

*Supplementary material related to the article*

## **Hybridization approach to identify salicylanilides as inhibitors of tubulin polymerization and signal transducer and activator of transcription 3 (STAT3)**

**Marta Gargantilla <sup>1</sup>, Leentje Persoons <sup>2</sup>, Tereza Kauerová <sup>3</sup>, Natalia del Río <sup>1</sup>, Dirk Daelemans <sup>2</sup>, Eva-María Priego <sup>1</sup>, Peter Kollar <sup>3\*</sup> and María-Jesús Pérez-Pérez <sup>1\*</sup>**

<sup>1</sup> Instituto de Química Médica (IQM, CSIC) c/Juan de la Cierva 3, 28006-Madrid, Spain;

mgargantilla@iqm.csic.es (M.G.), natalia.delrio@iqm.csic.es (N. R.), empriego@iqm.csic.es (E.-M.P.).

<sup>2</sup> KU Leuven Department of Microbiology, Immunology and Transplantation, Laboratory of Virology and Chemotherapy, Rega Institute for Medical Research, KU Leuven, Herestraat 49, 3000 Leuven, Belgium; leentje.persoons@kuleuven.be (L.P.); dirk.daelemans@kuleuven.be (D.D.)

<sup>3</sup> Department of Pharmacology and Toxicology, Faculty of Pharmacy, Masaryk University, Palackého tr. 1946/1, 602 00 Brno, Czech Republic; kauerovat@pharm.muni.cz (T. K.)

\* Correspondence: kollarp@pharm.muni.cz (P. K.); mjperez@iqm.csic.es (M.-J.P.-P.); Tel.: +34-91-2587516.

Includes:

Computational methods	S2
Figure S1: Immunofluorescence staining of $\alpha$ -tubulin in Hep-2 cells	S3
Figure S2: Proposed binding pose for compound 6 at the colchicine site	S4
<sup>1</sup> H and <sup>13</sup> C NMR spectra of selected compounds	S5

## Computational methods

The 3D structure of compound **6** was generated using the tool Maestro, implemented in the Schrodinger Suite (Schrödinger Release 2017-2: Maestro, Schrödinger, LLC, New York, NY, 2017) and optimized using the tool Macromodel.

The automated docking experiment was carried out using TUB075-tubulin complex (pdb id: 6FKJ). A three-dimensional cubic grid, consisting of 50x50x50 points with a spacing of 0.375 Å, was defined at the colchicine binding site. Electrostatic, desolvation, and affinity maps for the atom types present in the ligand was calculated using AutoGrid 4.2.6 and then the Lamarckian genetic algorithm implemented in the automated docking program AutoDock4.2.20. Intra- and intermolecular energy evaluation of each configuration allowed the selection of the best-scoring solutions.

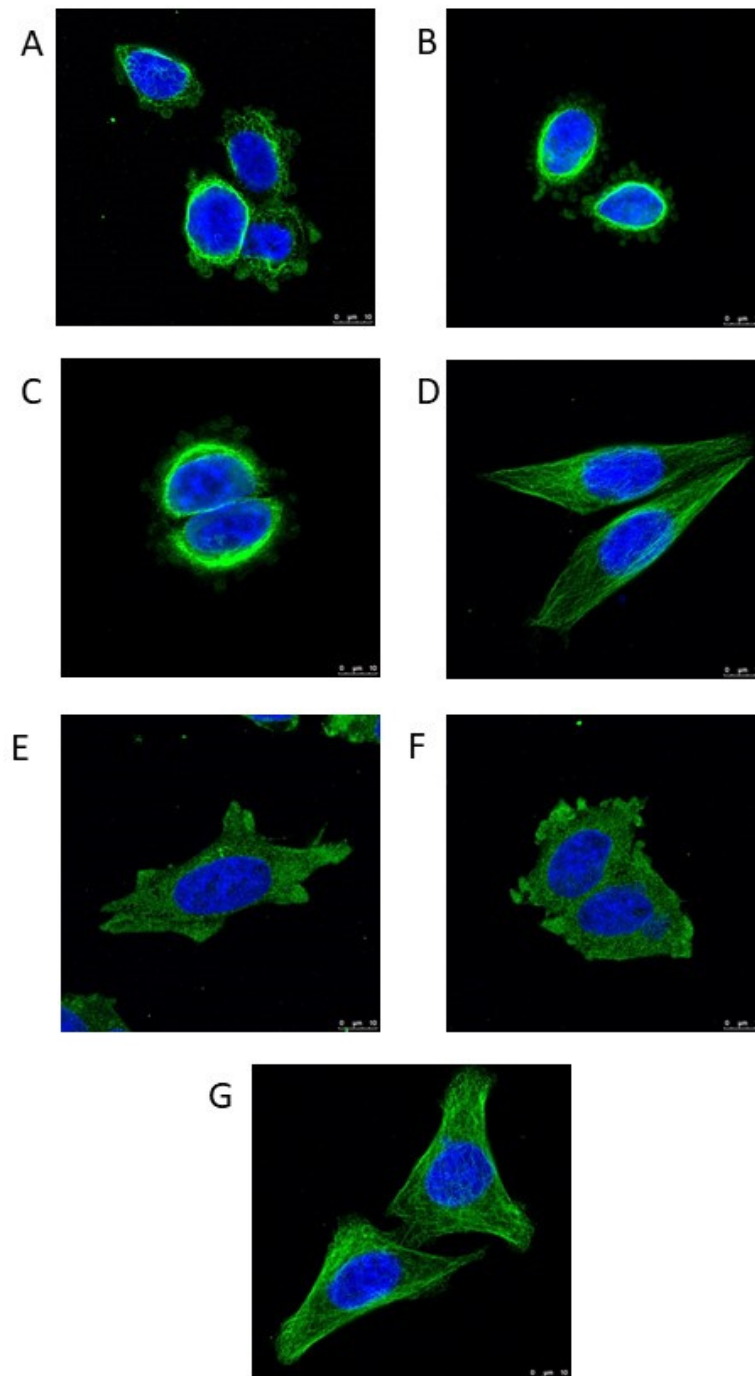


Figure S1. Immunofluorescence staining of  $\alpha$ -tubulin in Hep-2 cells: (A) SAL012 at 100  $\mu$ M; (B) SAL012 at 10  $\mu$ M; (C) SAL012 at 1  $\mu$ M; (D) SAL012 at 0,3  $\mu$ M; (E) TUB015 at 10  $\mu$ M; (F) nocodazole at 10  $\mu$ M; (G) Control (DMSO)

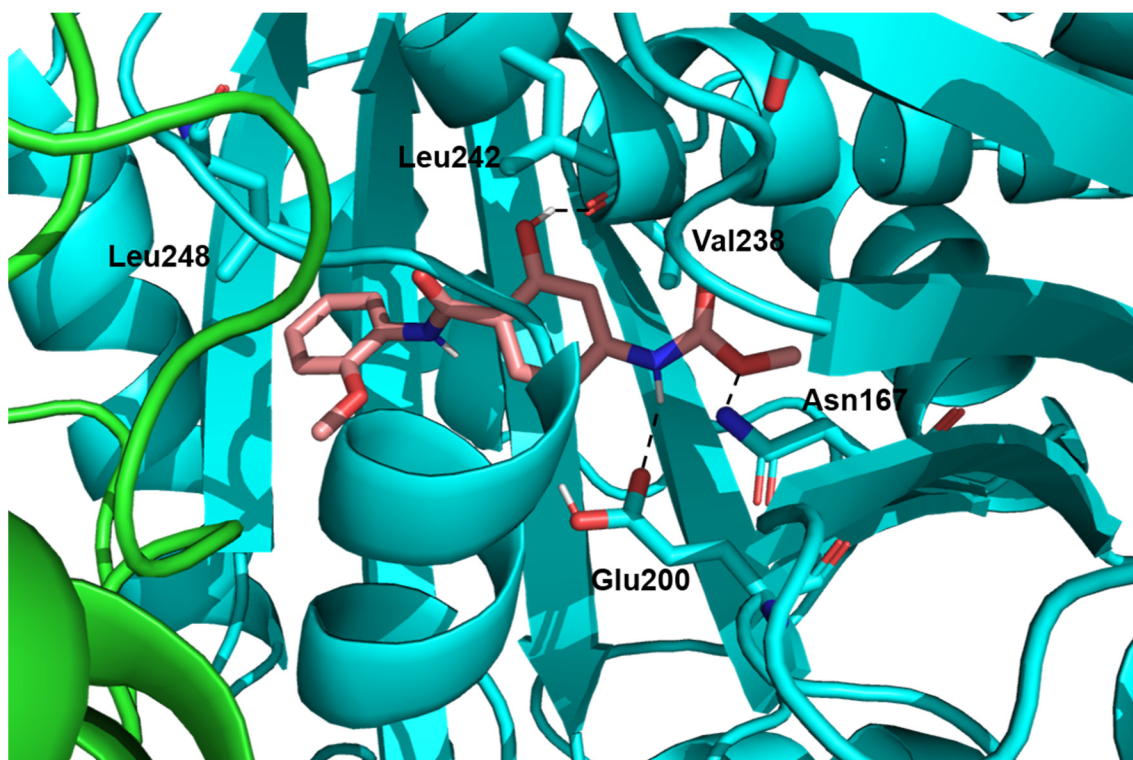
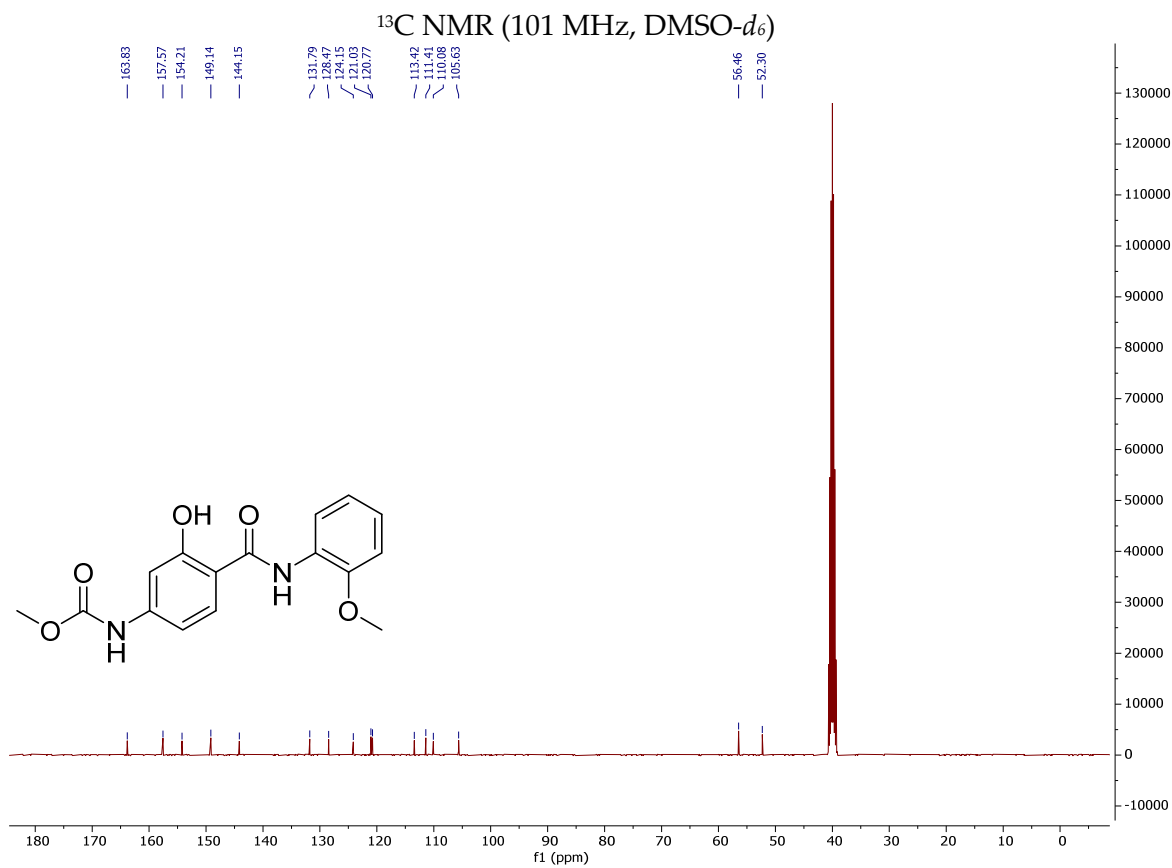
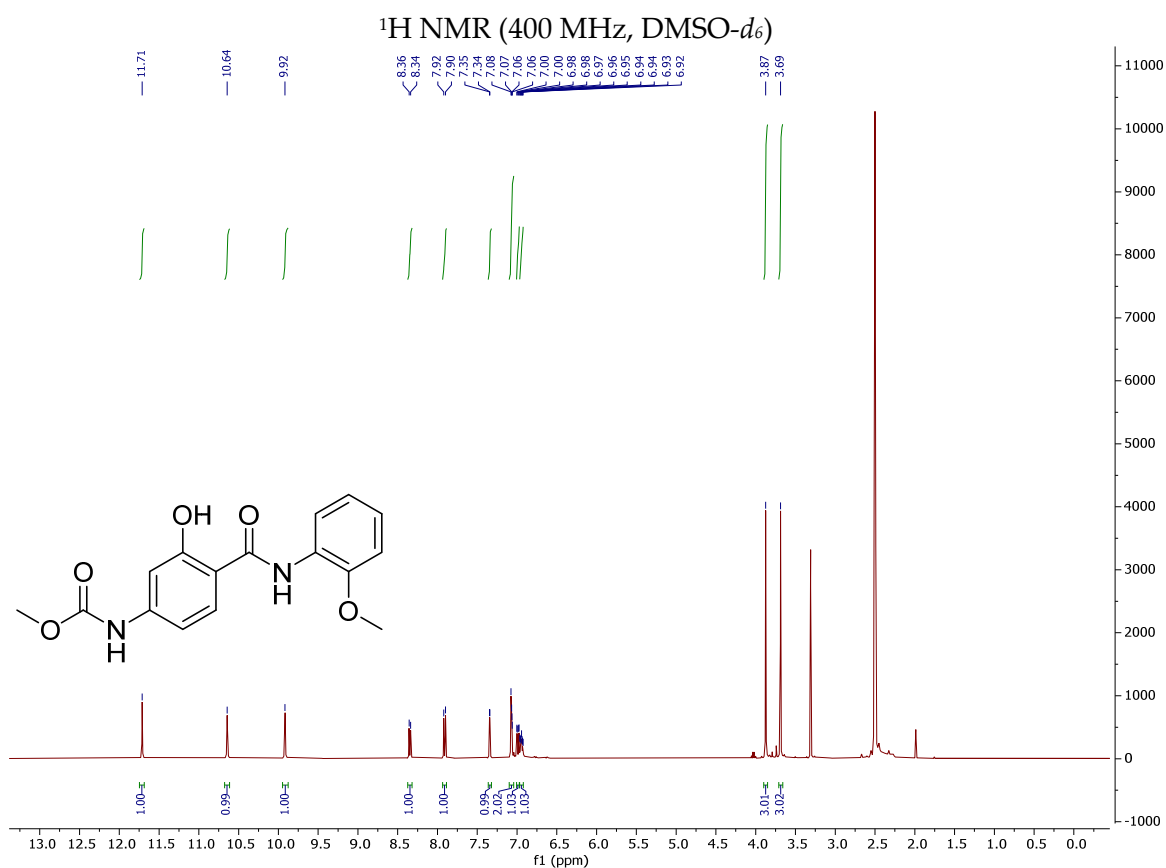
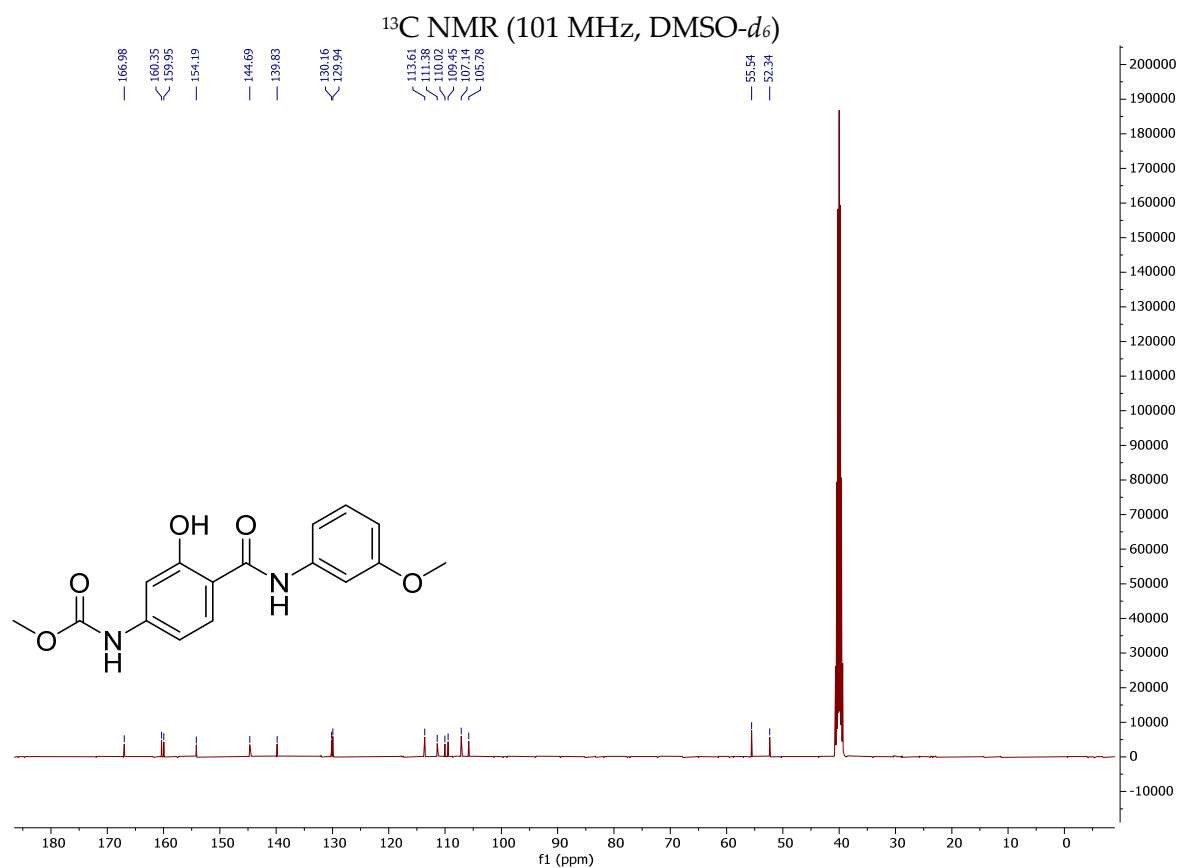
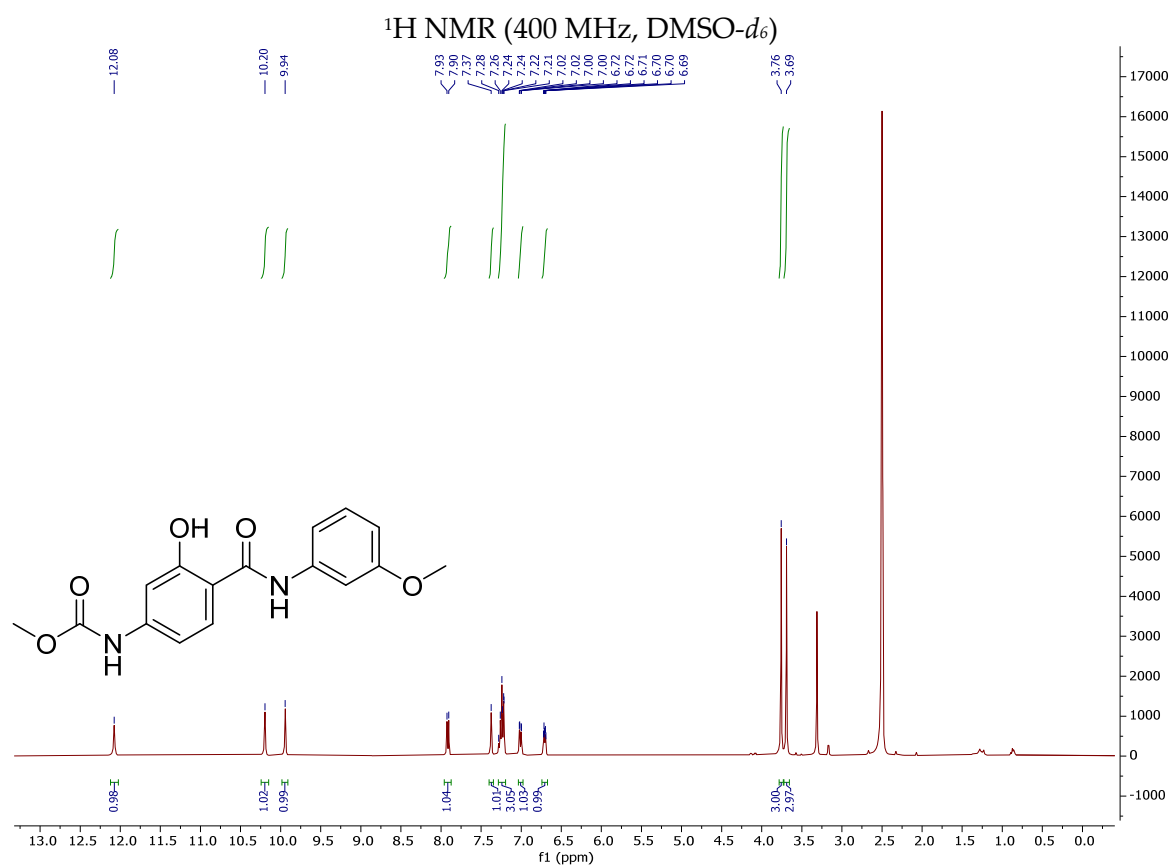


Figure S2. Proposed binding pose for compound **6** (salmon sticks) at the colchicine binding site in tubulin (PDB: 6FKJ) ( $\alpha$ -tubulin shown in green and  $\beta$ -tubulin in cyan). Selected residues of the binding pocket are shown in sticks and labelled. Dashed lines represent hydrogen bonds.

# Compound 6

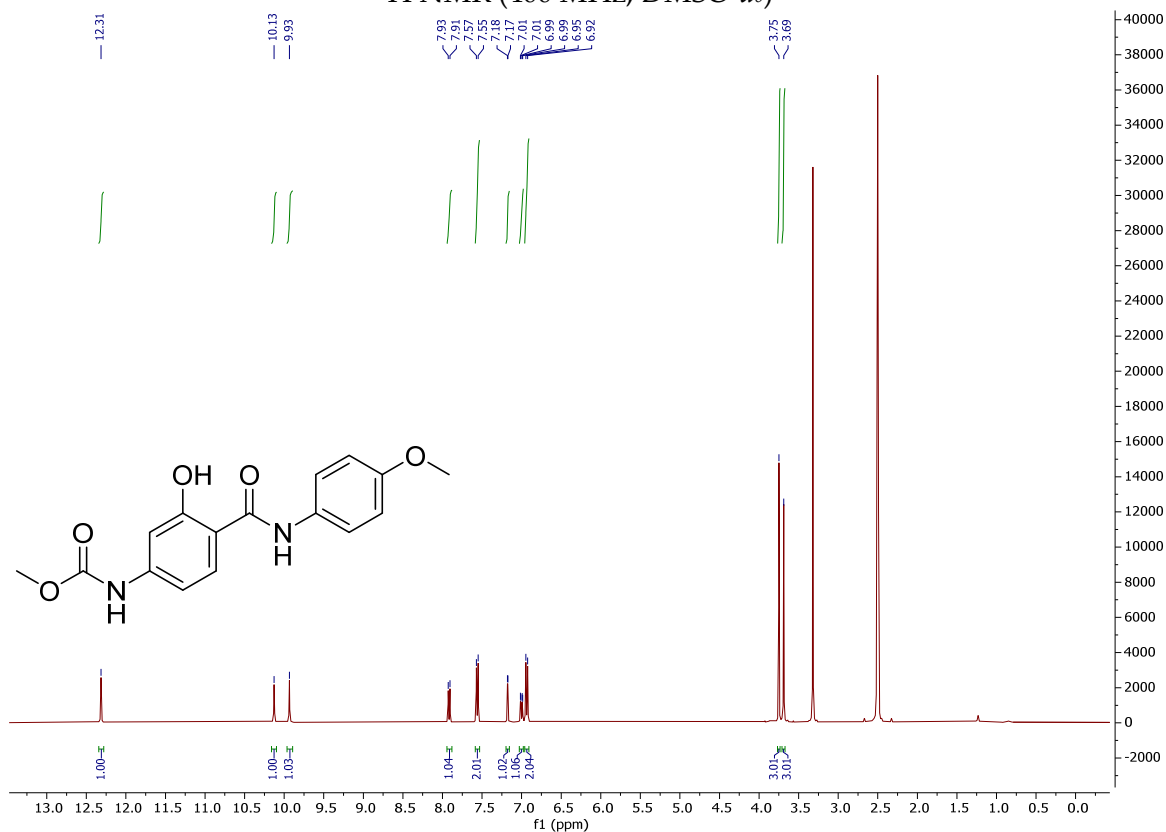


# Compound 12

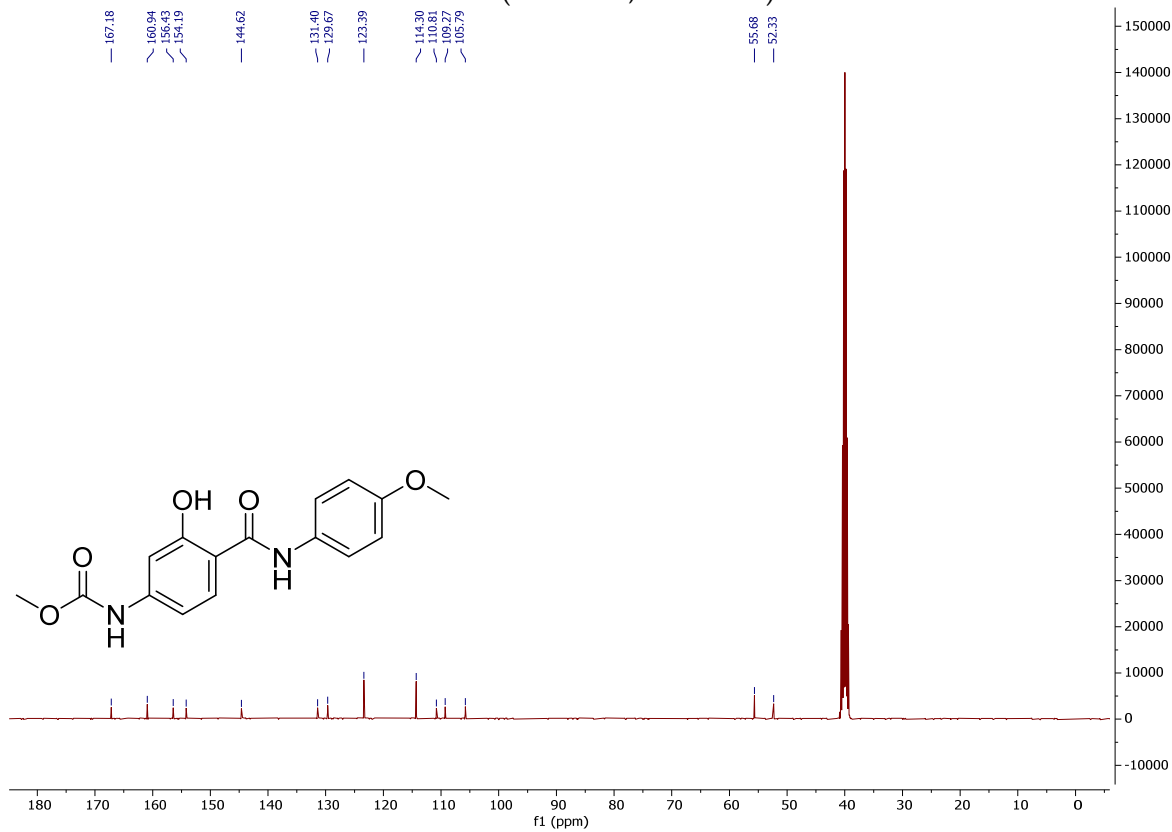


# Compound 13

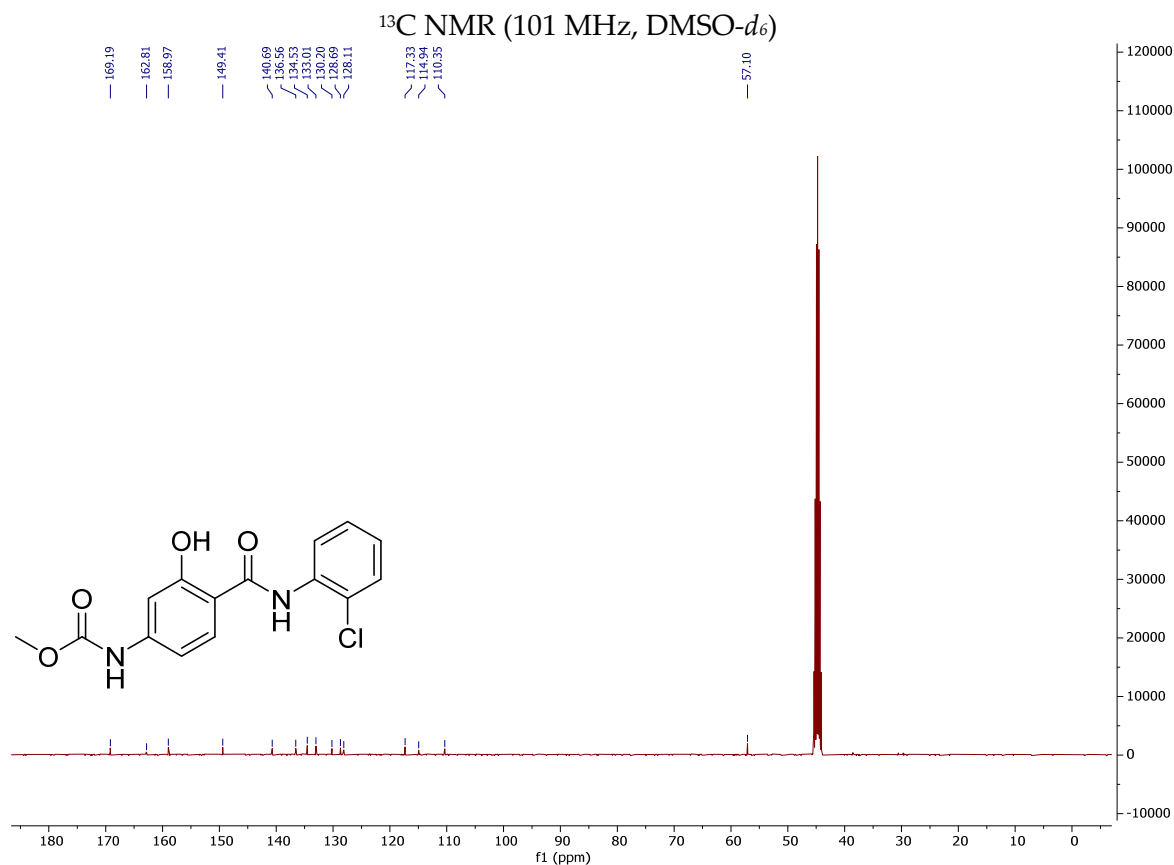
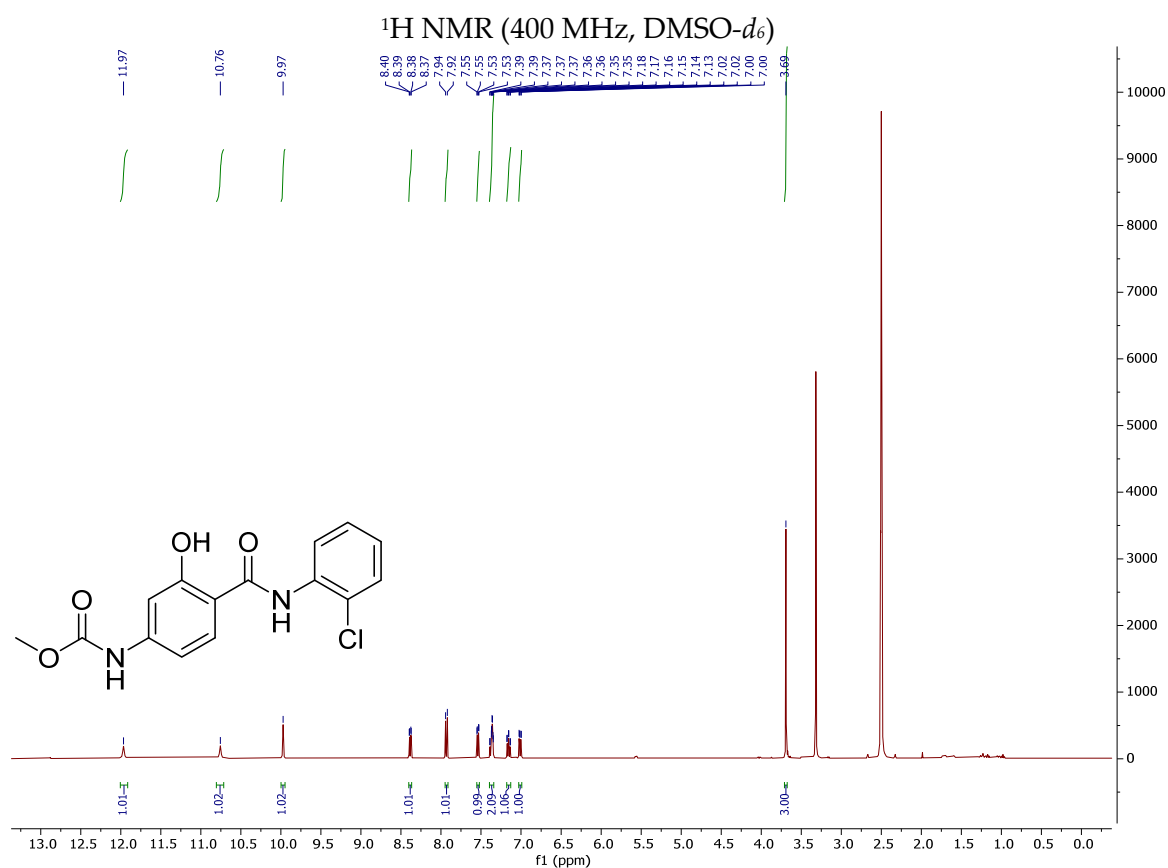
$^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )



$^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )

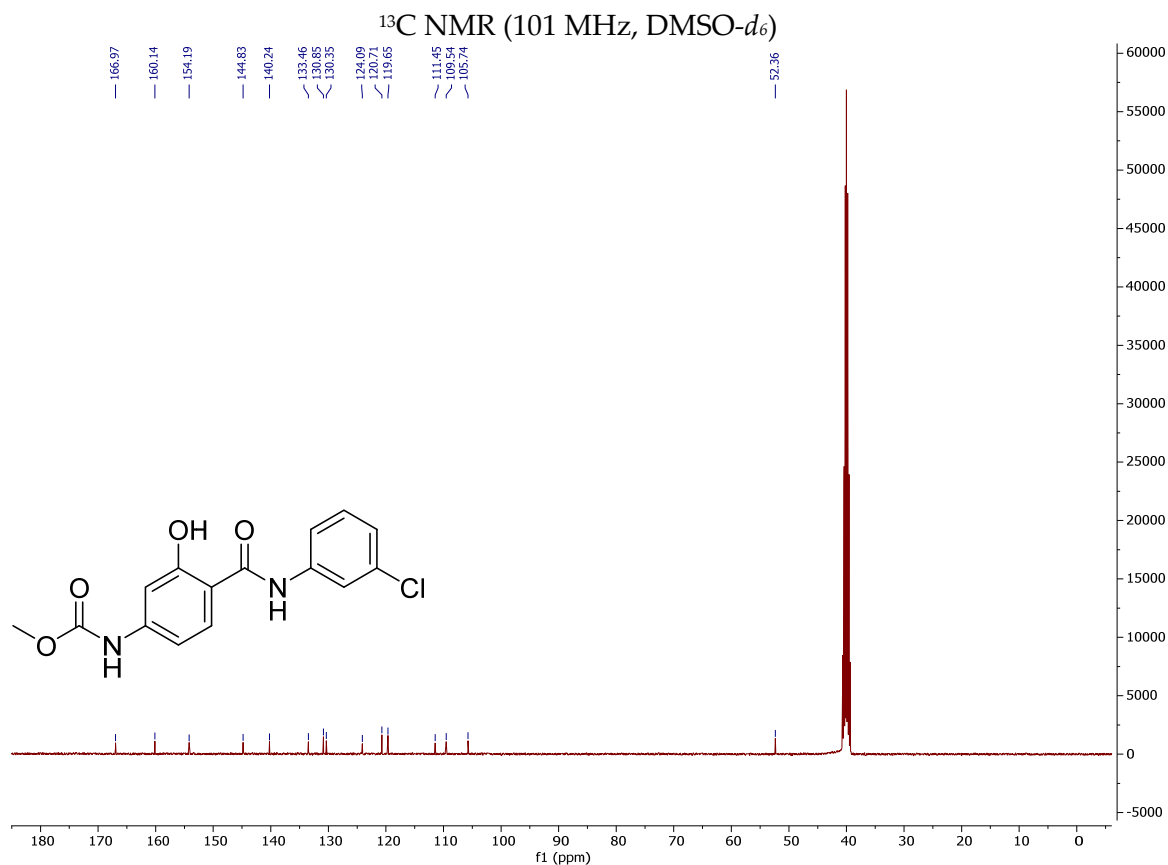
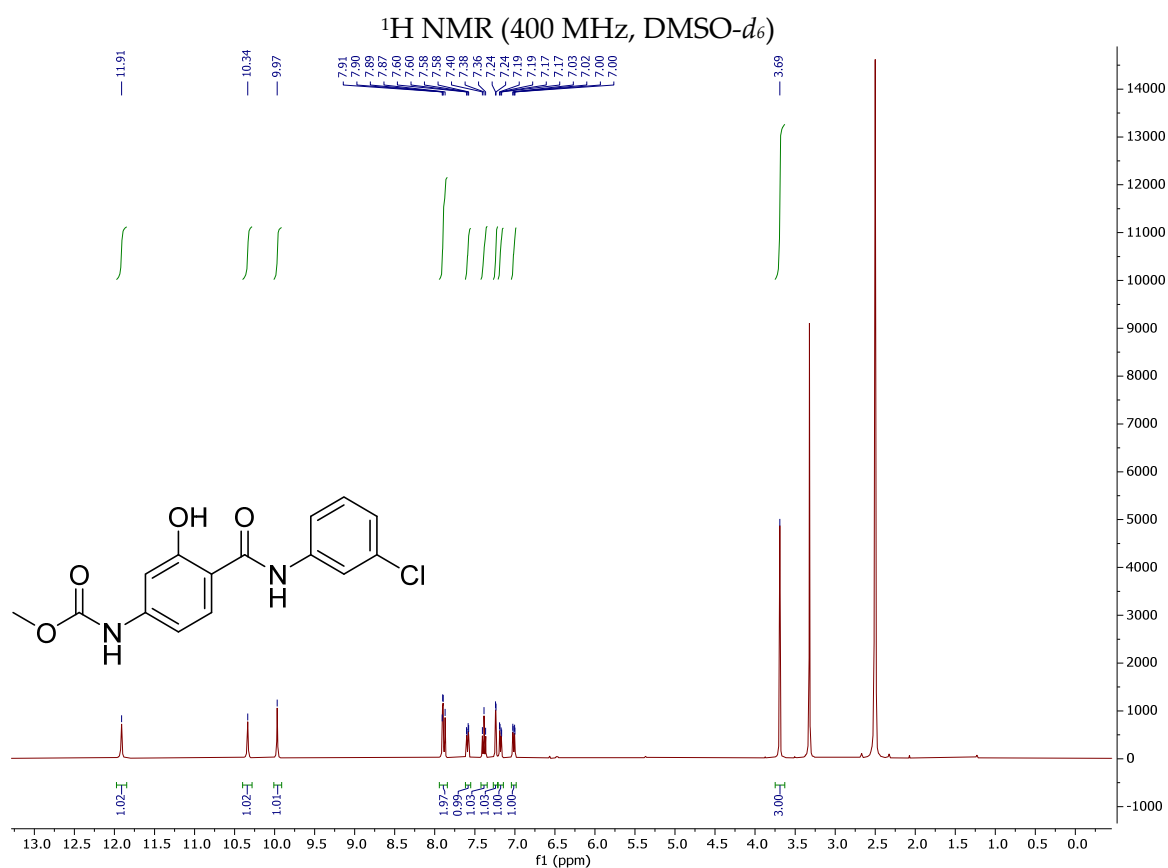


# Compound 14



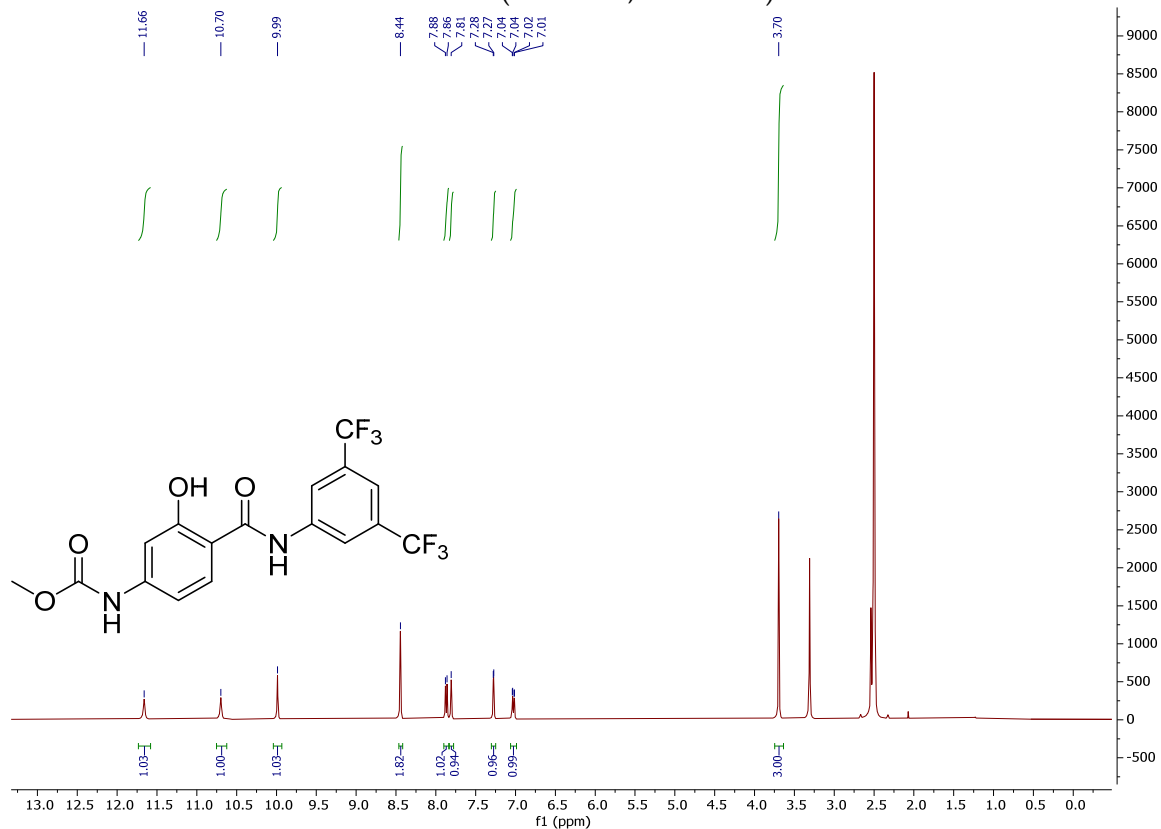


# Compound 15

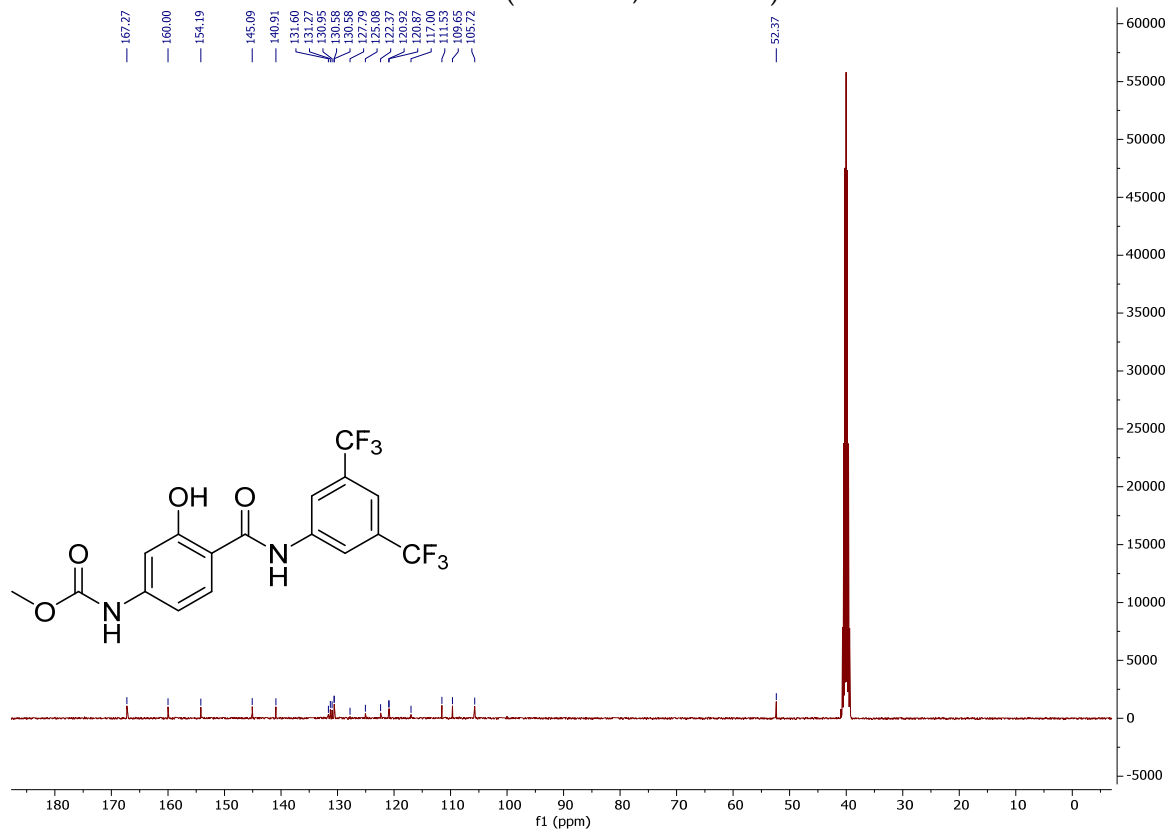


# Compound 16

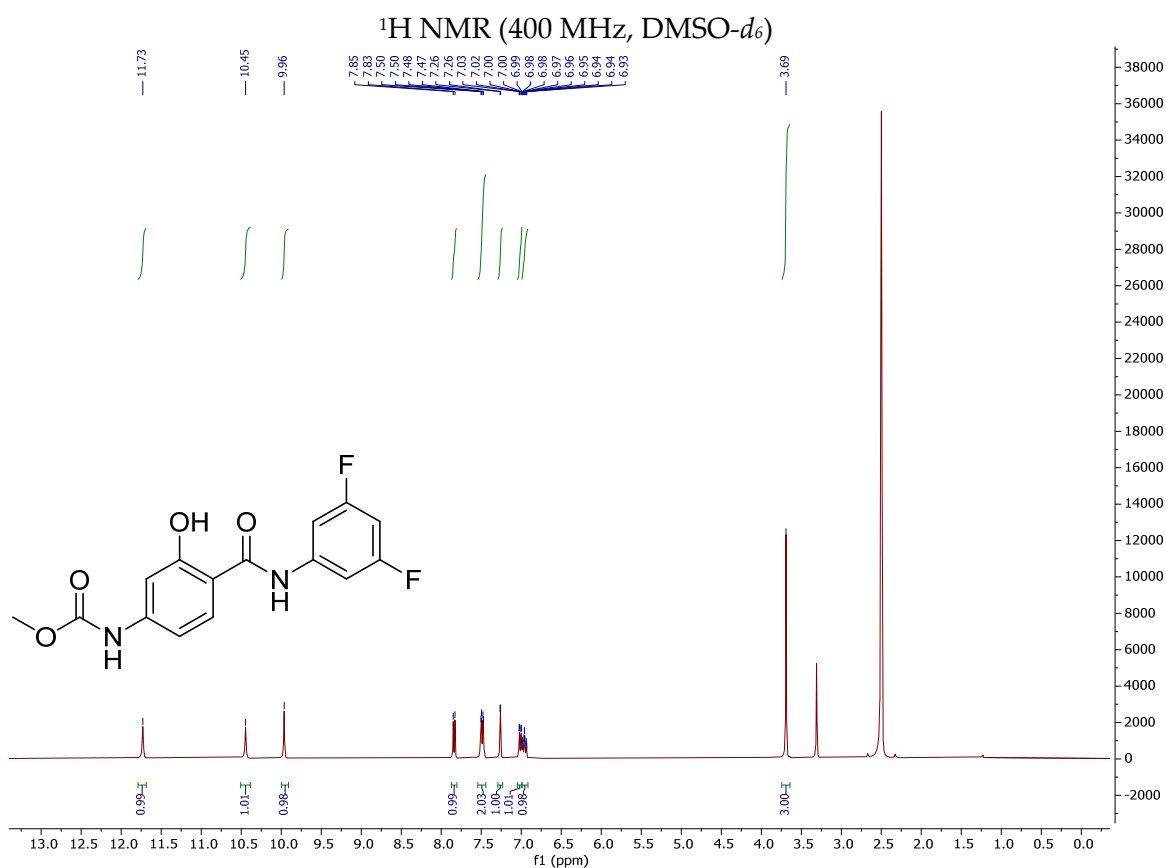
$^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )



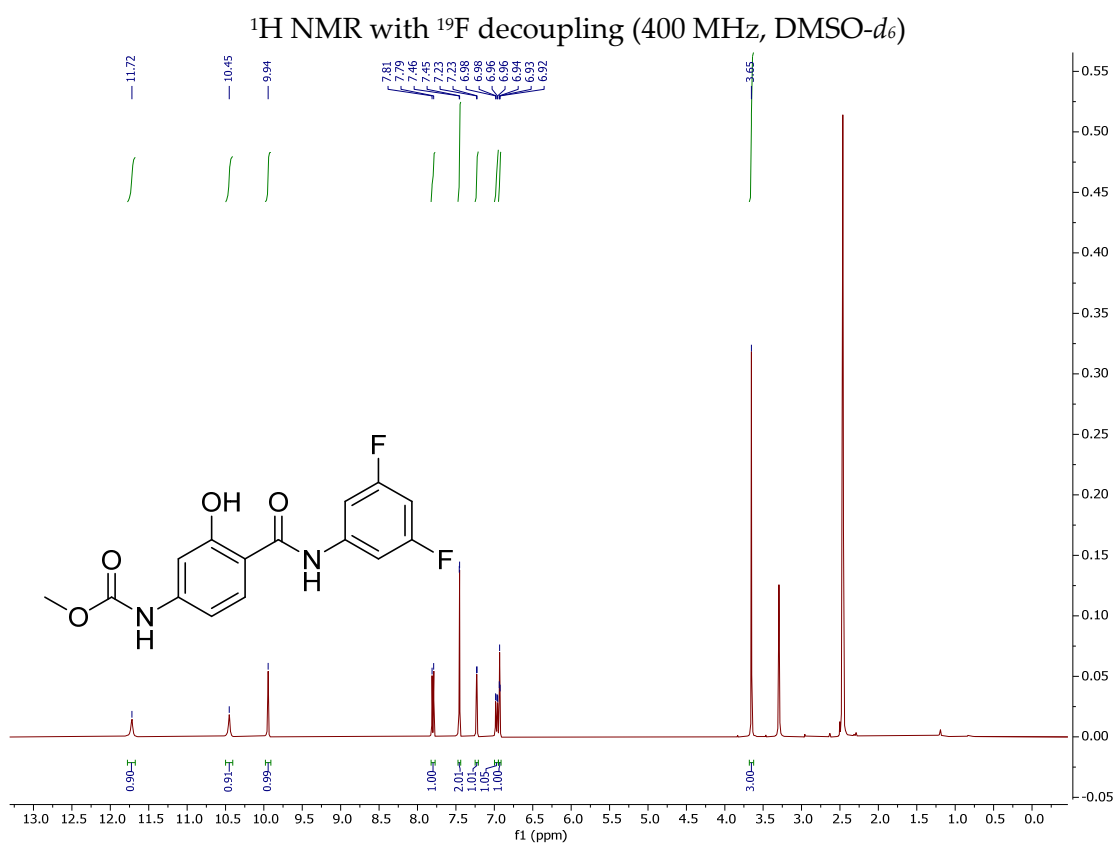
$^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )

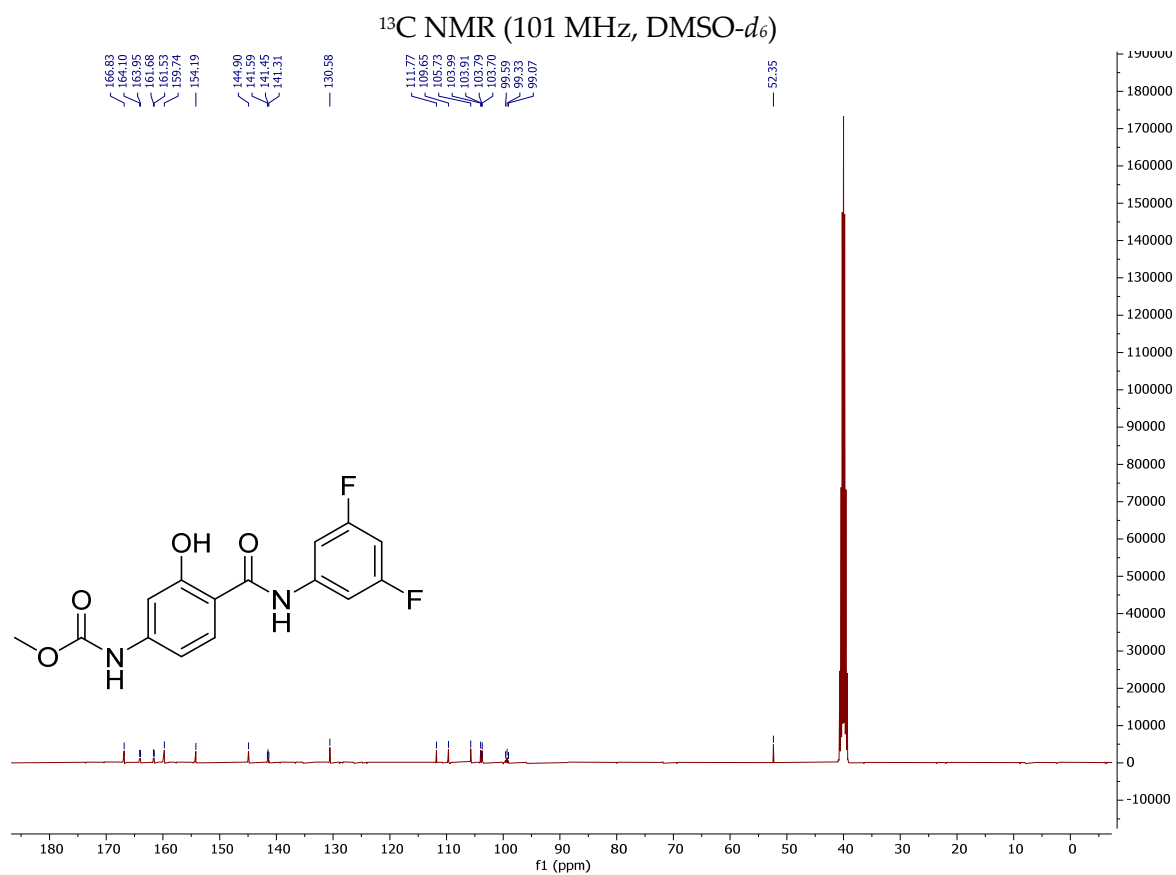


# Compound 17

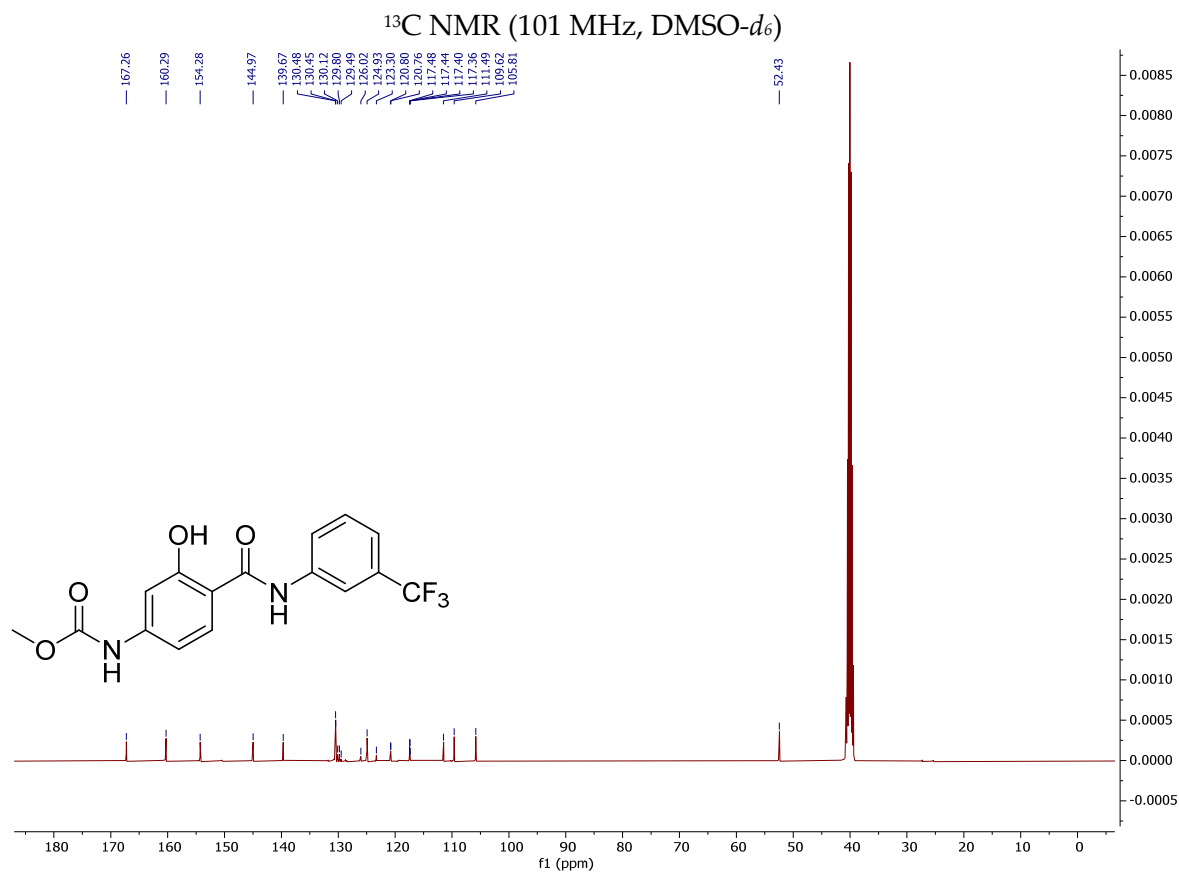
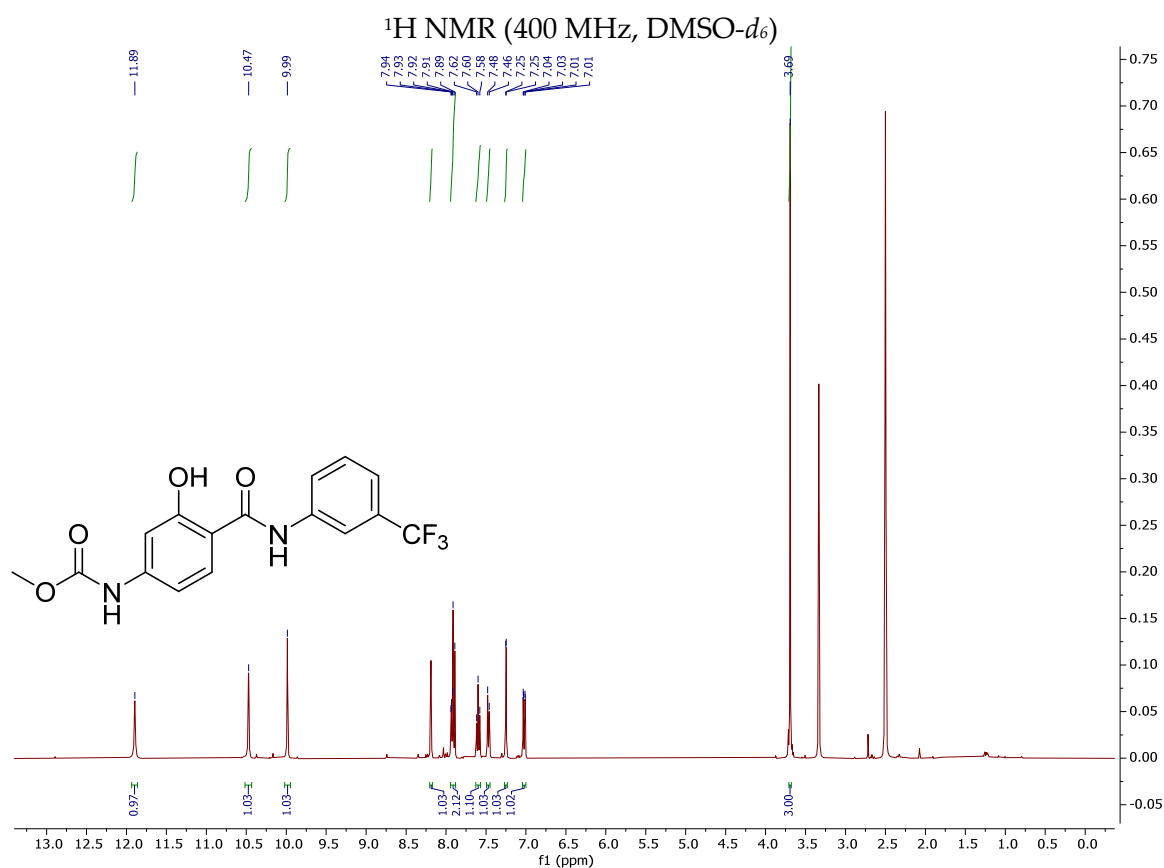


# Compound 17





# Compound 18



# Compound 21

