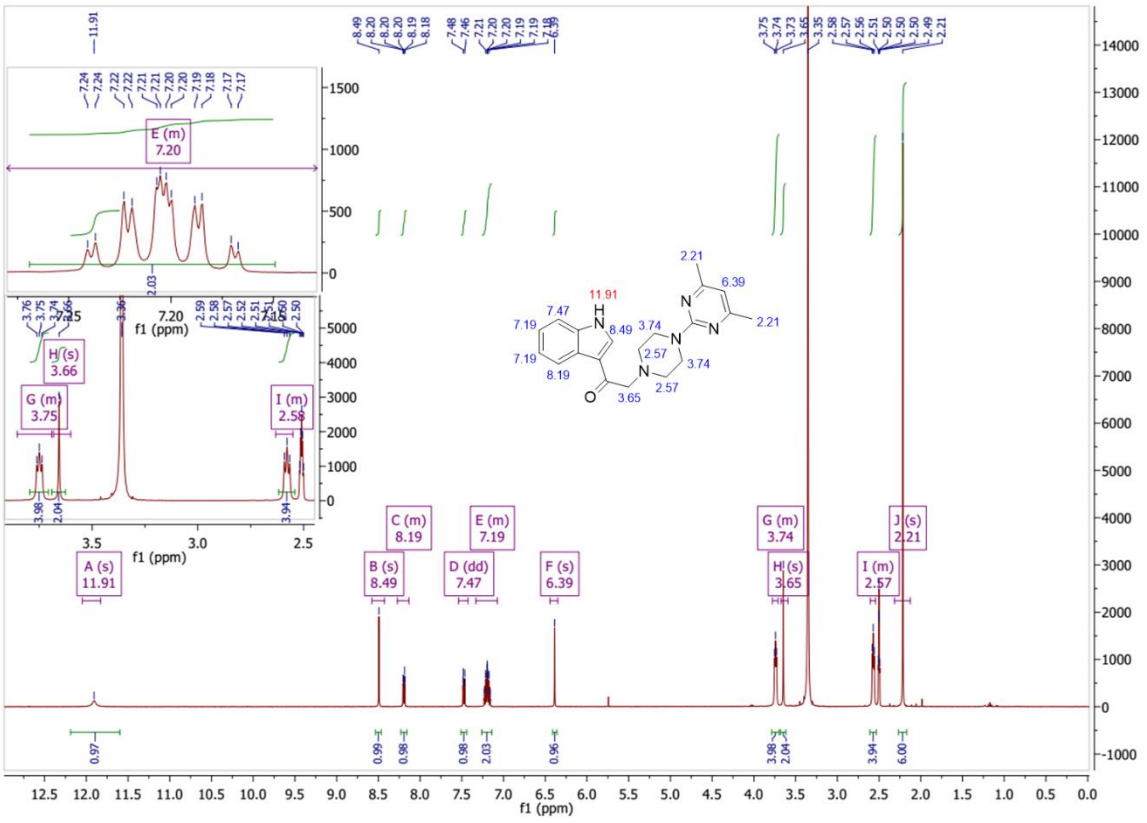


Figure S1: ^{1}H NMR of Compound 3.

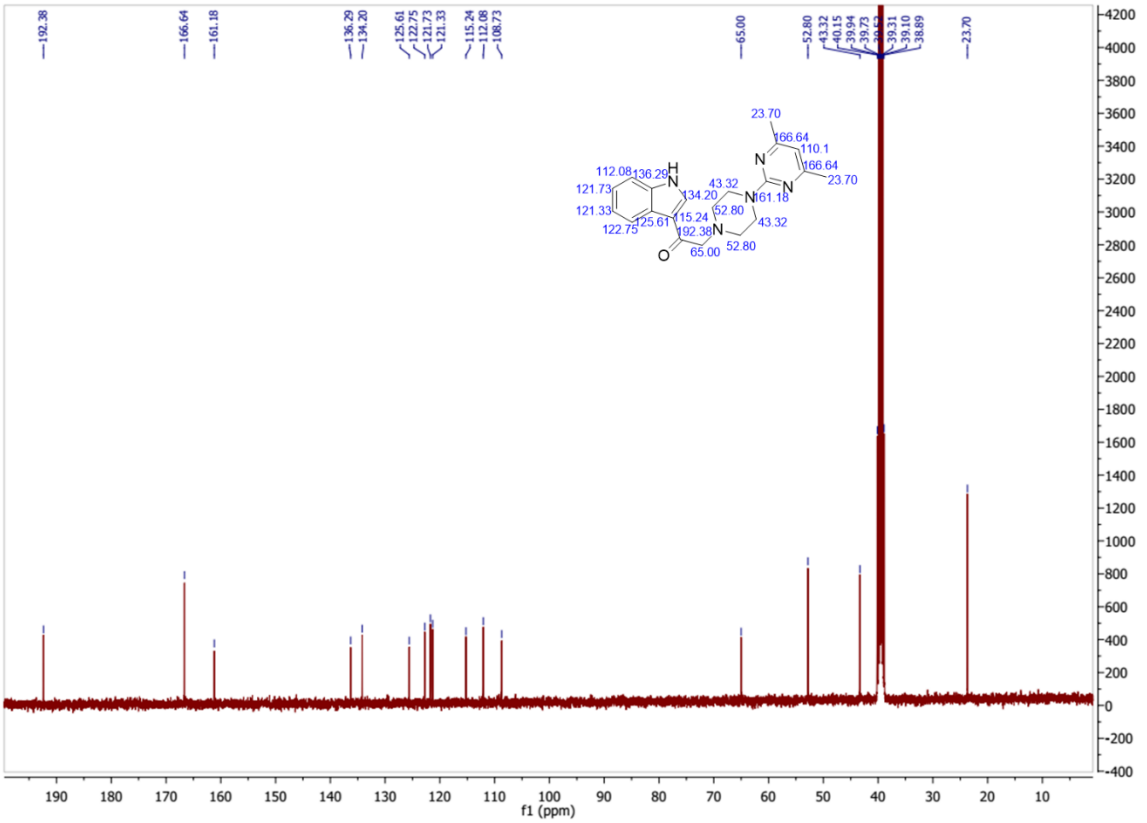


Figure S2: ^{13}C NMR of Compound 3.

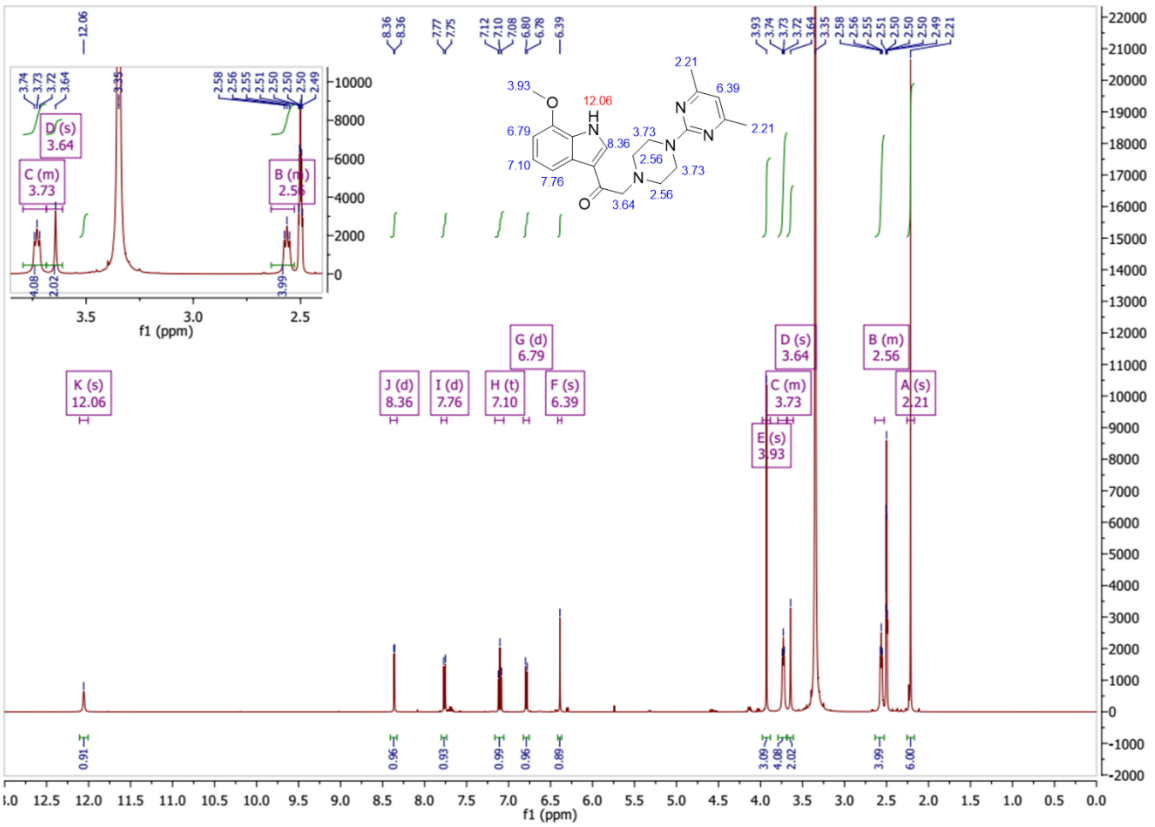


Figure S3: ^{1}H NMR of Compound 4.

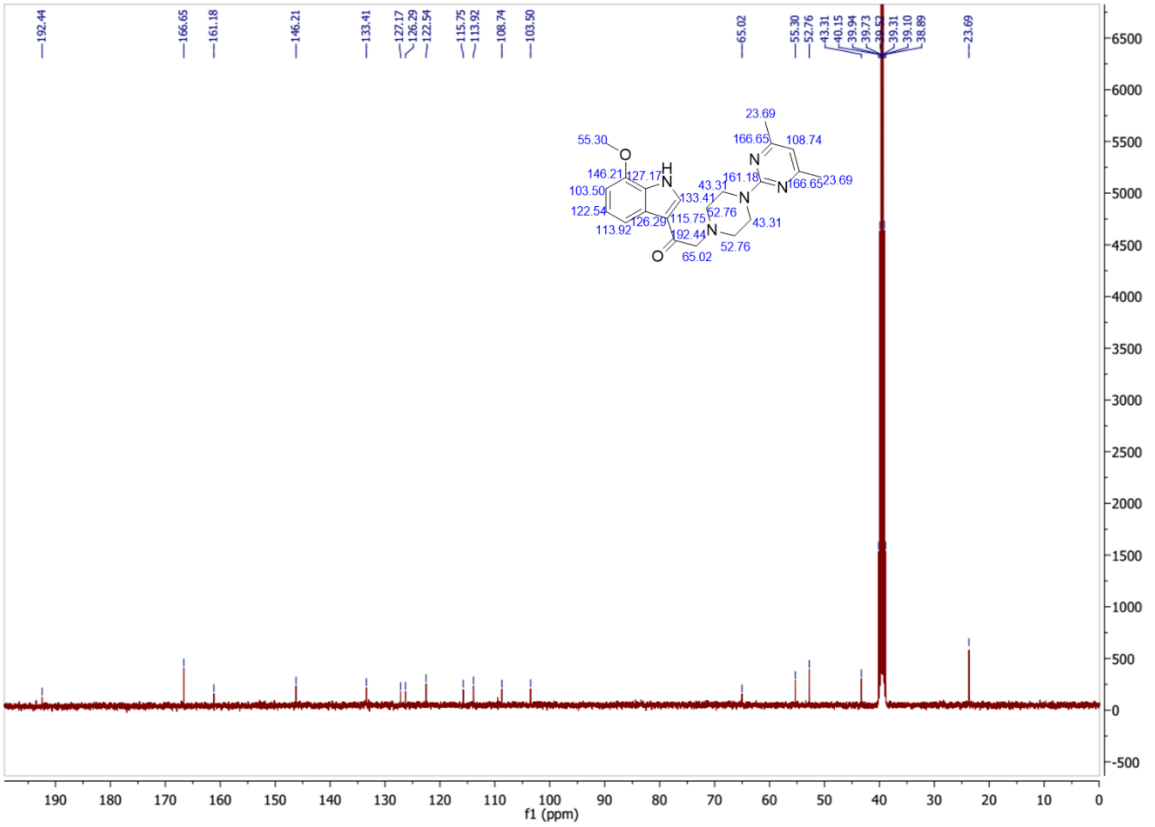


Figure S4: ^{13}C NMR of Compound 4.

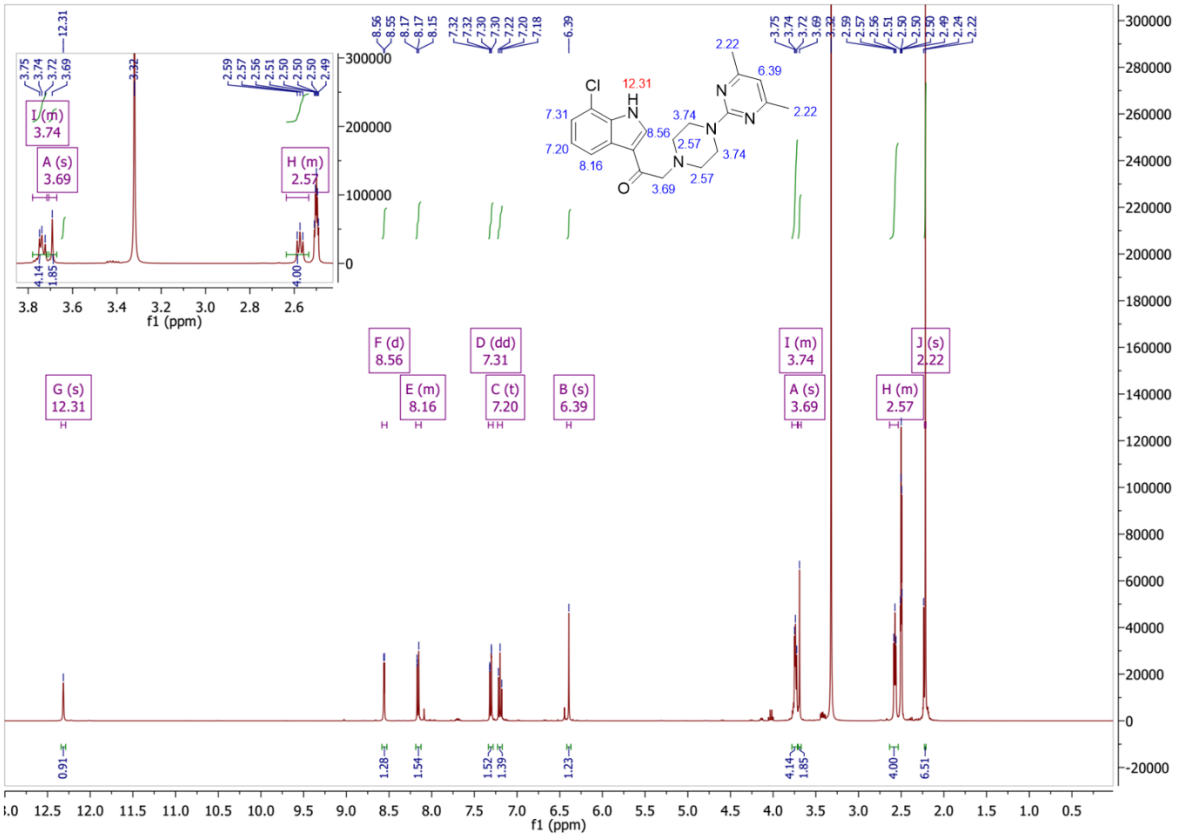


Figure S5: ^{1}H NMR of Compound 5.

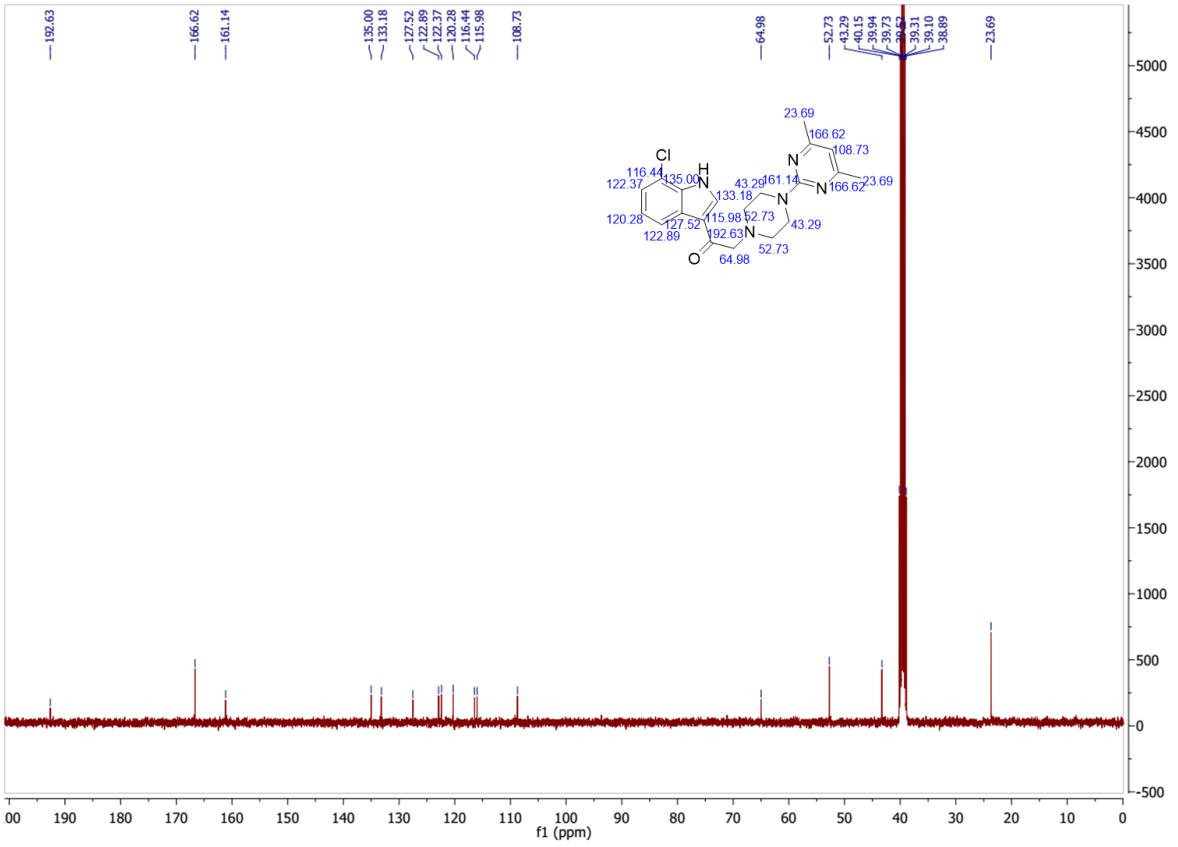


Figure S6: ^{13}C NMR of Compound 5.

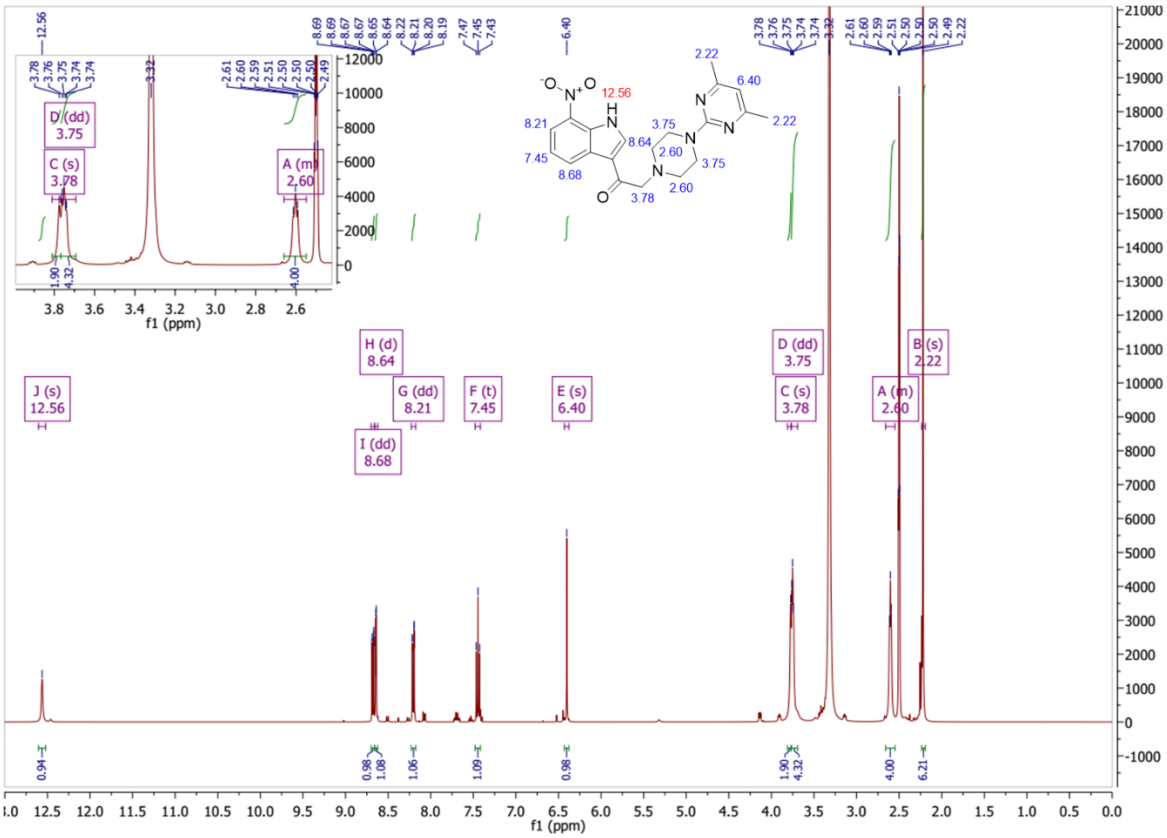


Figure S7: ^{1}H NMR of Compound 6.

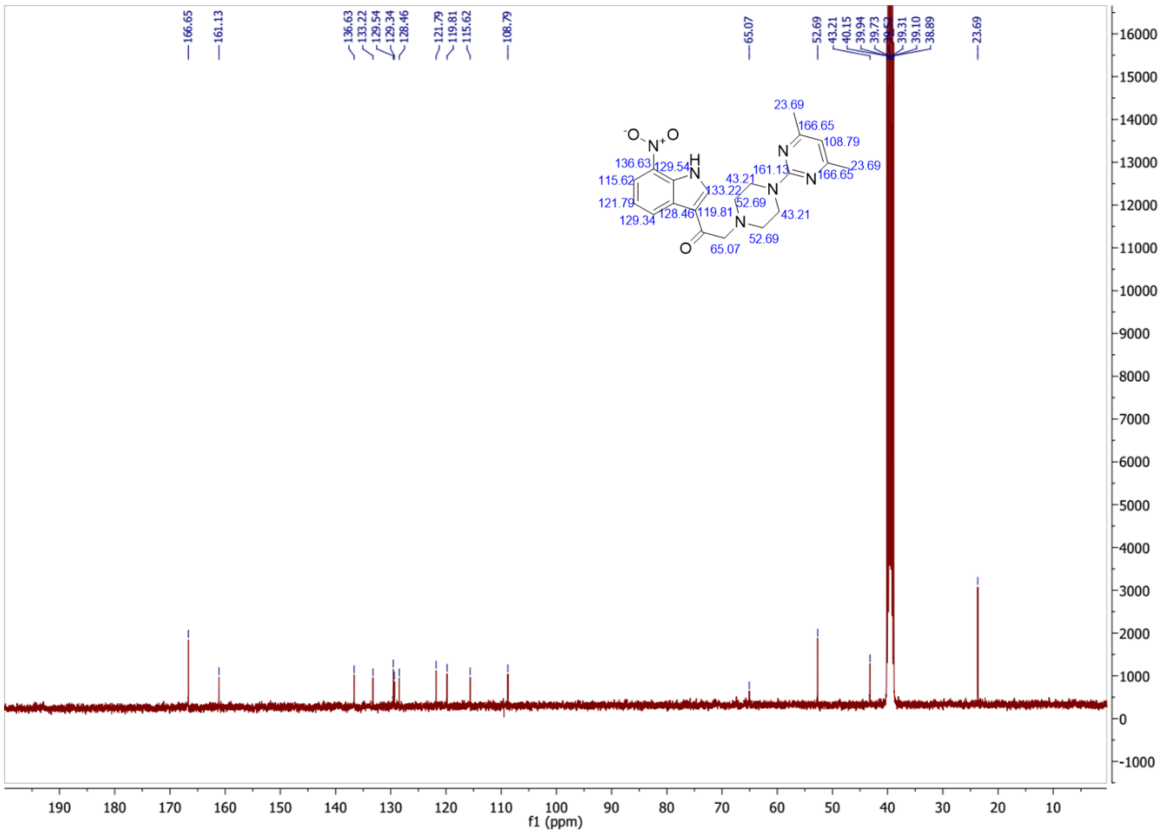


Figure S8: ^{13}C NMR of Compound 6.

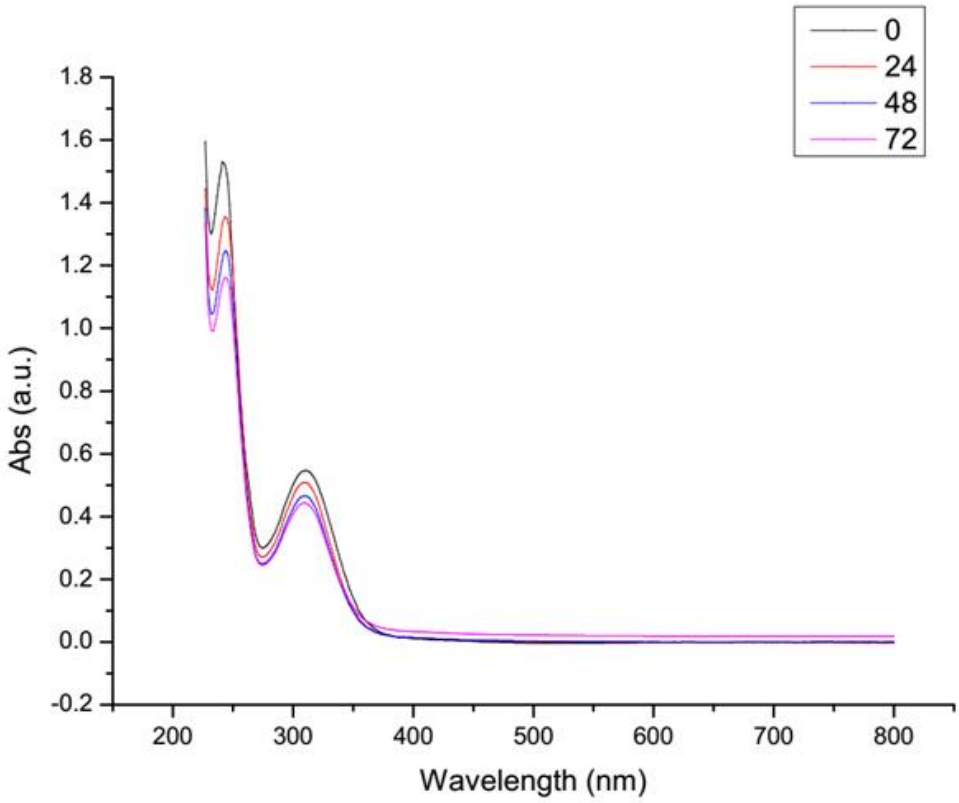


Figure S9: UV-stability of Compound 4 in water over 72h.

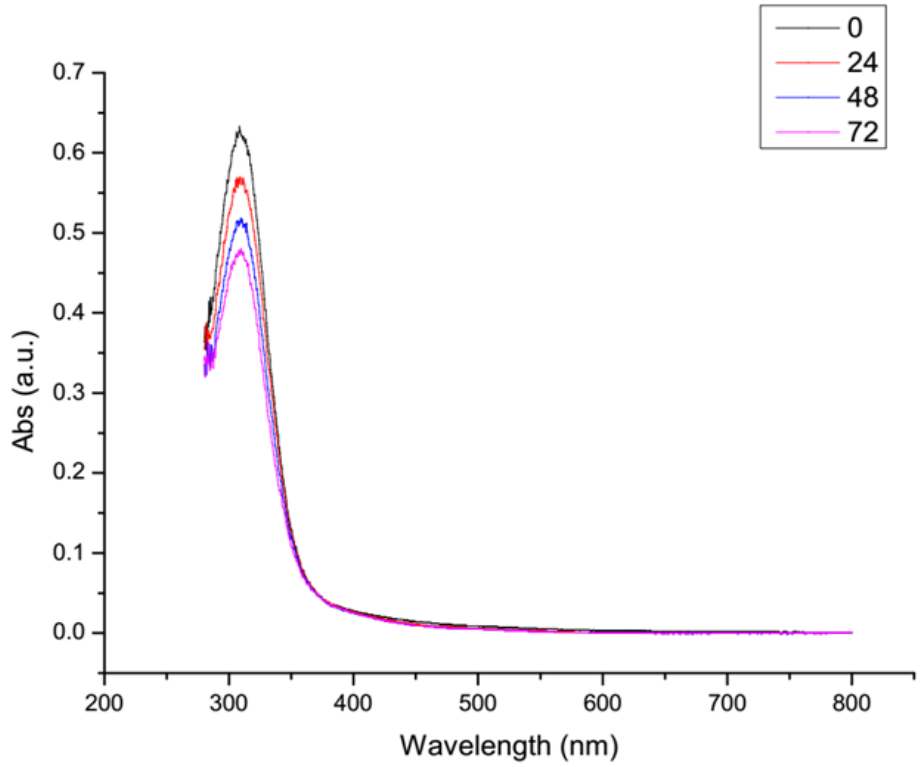


Figure S10: UV-stability of Compound 4 in DMEM over 72h.

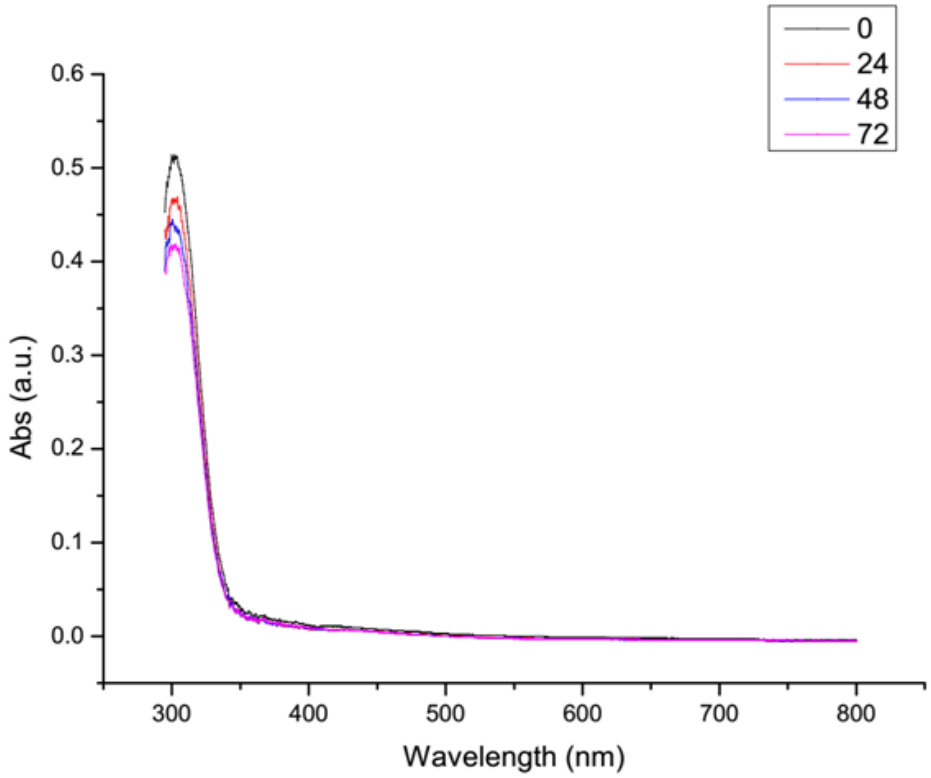
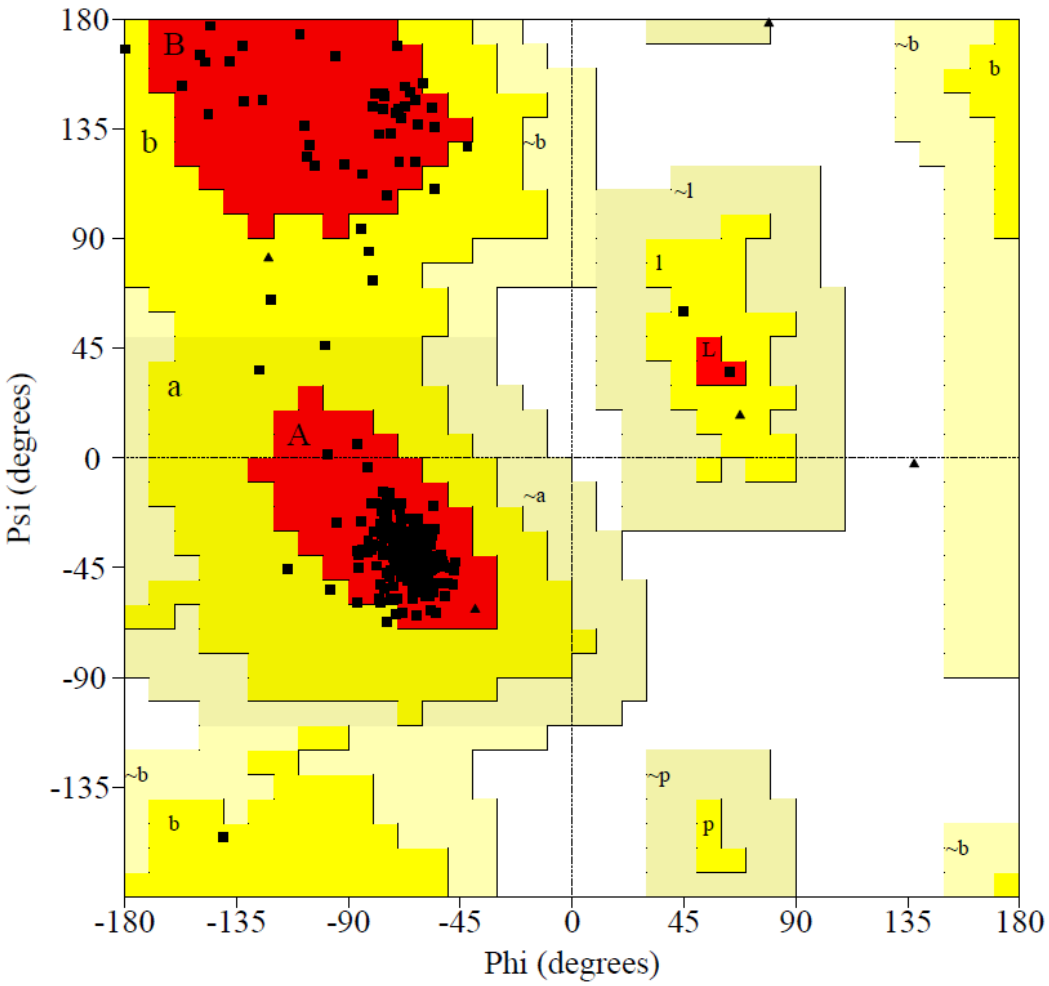


Figure S11: UV-stability of Compound 4 in RPMI-1640 over 72h.



Plot statistics

Residues in most favoured regions [A,B,L]	268	94.7%
Residues in additional allowed regions [a,b,l,p]	15	5.3%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
Number of non-glycine and non-proline residues	283	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	11	
Number of proline residues	8	
Total number of residues	304	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Figure S12: Ramachandran plot for hA$_3$AR homology model (PROCHECK analysis).