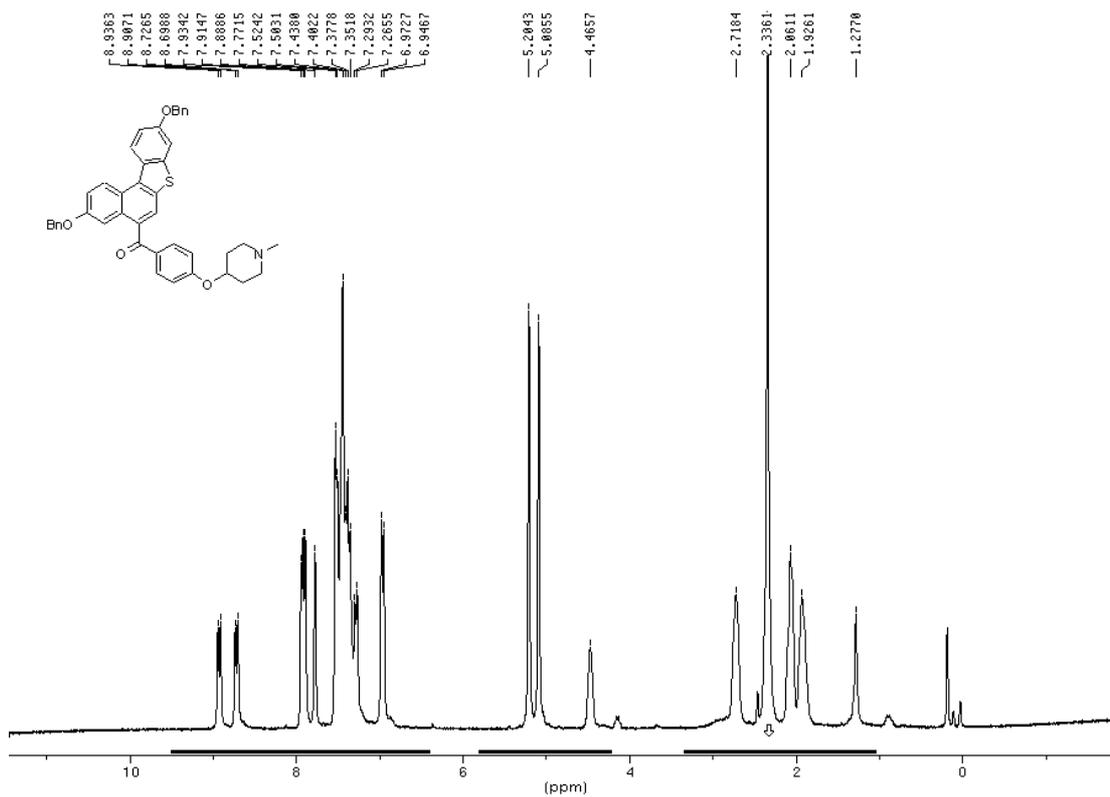


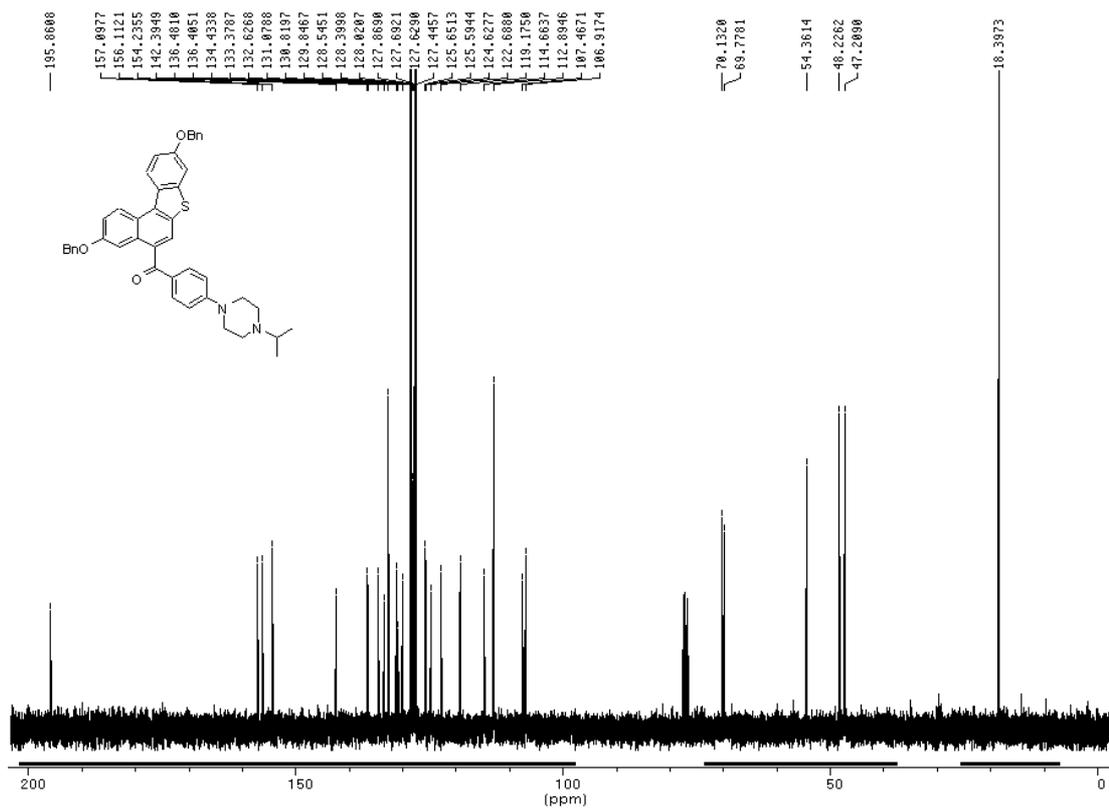
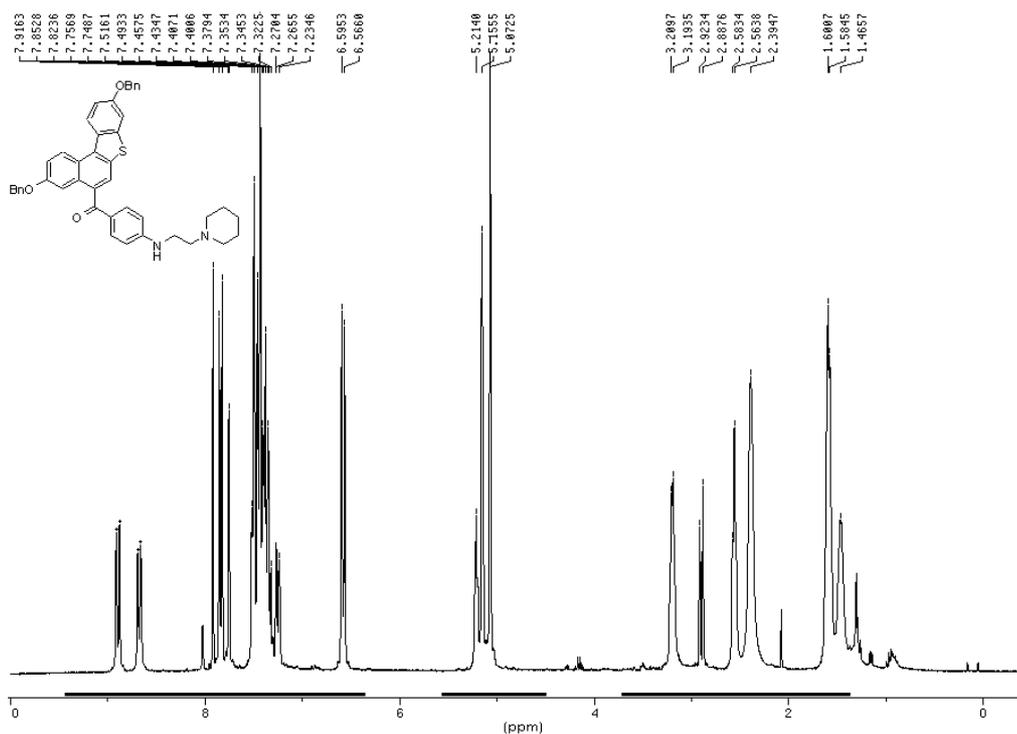


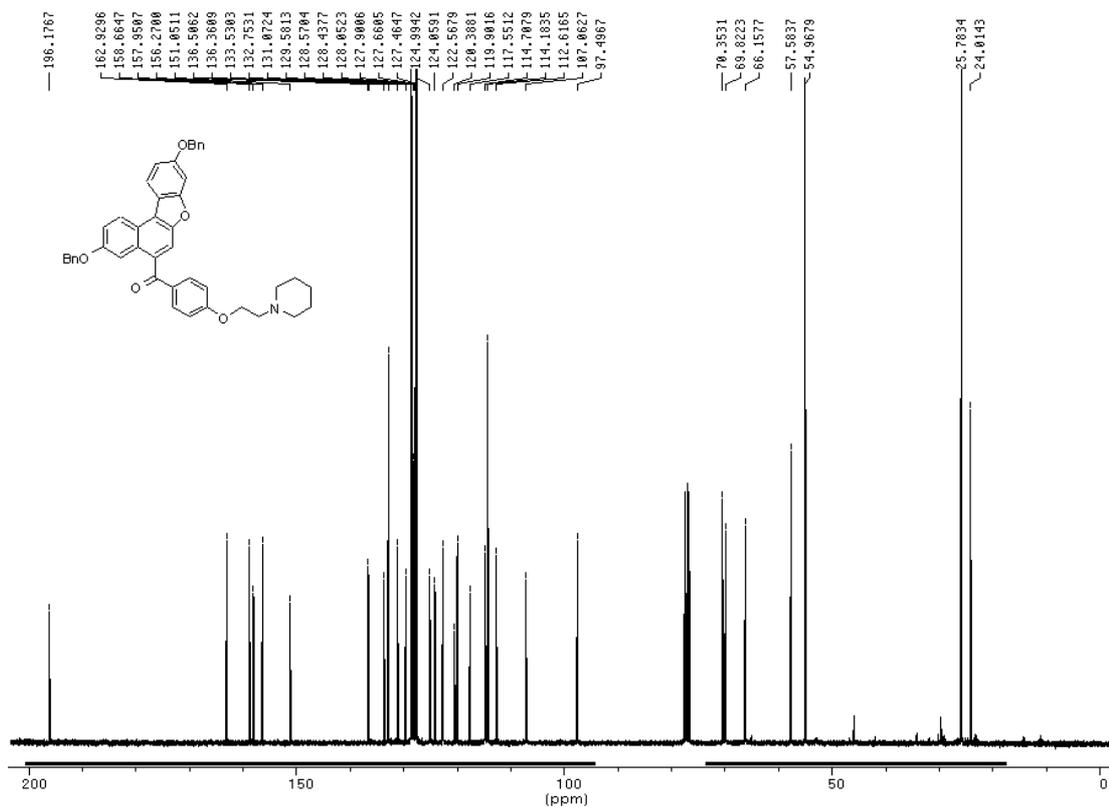
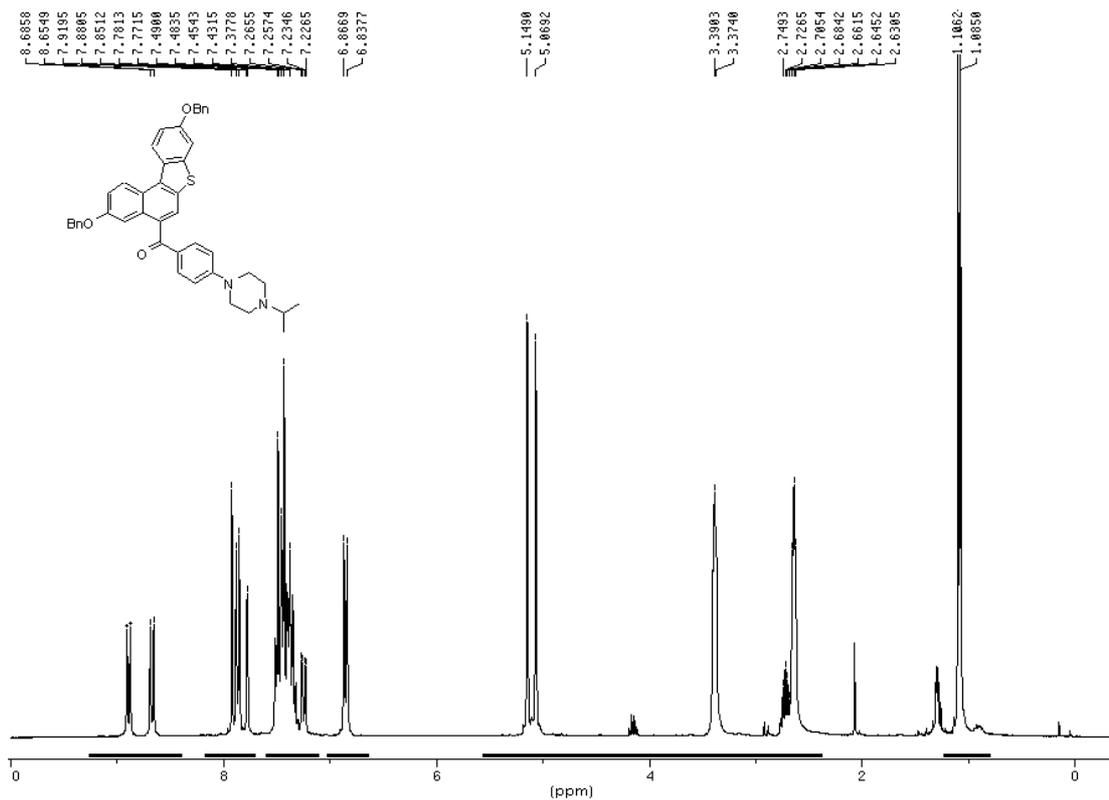


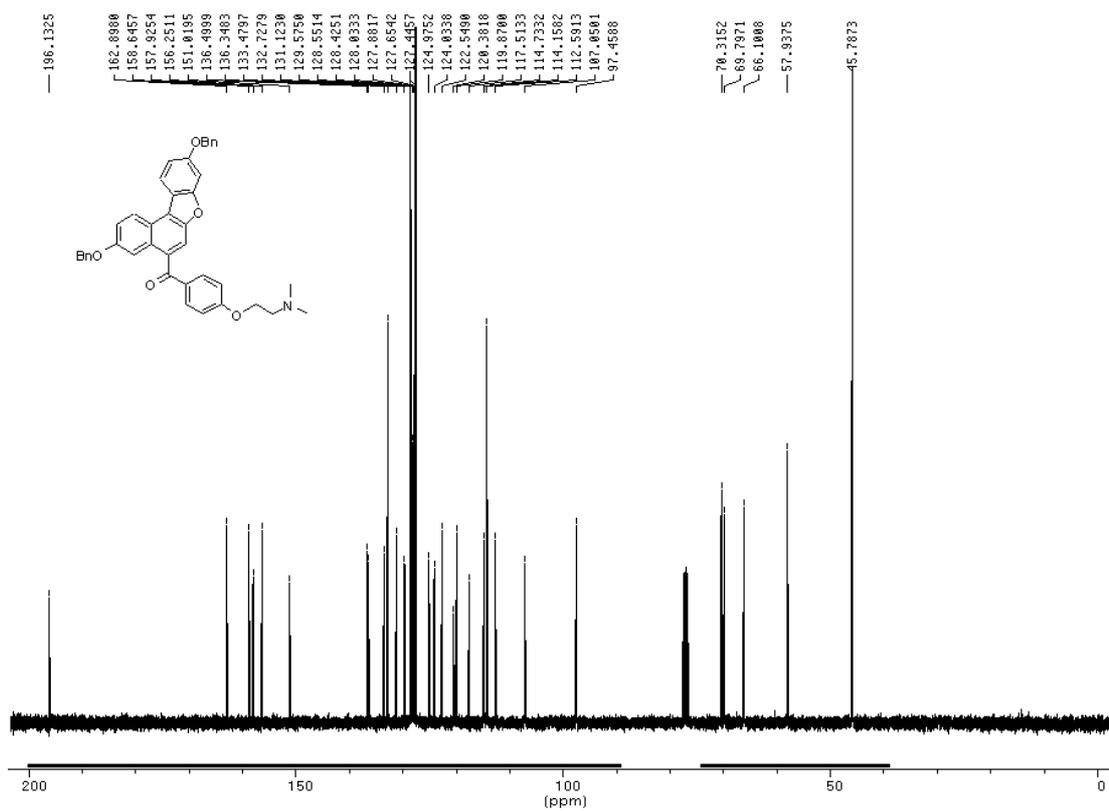
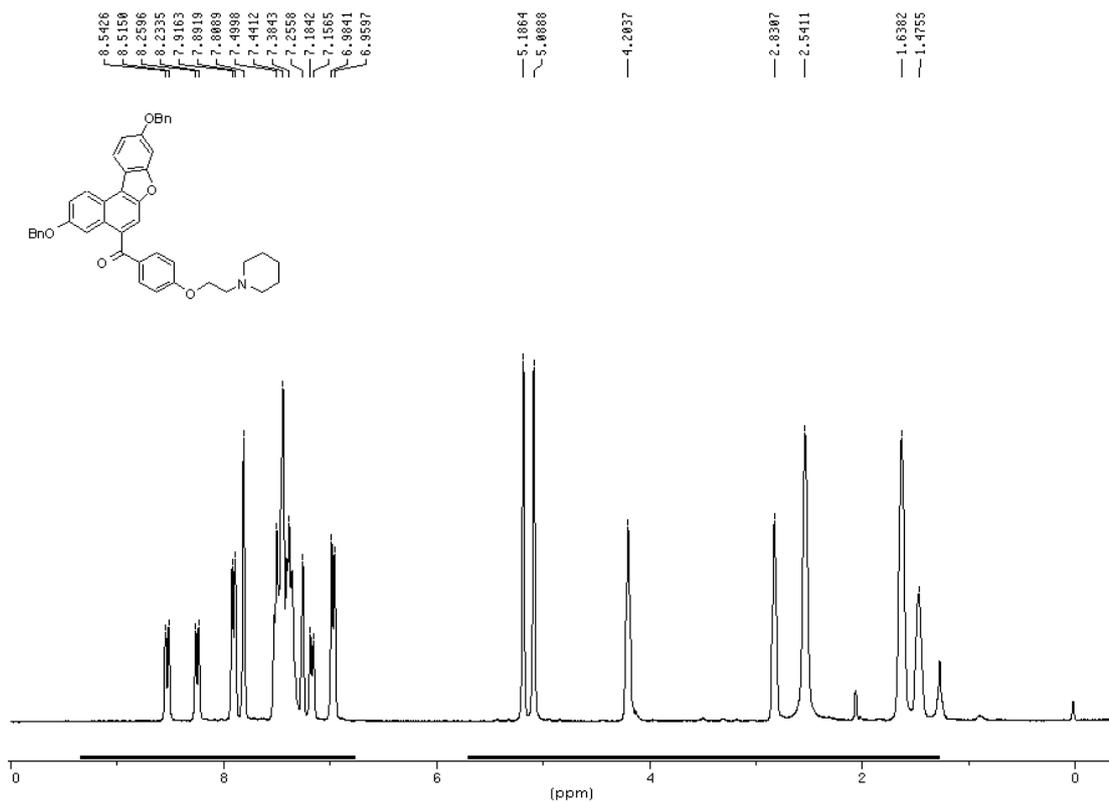


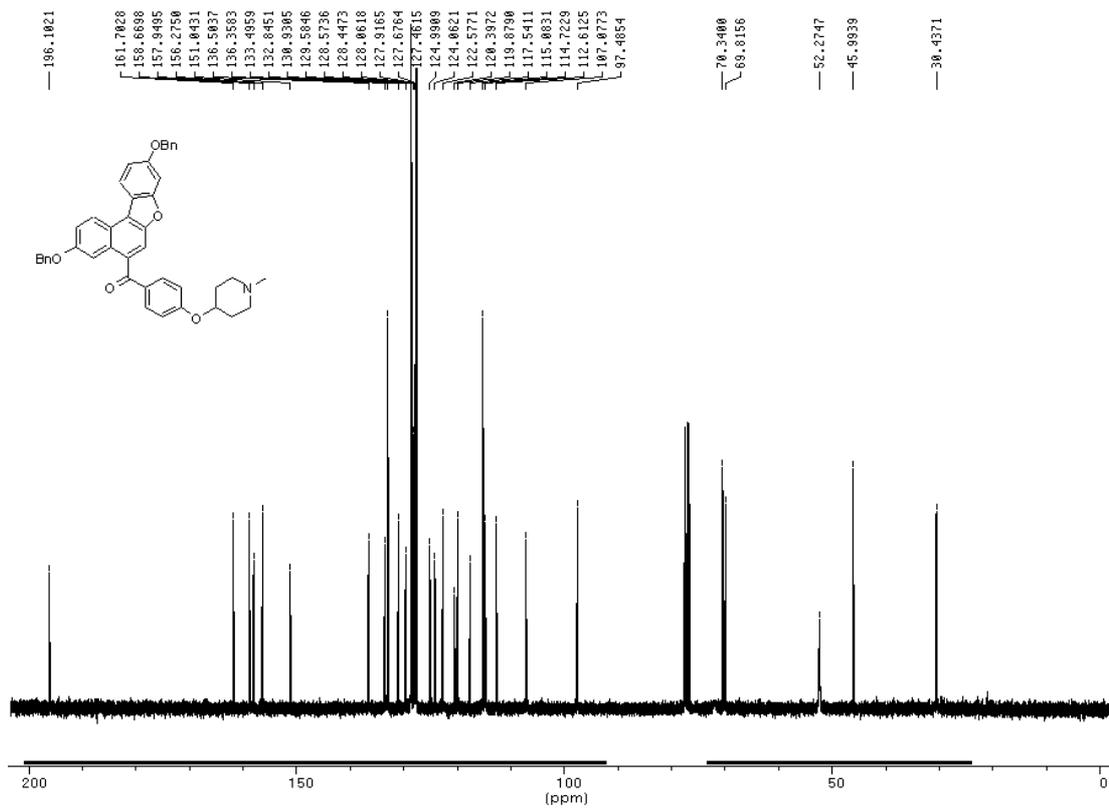
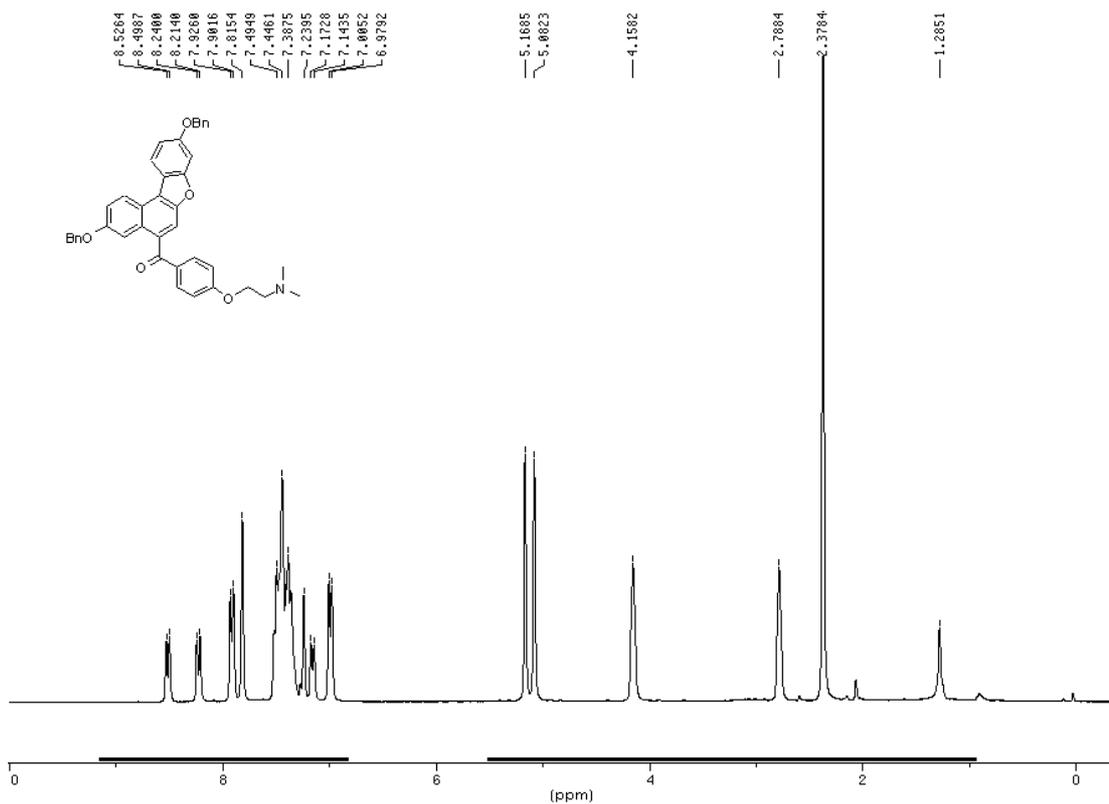


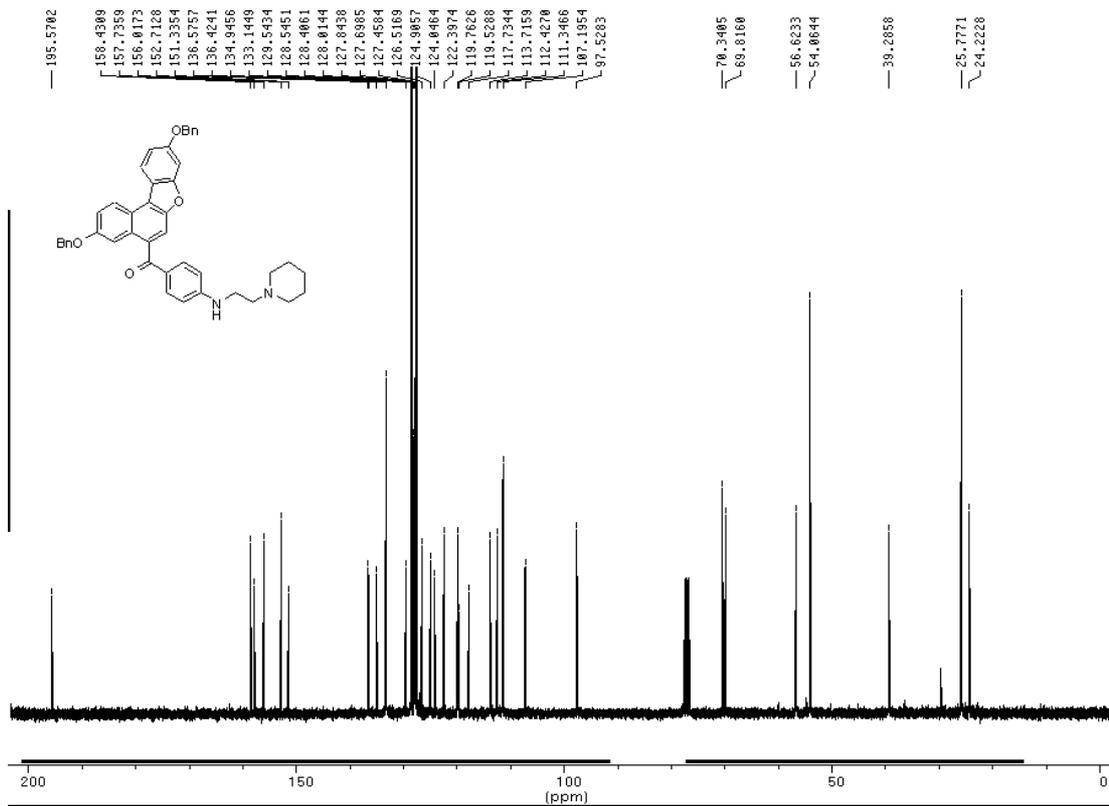
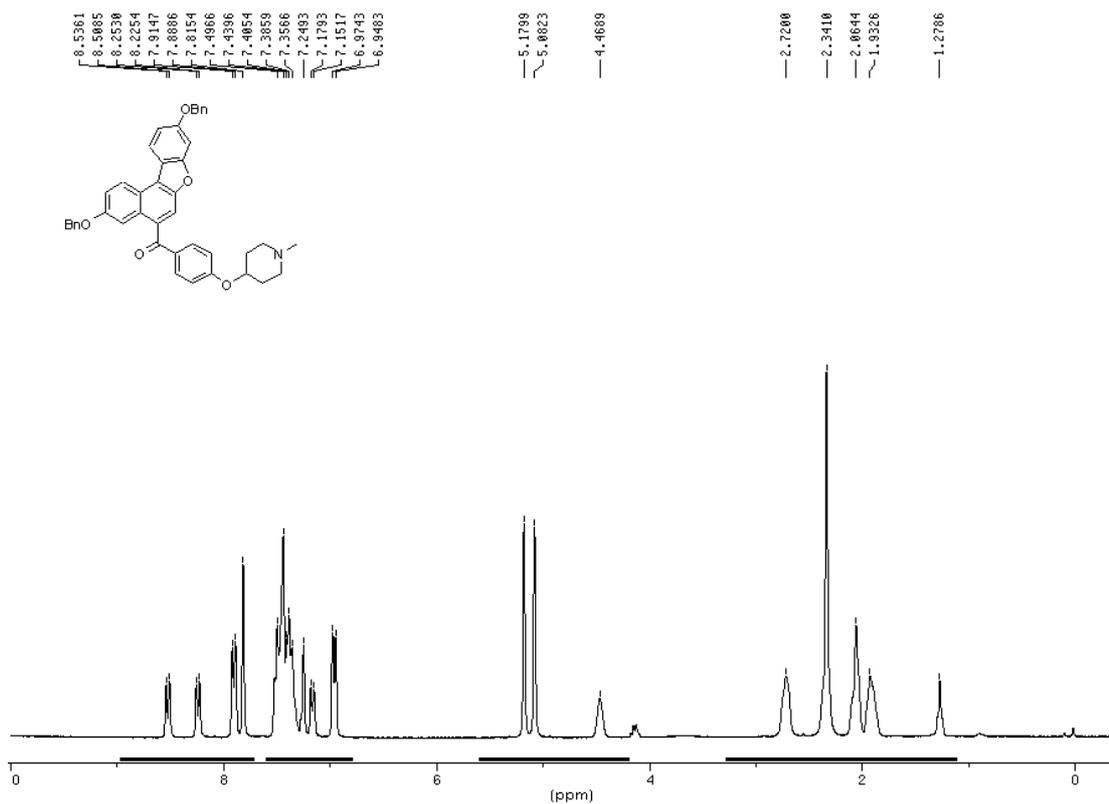


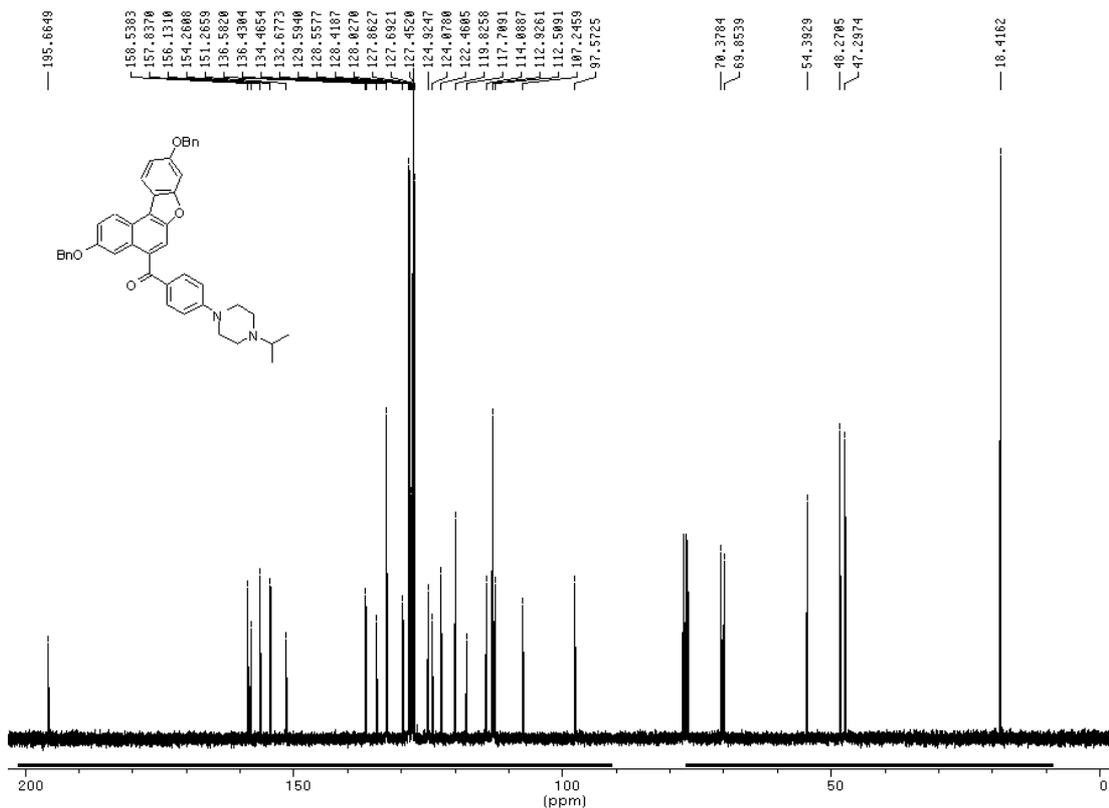
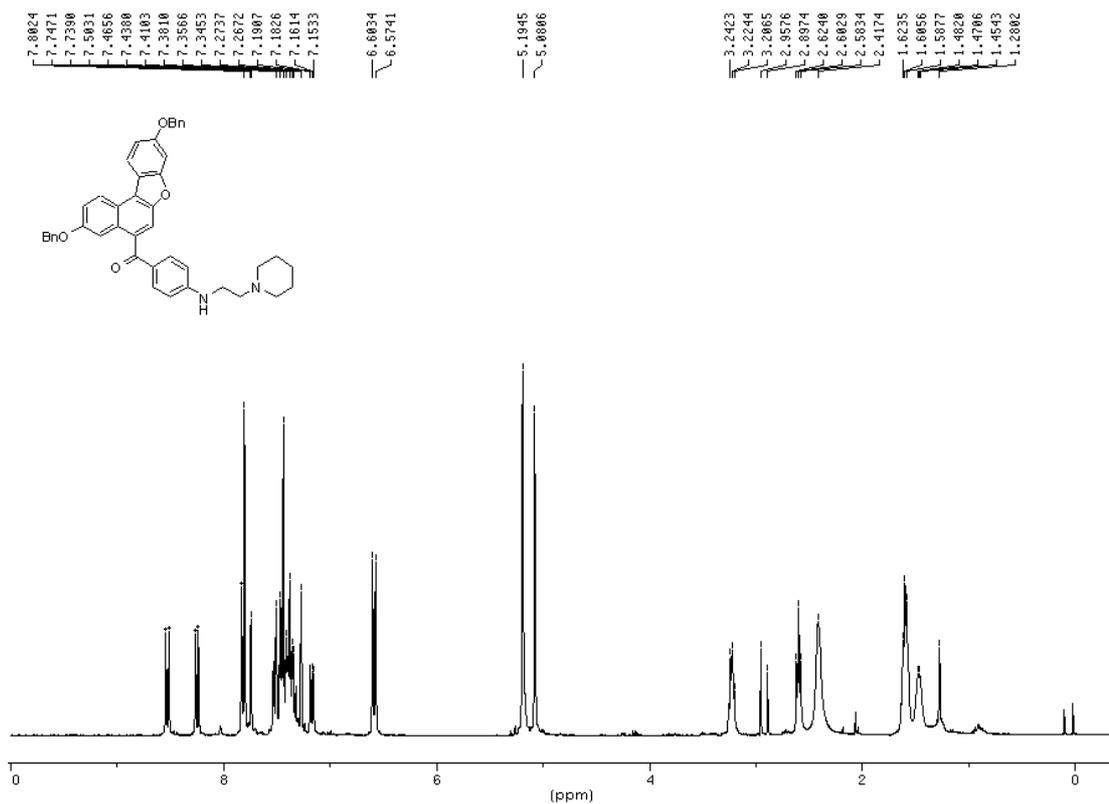


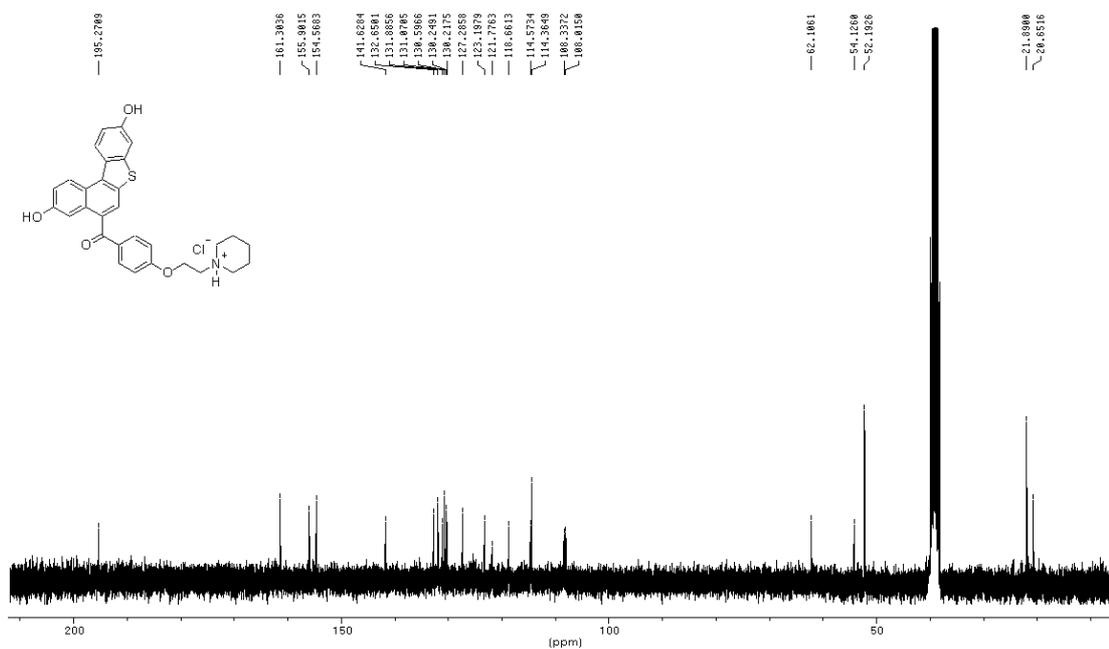
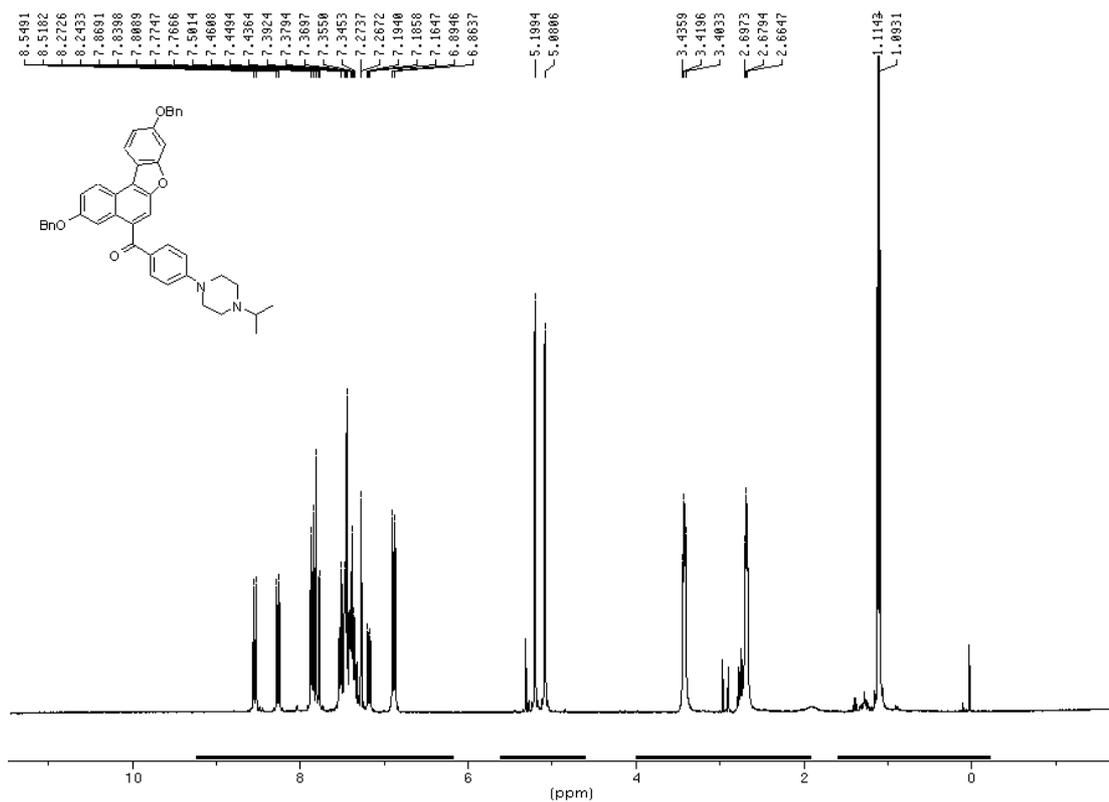


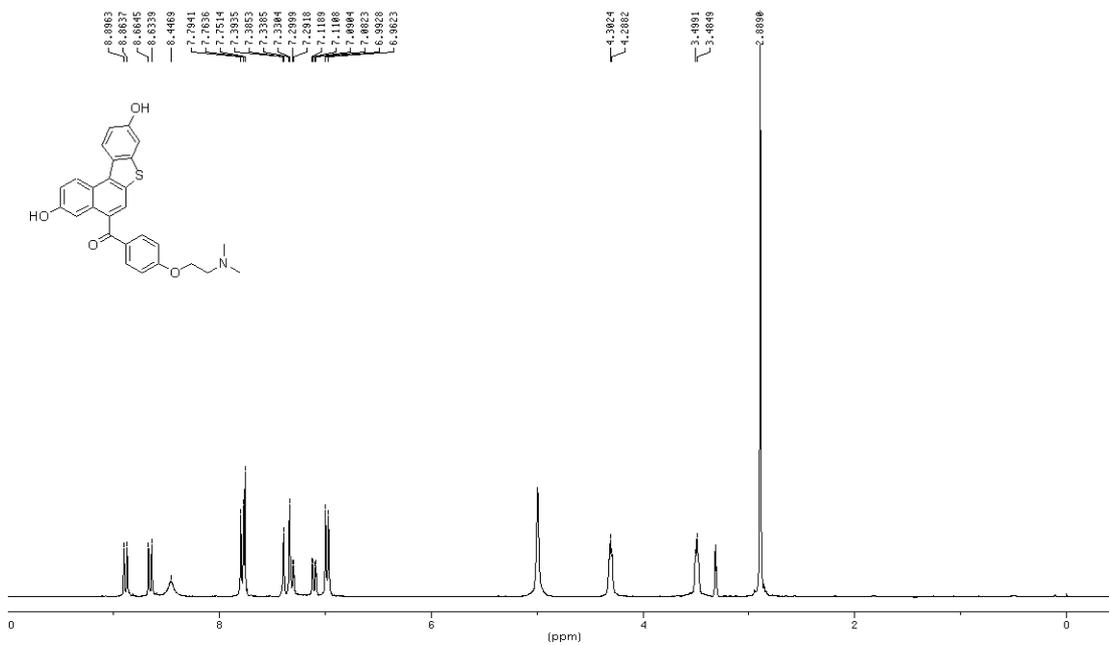
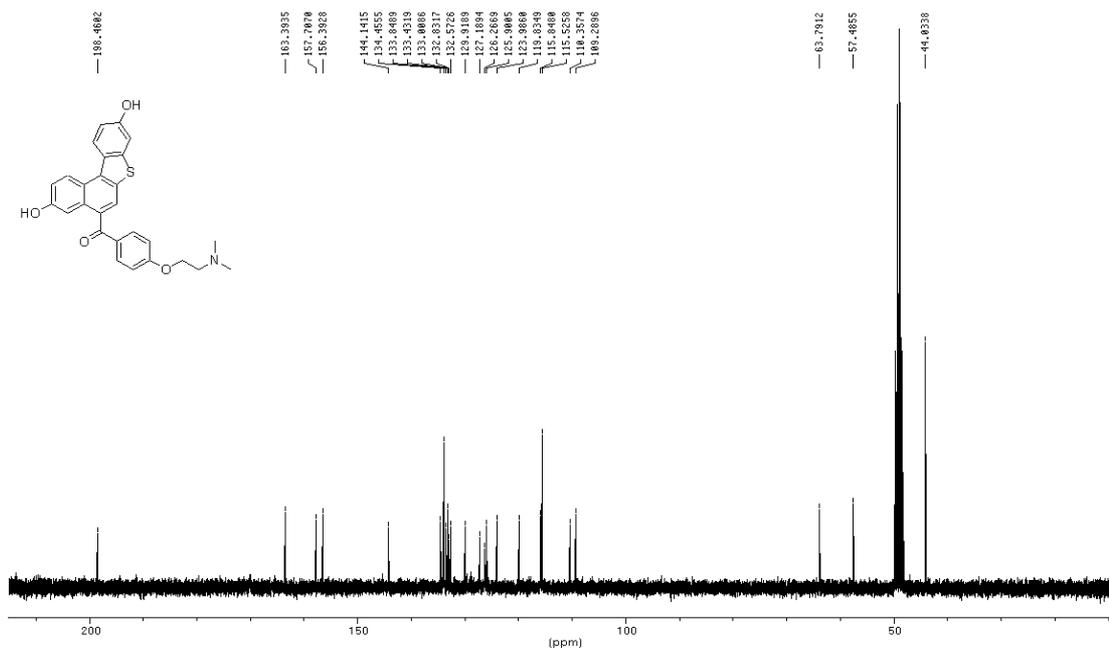


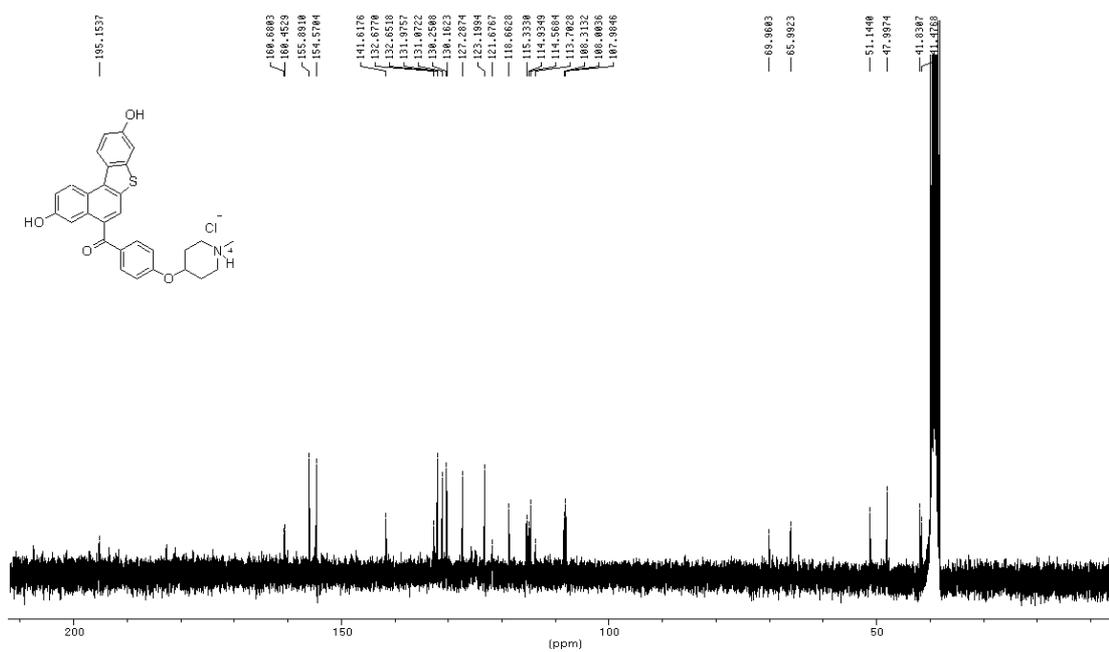
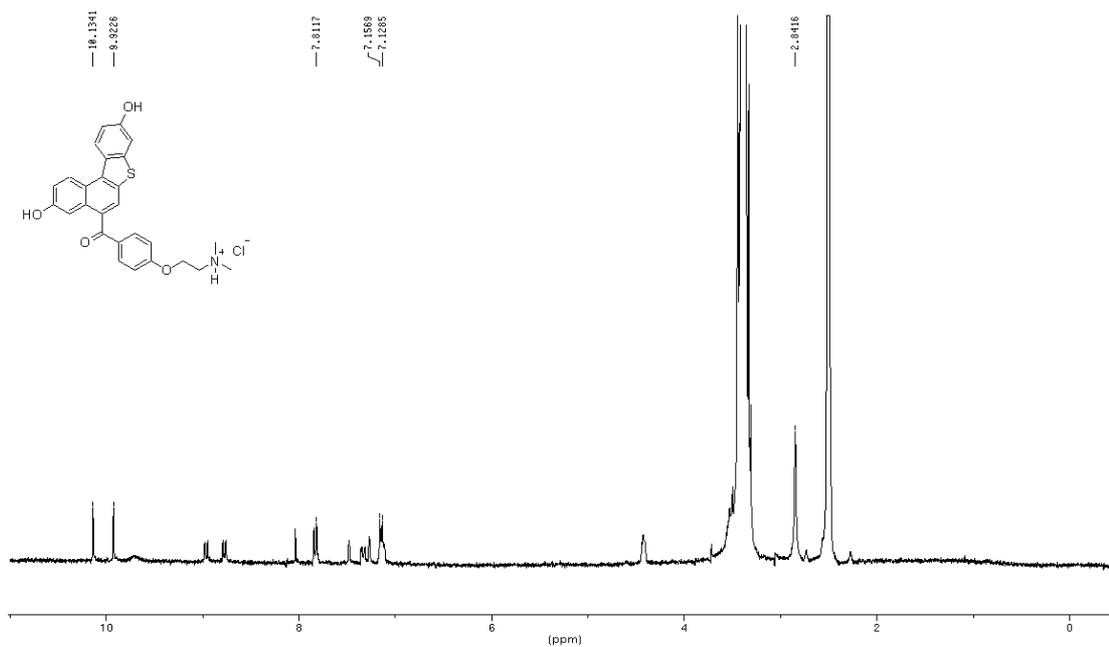


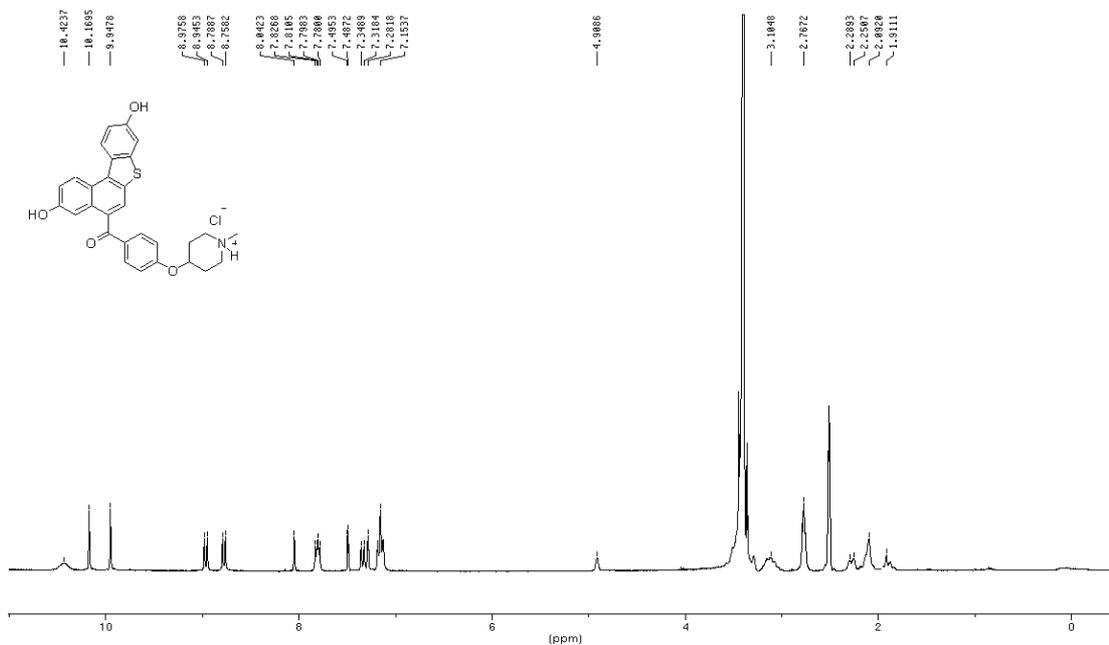
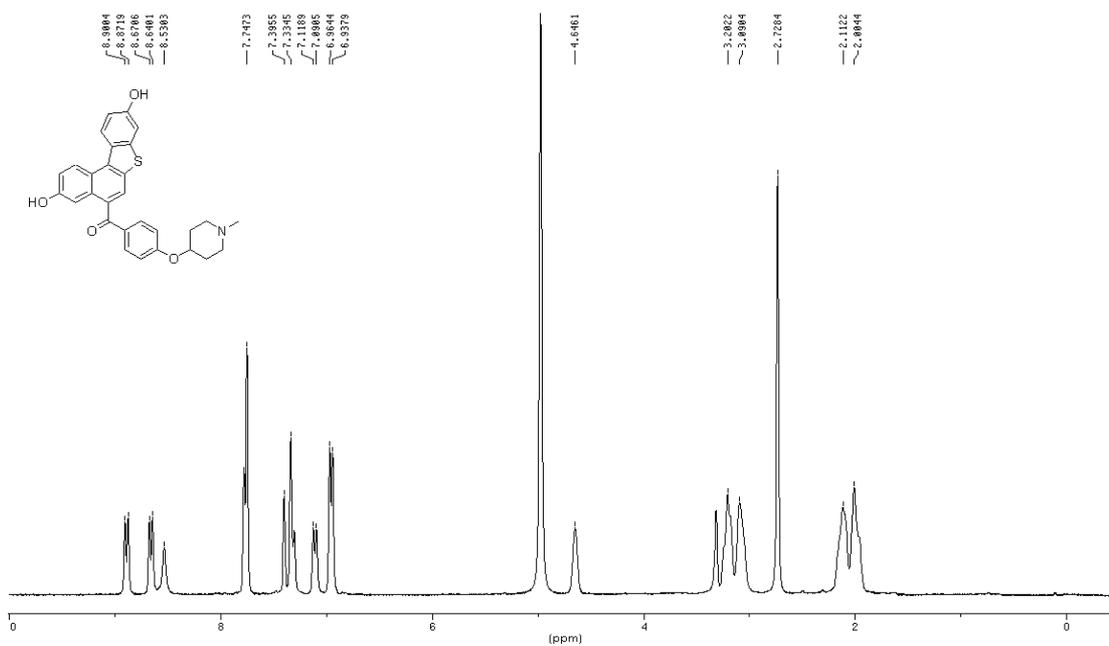


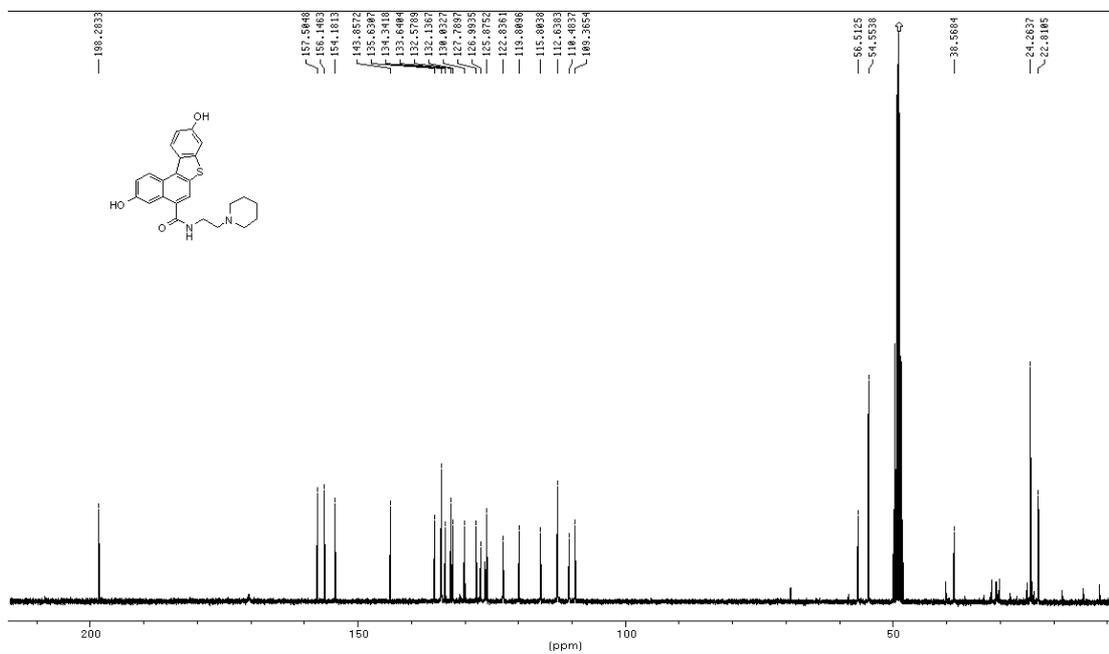
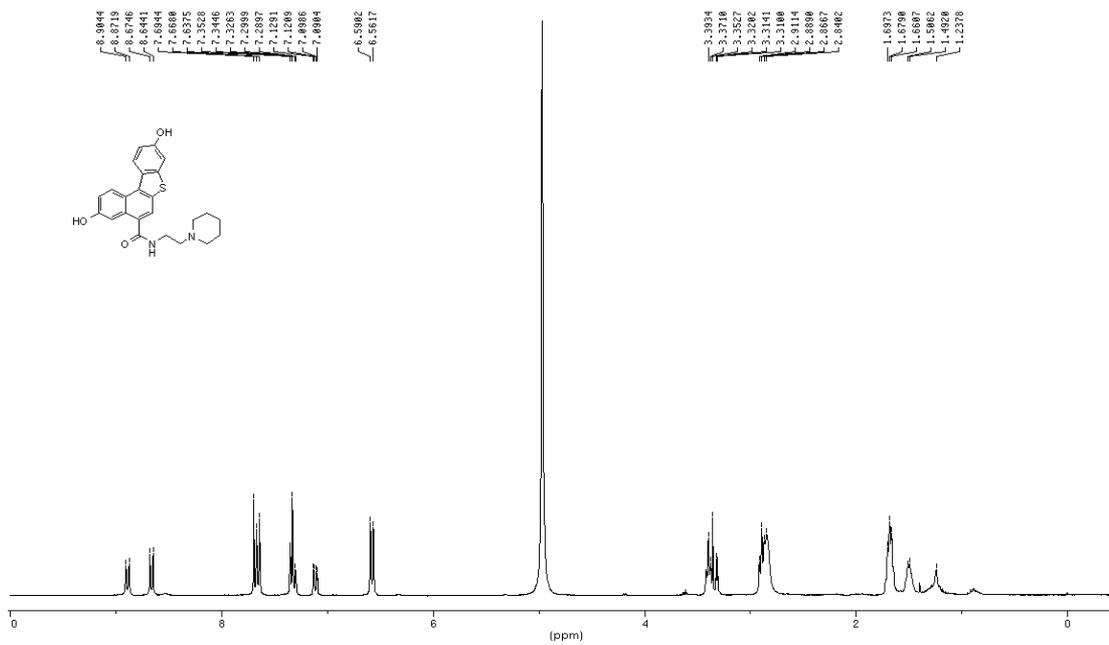


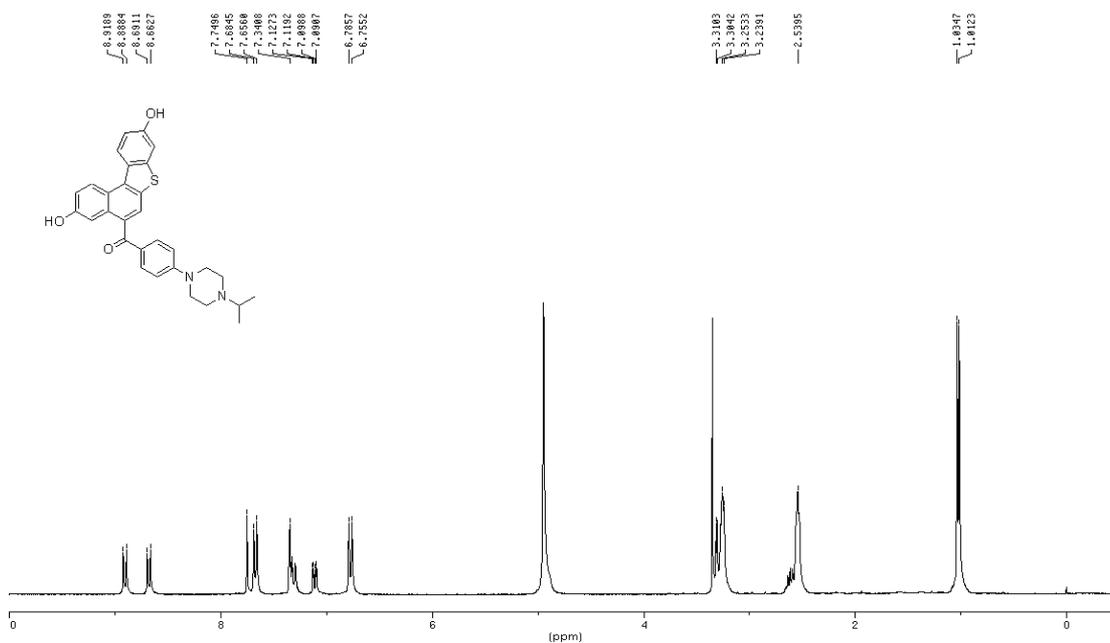
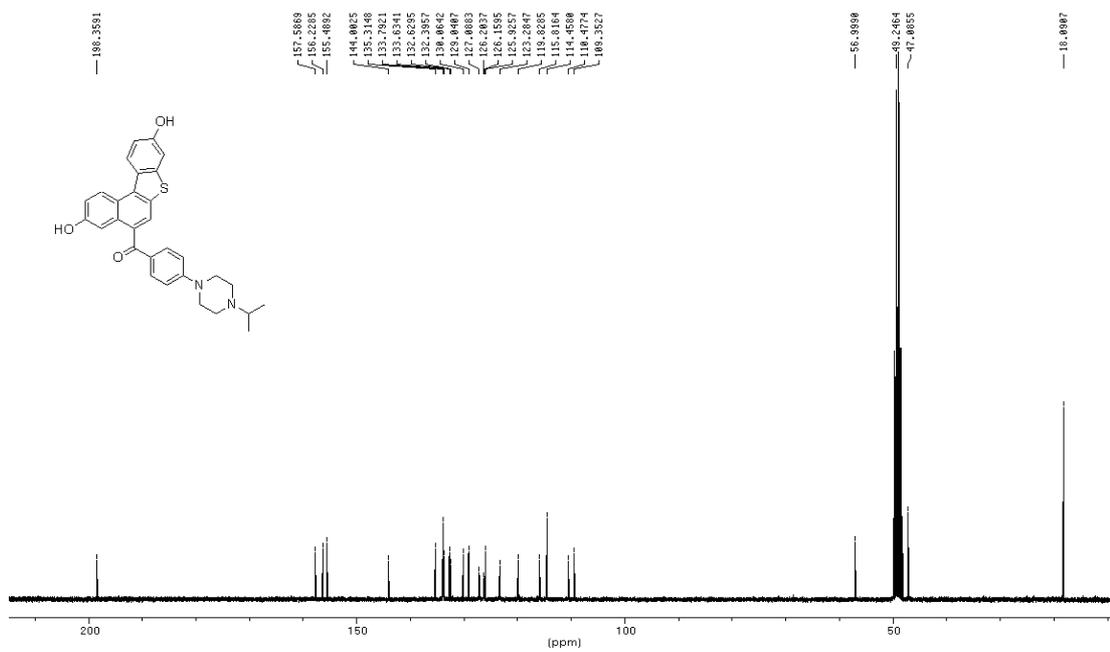


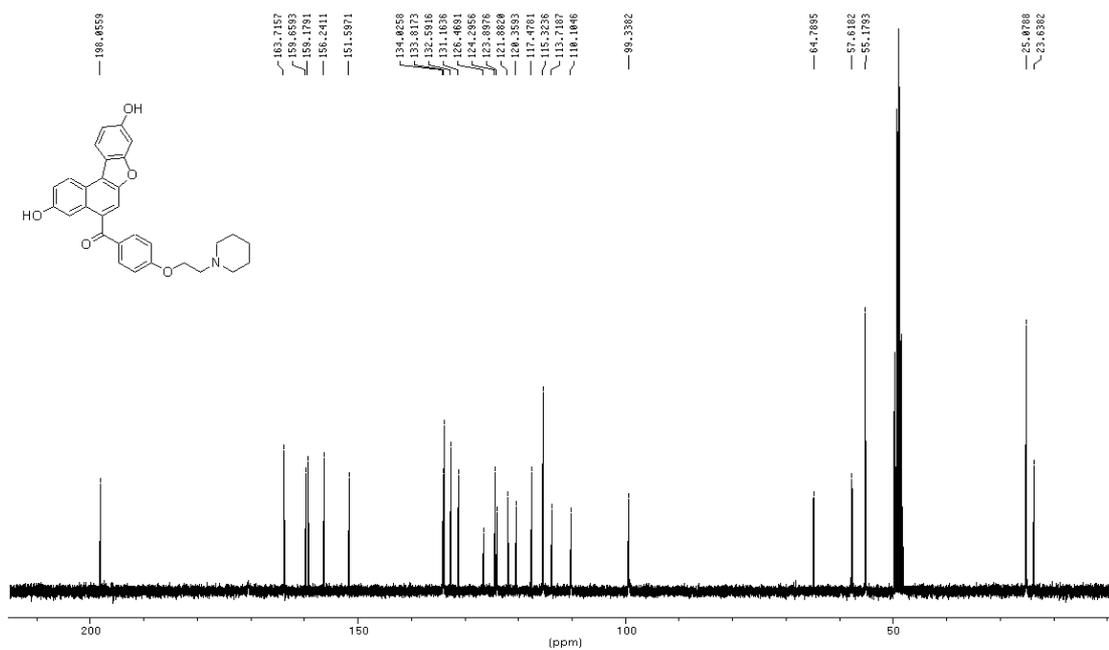
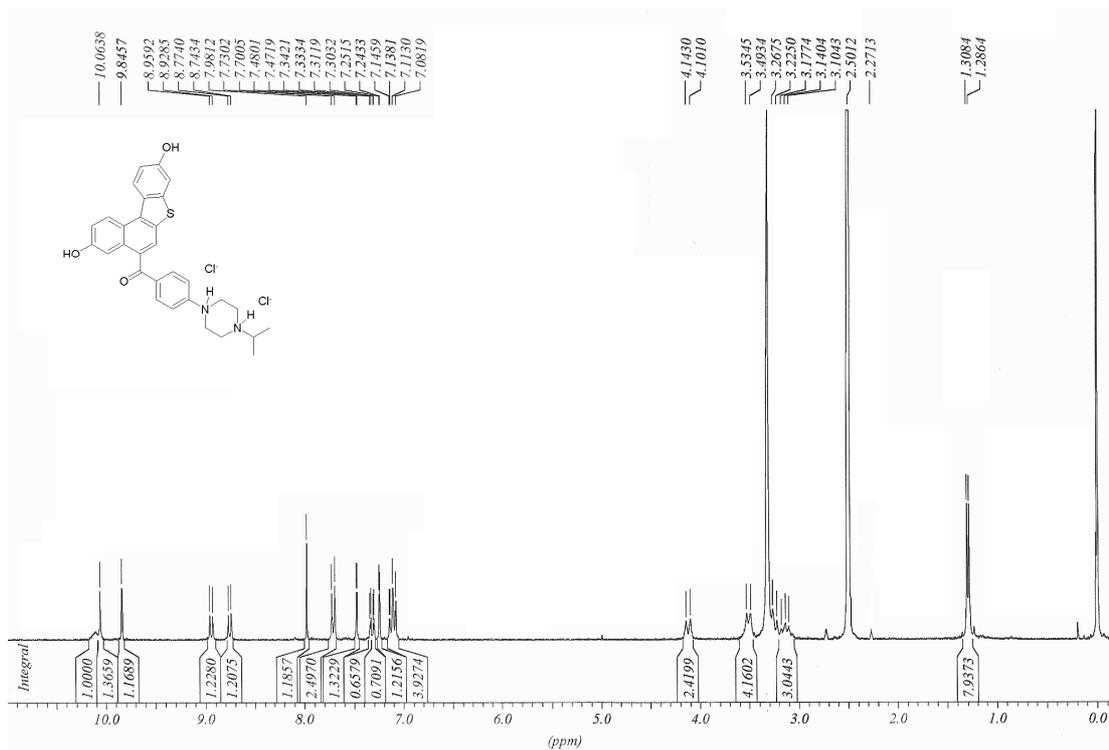


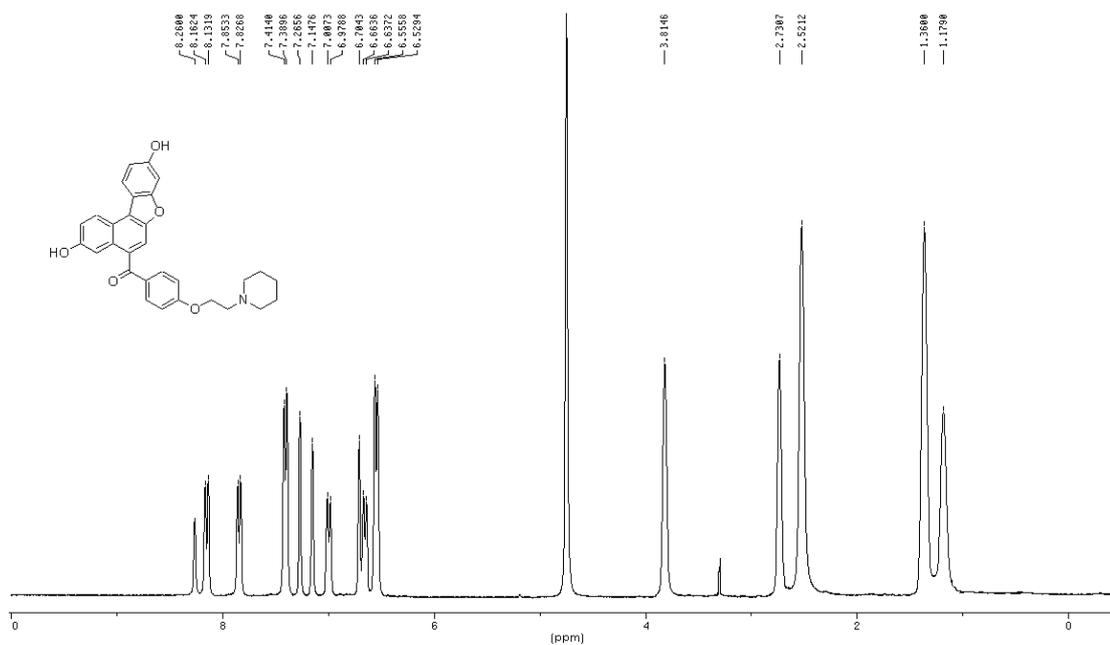
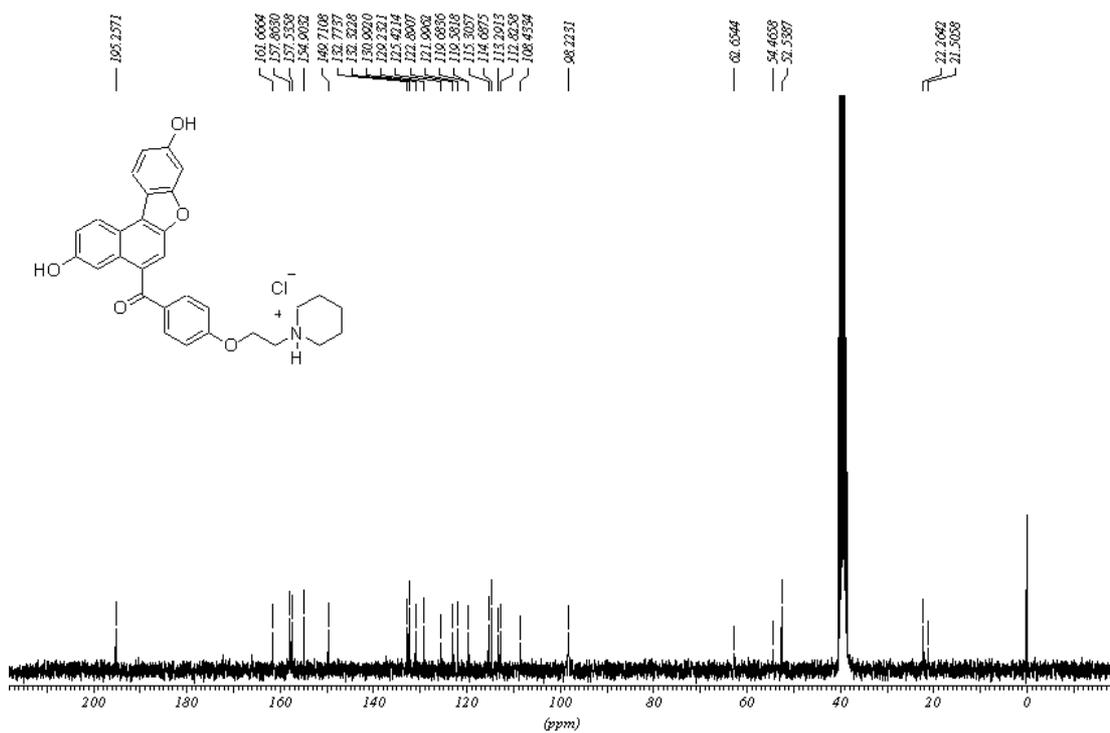


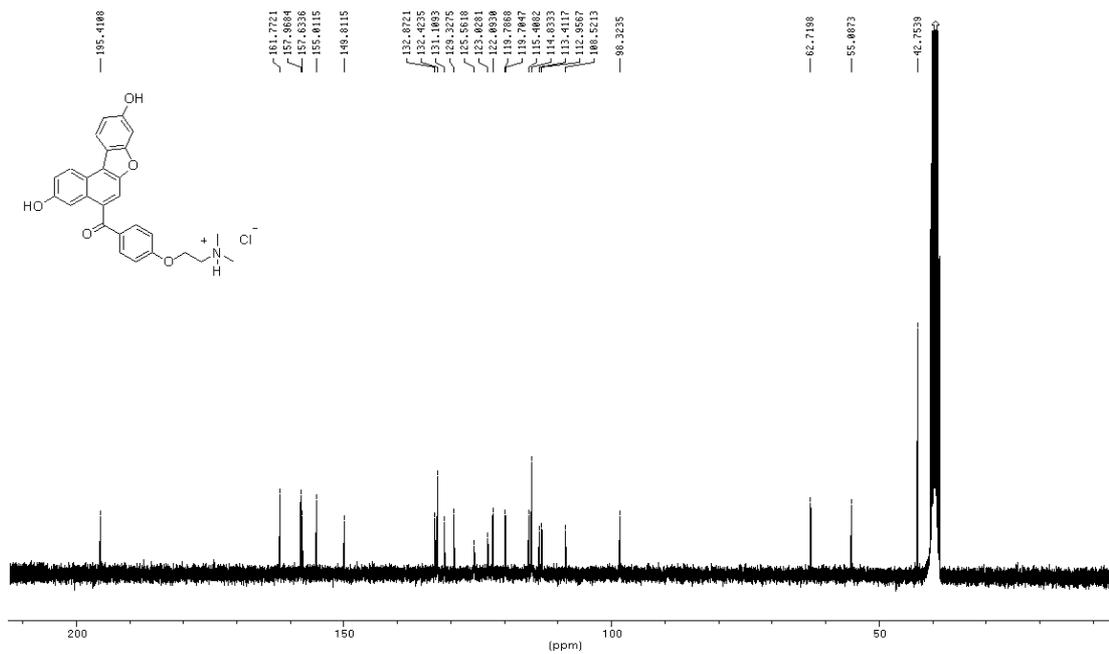
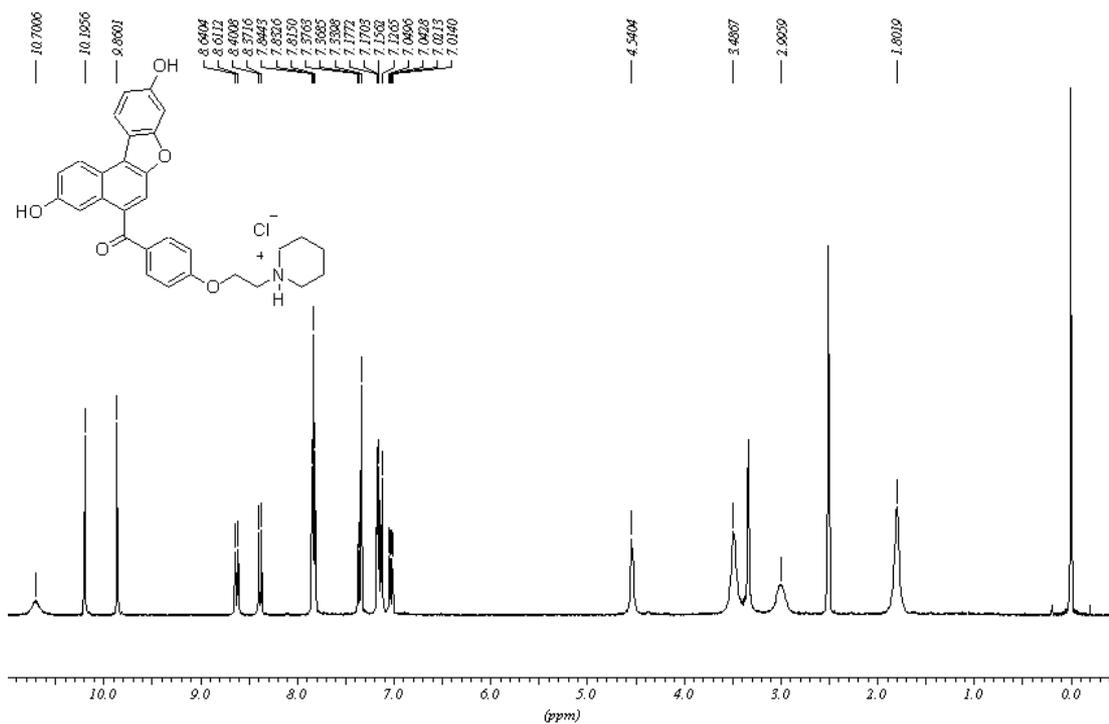


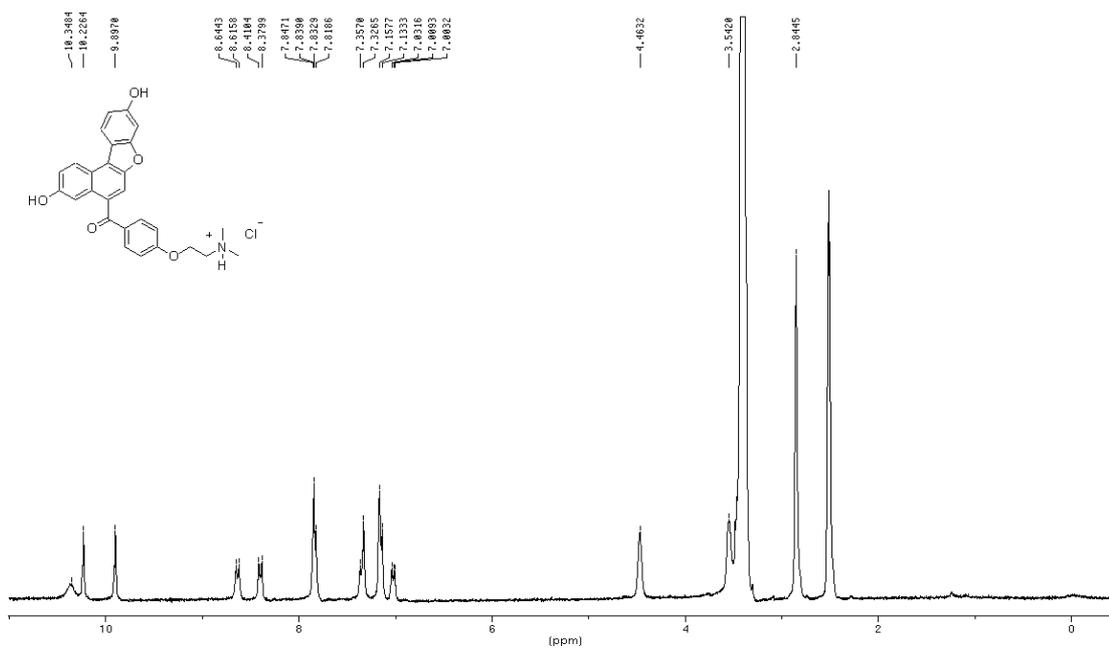
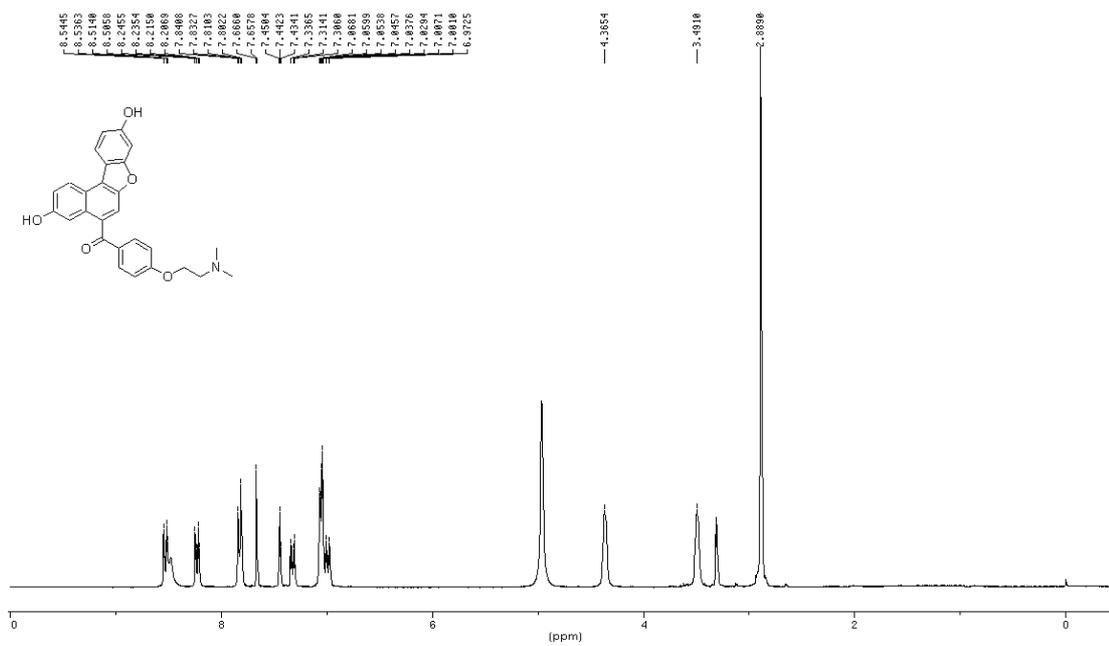


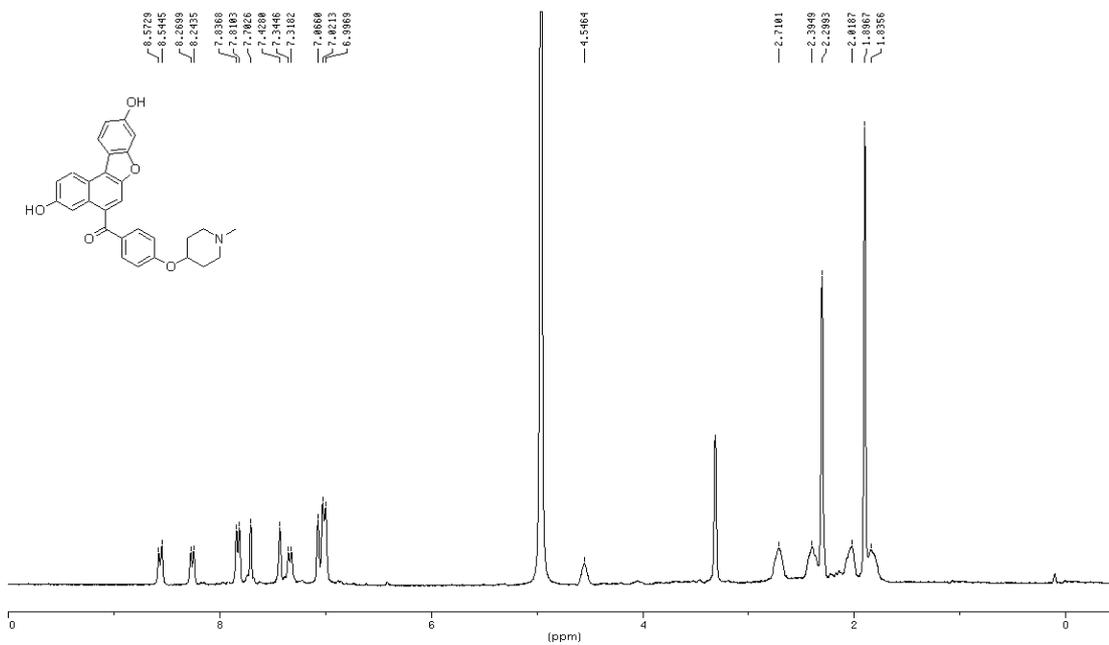
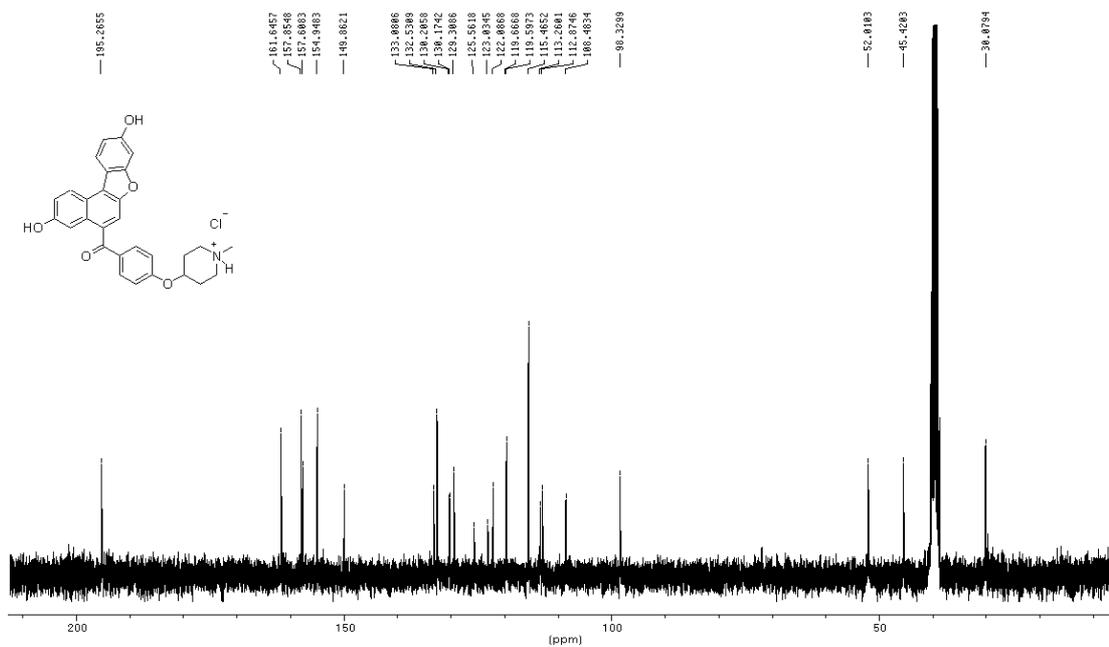


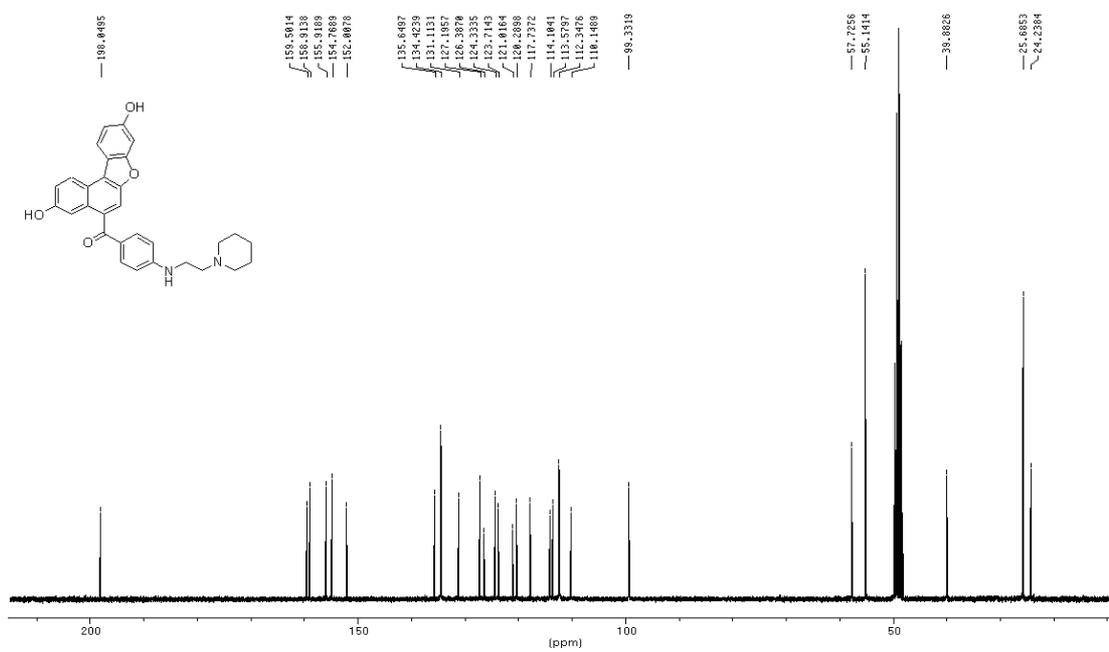
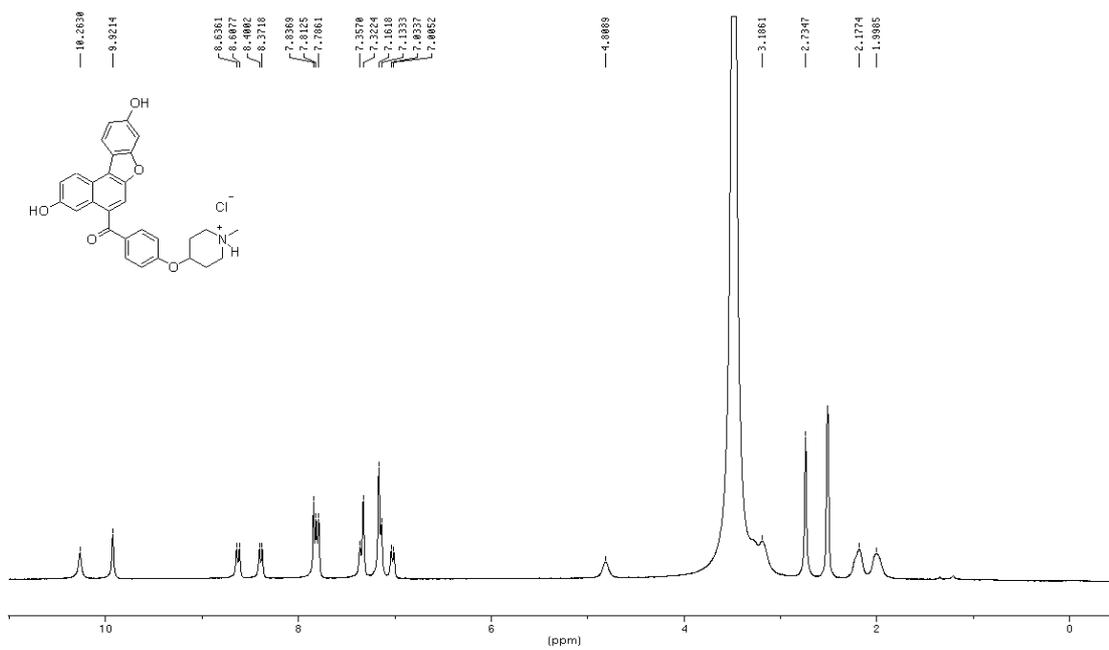


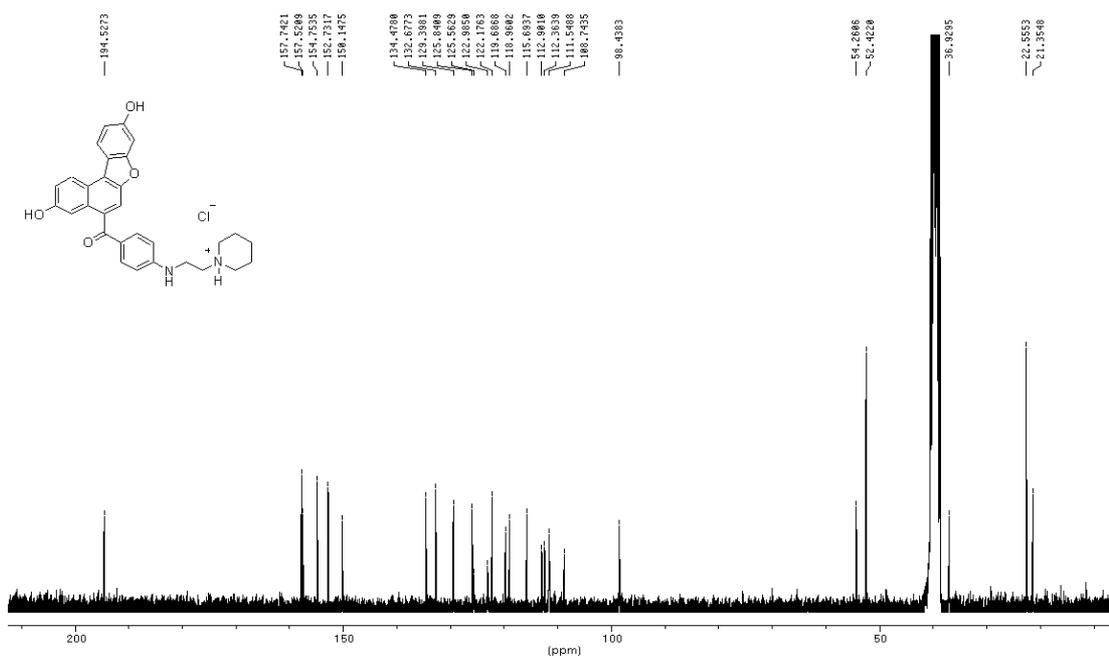


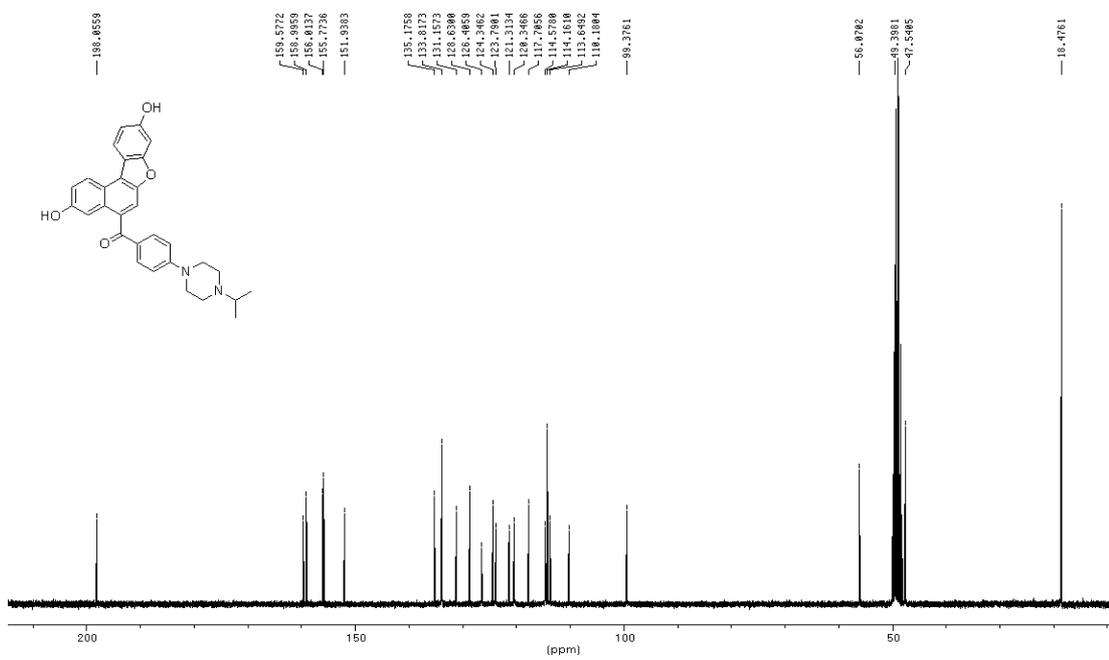
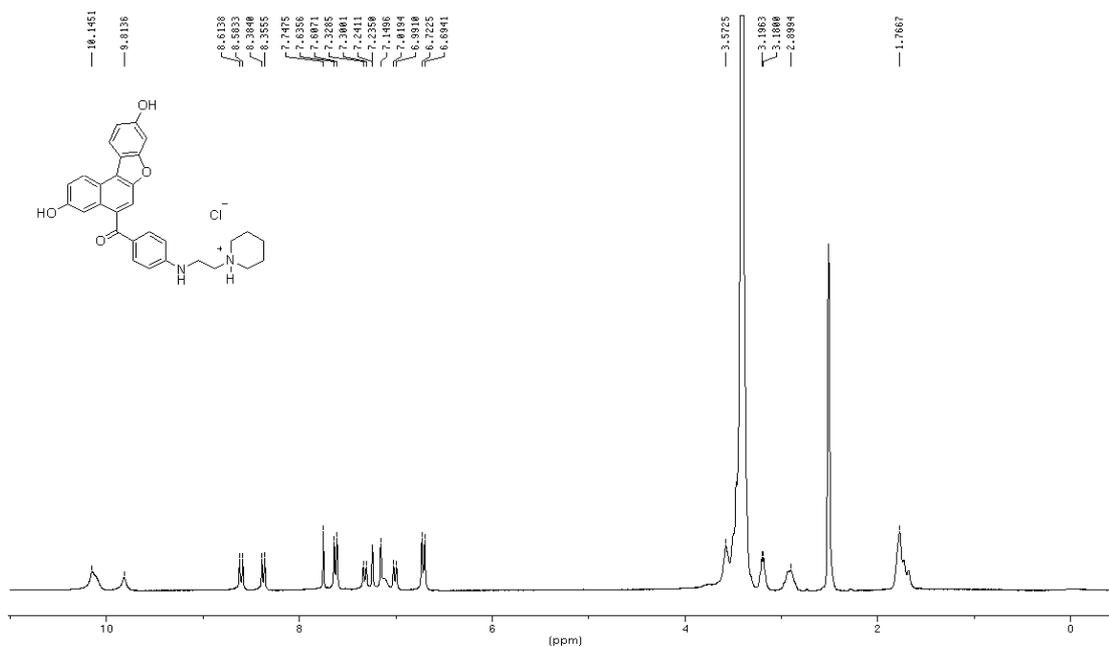


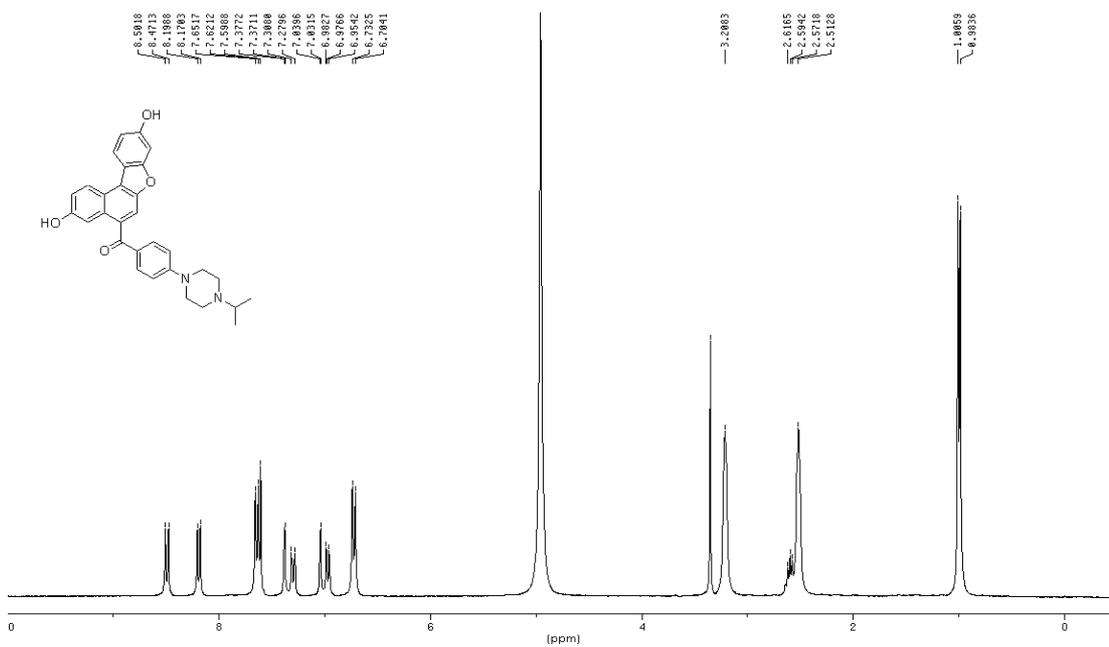
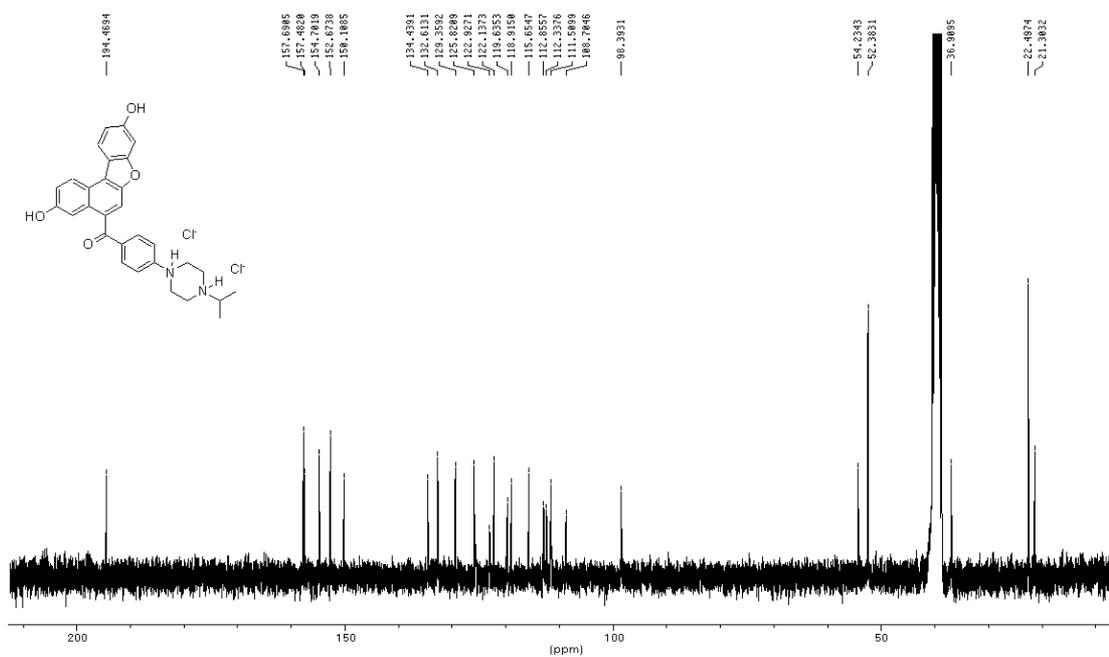


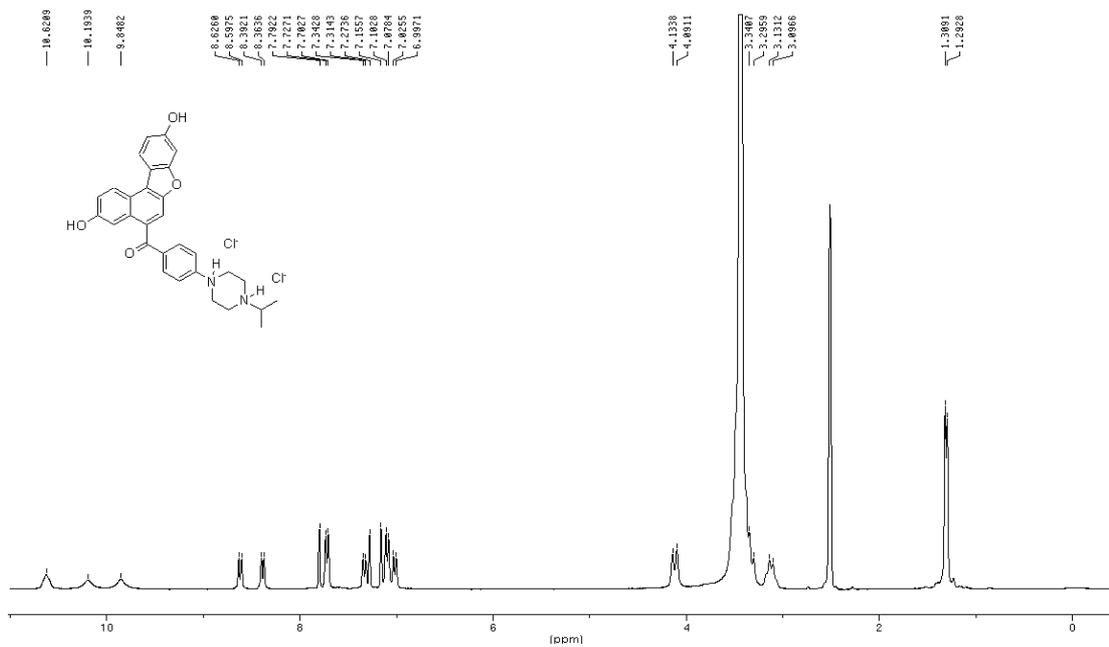




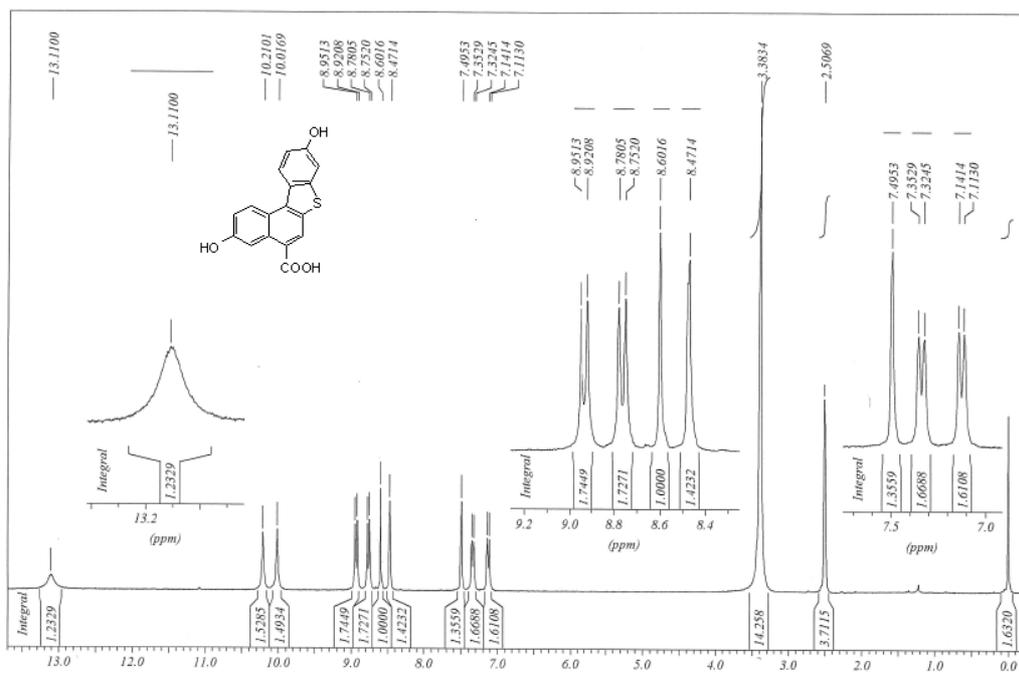




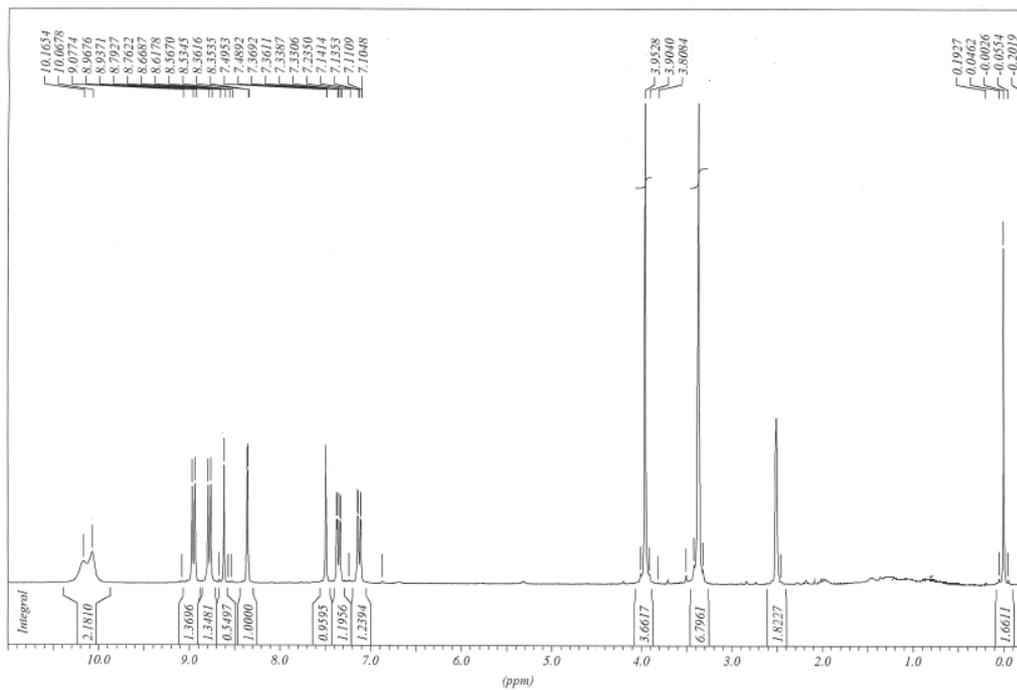




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SD7 DMSO 5.07.2010



SD7C13.073 DMSO 05-06-2010

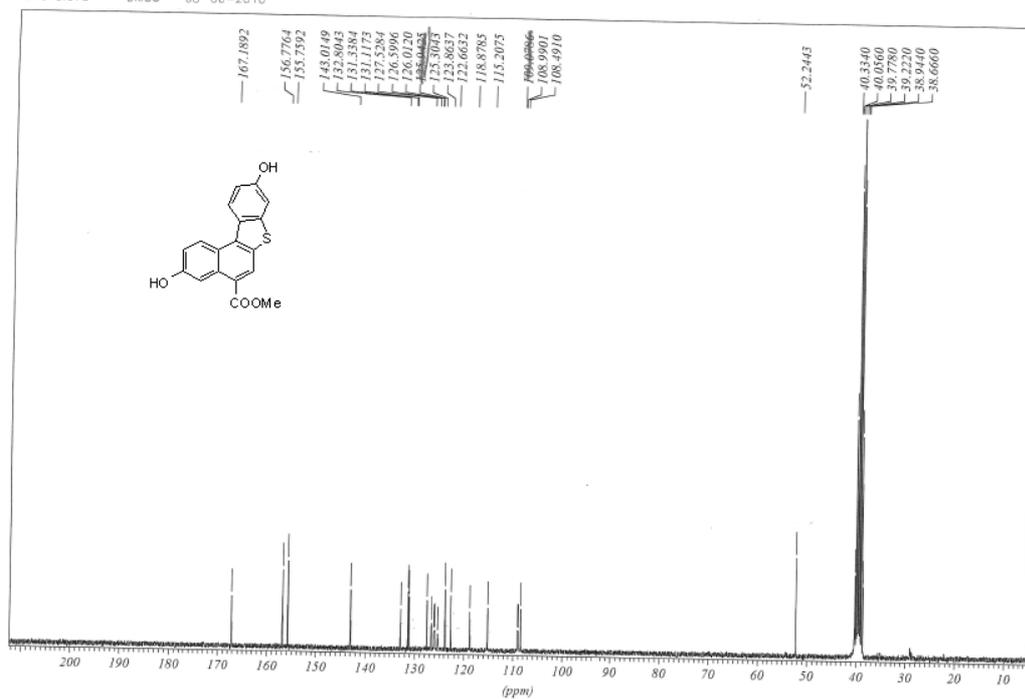
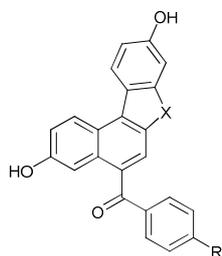


Table S1. Predicted binding energy from the docking studies with **Glide** and *AutoDock*, corresponding to estradiol-like binding modes within the LBD. No value provided means that the docking calculation did not yield any binding pose within the LBD.



Comp.	X	R	Binding energy in ER α (kcal/mol ⁻¹)	Binding energy in ER β (kcal/mol ⁻¹)
6b	O	F	-7.6/-5.7	-10.0/-6.0
9a	S		--/--	-6.5/--
9b	S		--/-5.1	--/-4.7
9c	S		--/--	-6.6/--
9f	O		-6.3/--	-6.8/-6.6
9g	O		-6.1/-6.9	-6.7/-6.5
9h	O		-6.5/--	-6.8/-5.4
9i	O		-6.6/-7.0	-6.7/-7.8
9j	O		--/--	-7.8/-6.6

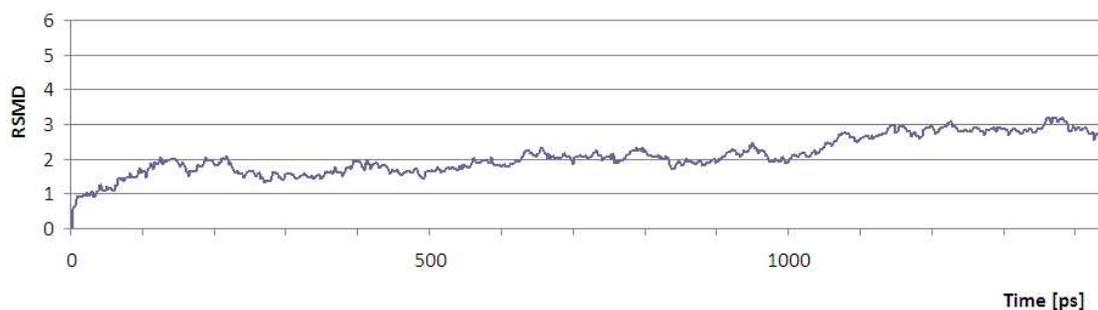


Figure S1. Evolution of the root-mean-square deviation (rmsd) of the $C\alpha$ atoms of ER β -**9f** complex with respect to the initial structure during the MD simulation (initial 500 ps with distance restriction).

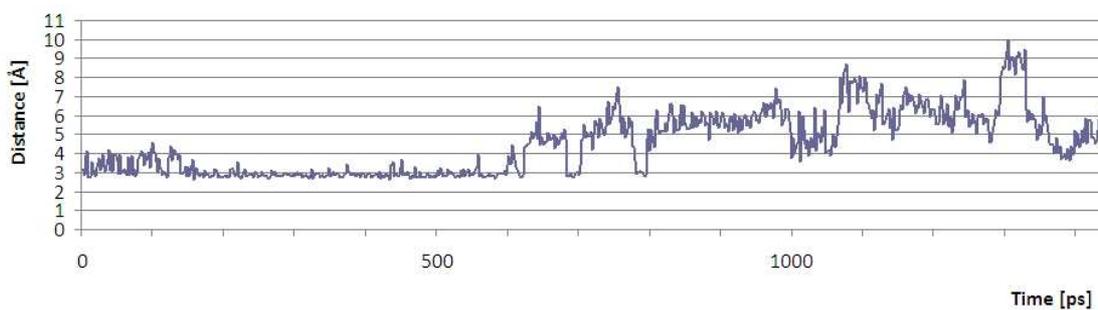


Figure S2. Evolution of the Asp303 $\text{COO}^- \cdots \text{NH}^+$ piperidinium distance (Å) of ER β -**9f** complex during the MD simulation (initial 500 ps with distance restriction).



Figure S3. Evolution of the root-mean-square deviation (rmsd) of the $C\alpha$ atoms of ER β -**9f** complex with respect to the initial structure during the MD simulation (with no restrictions).

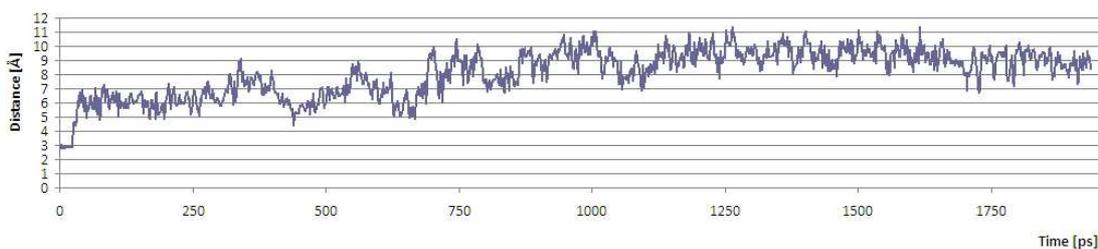


Figure S4. Evolution of the Asp303 $\text{COO}^- \cdots \text{NH}^+$ piperidinium distance (Å) of ER β -**9f** complex during the MD simulation (with no restrictions).

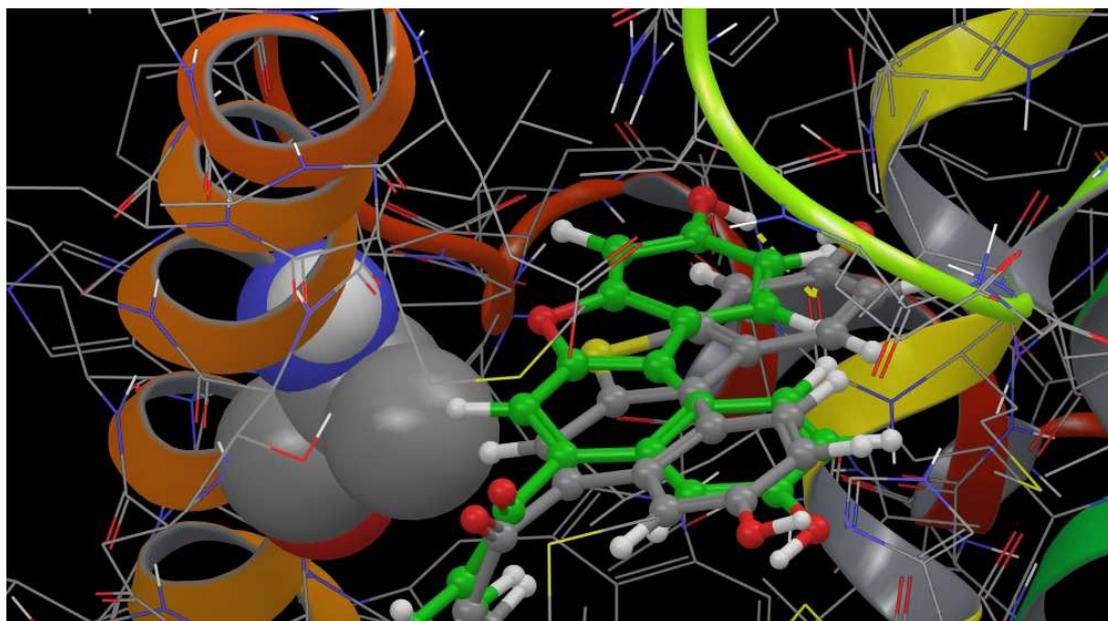


Figure S5. Superimposition of docked poses of compound **9f** (green) and the thioderivative **9a** (grey).