

Supporting information

1,4,9-Triazaspiro[5.5]undecan-2-one derivatives as potent and selective METTL3 inhibitors

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METTL3/METTL14

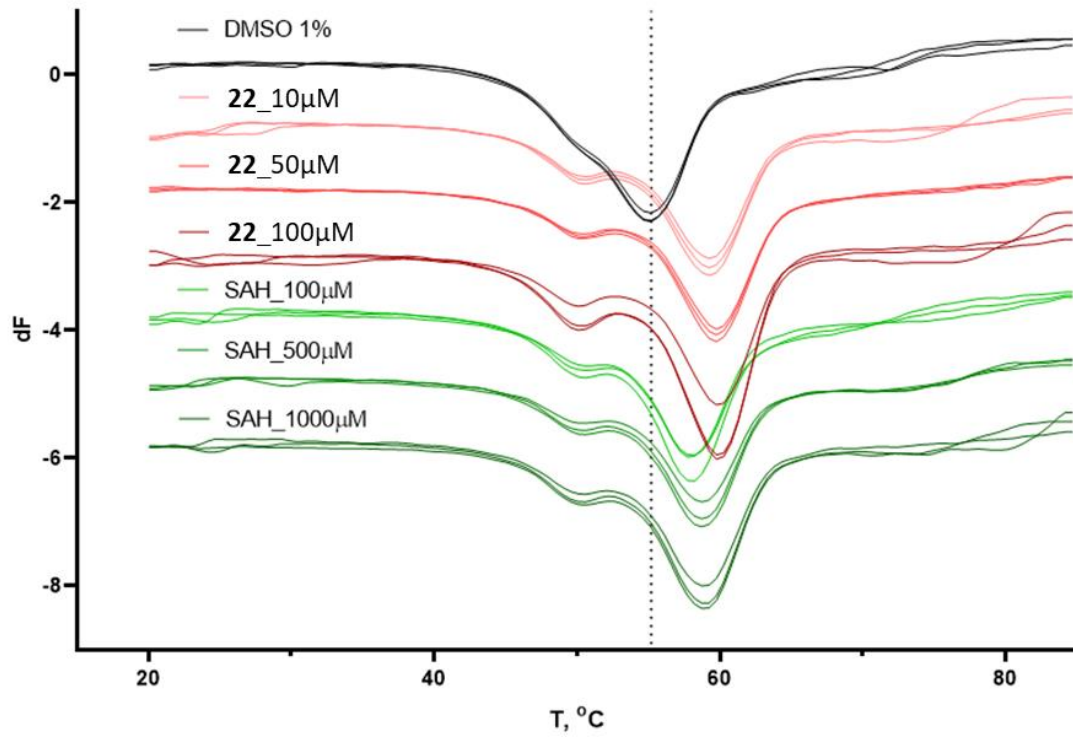


Figure S1: Thermal shift assay results. Shown are the first derivative of the melting curves of METTL3/METTL14 for inhibitor **UZH2** or **SAH**.

METTL16

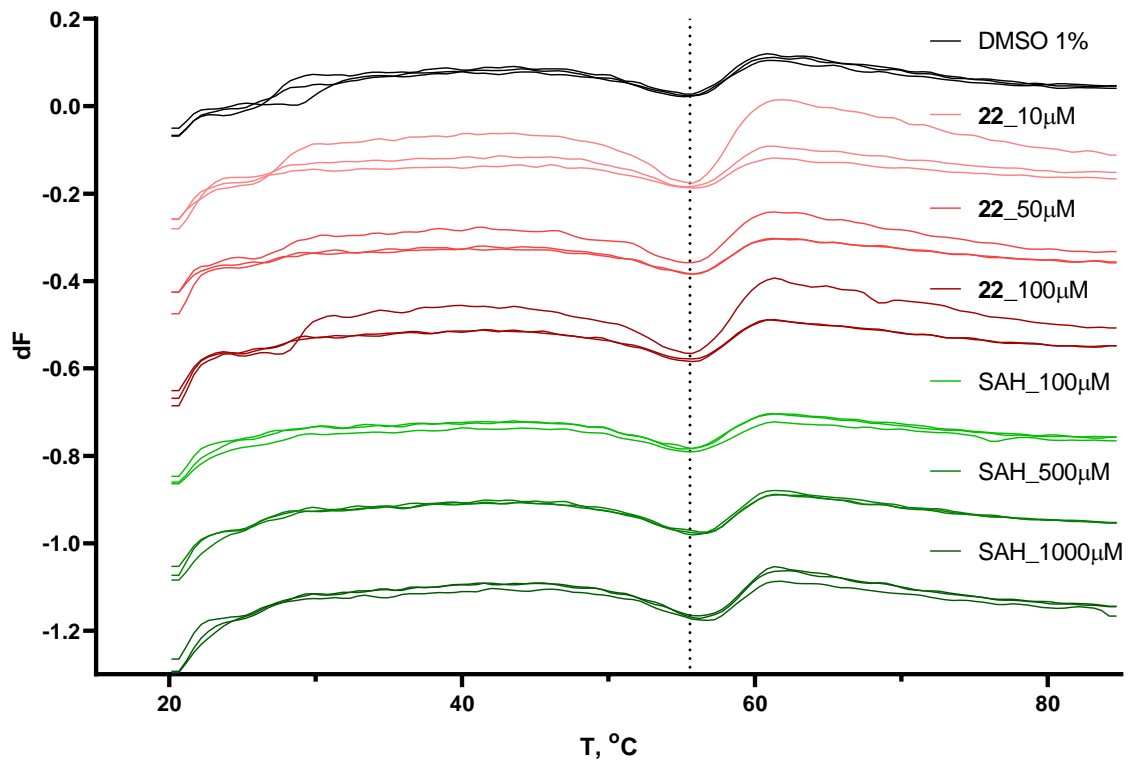
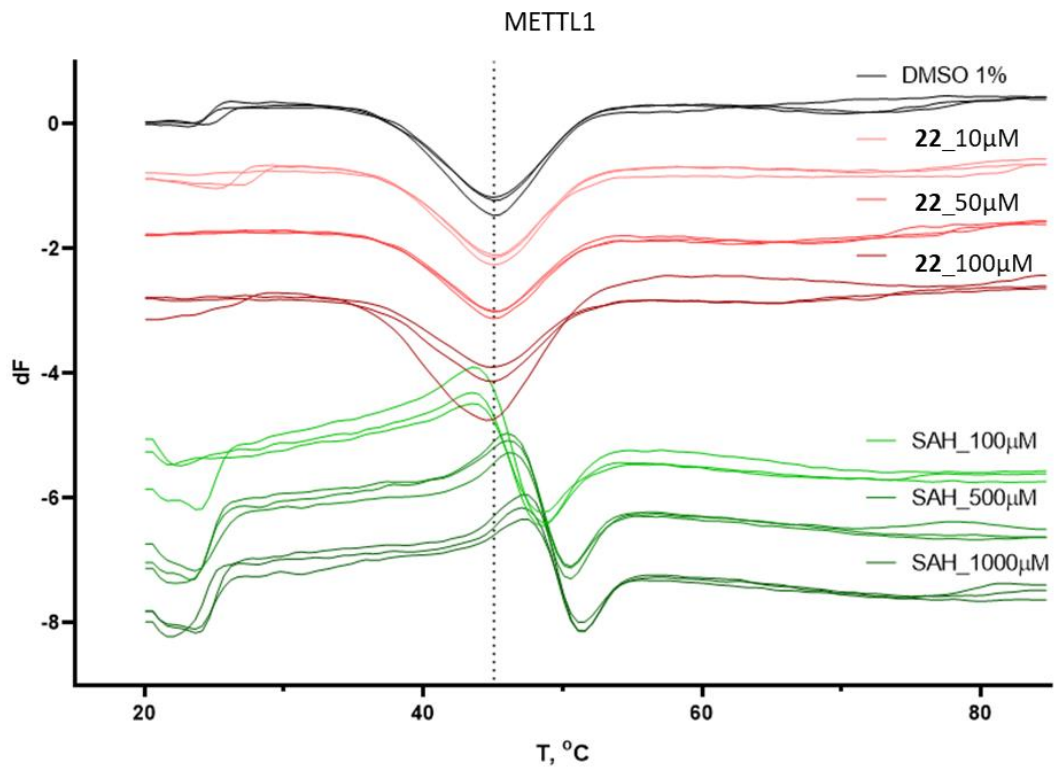


Figure S2: Thermal shift assay results. Shown are the first derivative of the melting curves of METTL16 for inhibitor **UZH2** or **SAH**. **UZH2** does not shift the melting temperature of METTL16.



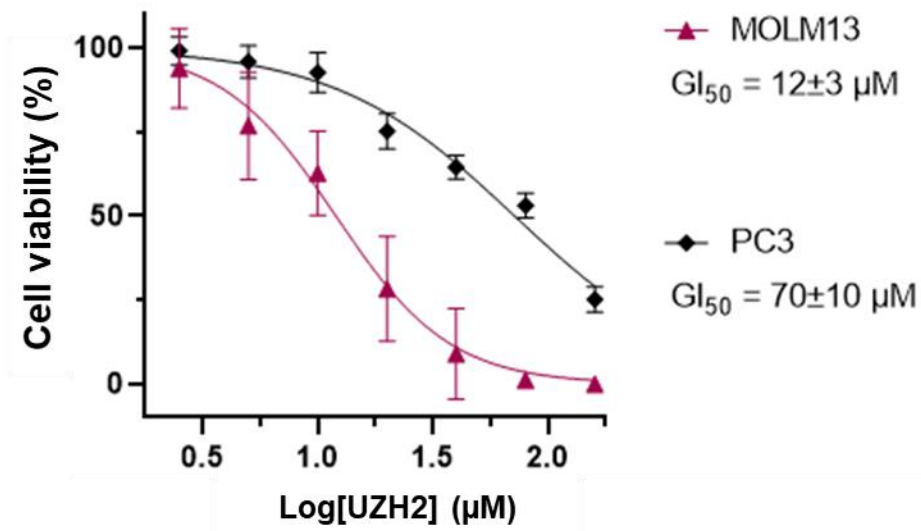


Figure S4: Cell viability curves of MOLM13 and PC-3 cells upon **UZH2** incubation for 3 days.

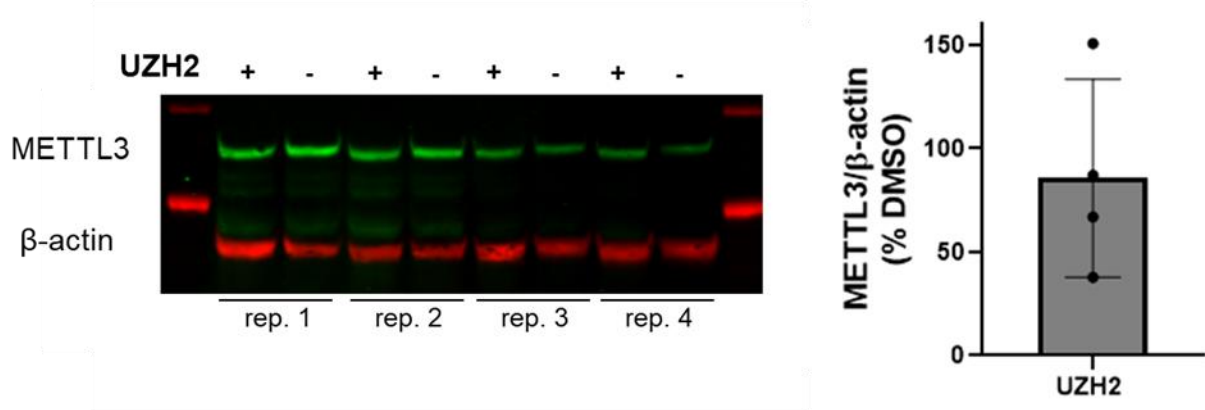


Figure S5: Western blotting of METTL3 in MOLM-13 cells after **UZH2** treatment (10 µM) for 16 h. METTL3/β-actin (90 ± 40)% of DMSO control.

X-ray data collection and refinement statistics

Table S1: PDB codes, X-ray data collection and refinement statistics for structures of ternary complexes of METTL3, METTL14 and selected compounds developed in this study.

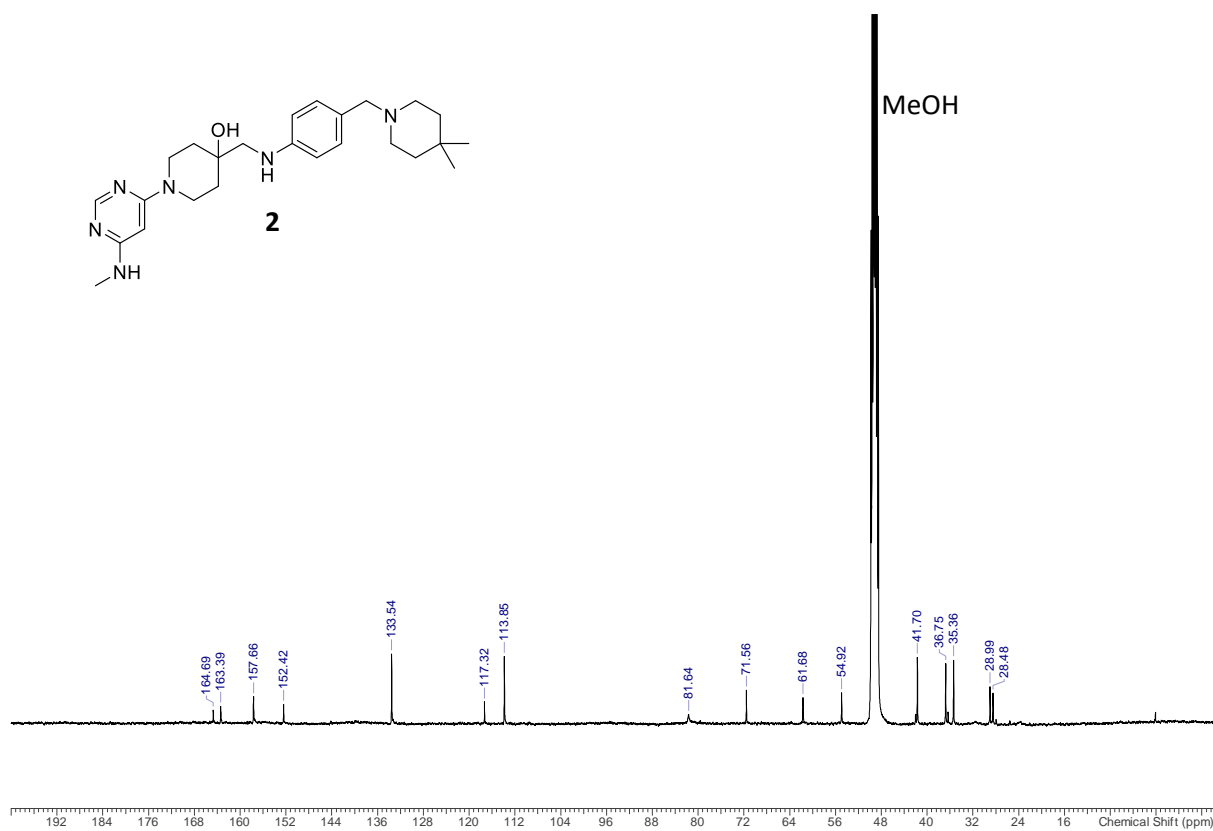
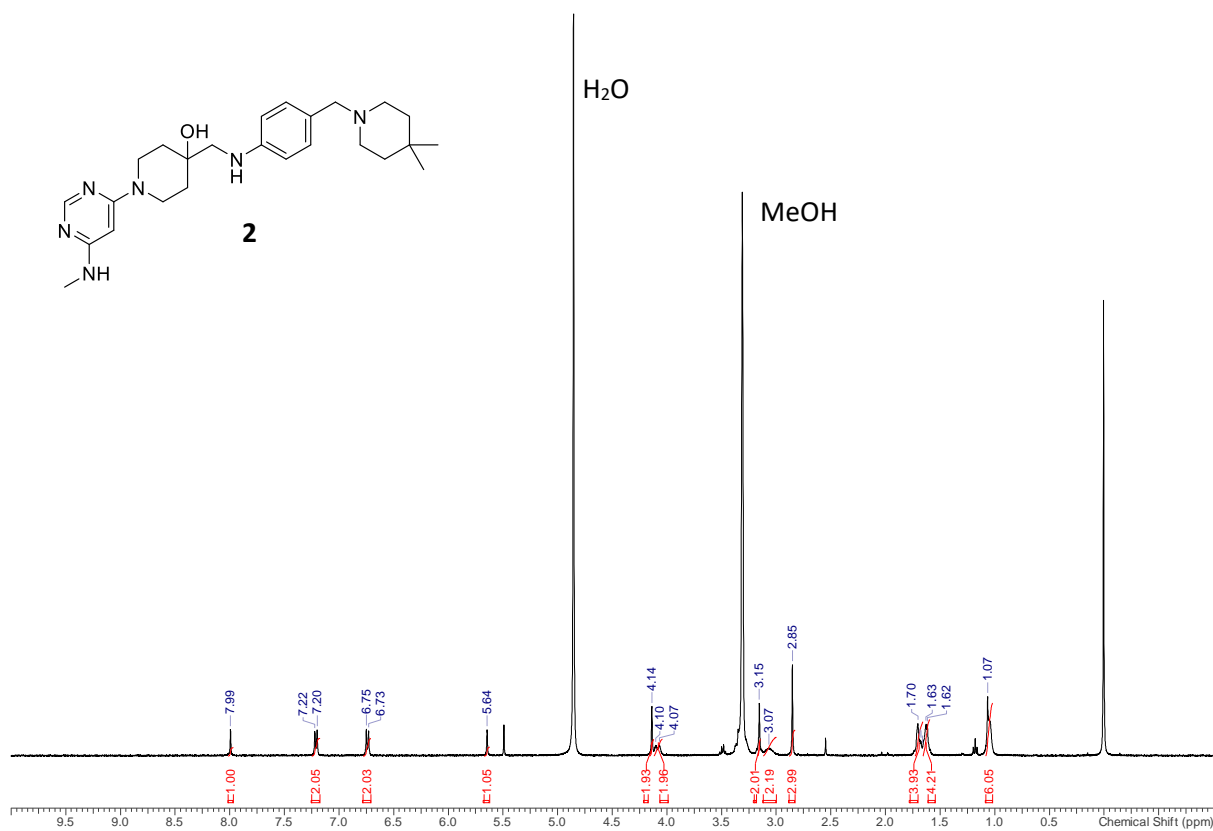
PDB ID:	7NHI	7O08	7O09
Compound	1	5	7
Data Collection			
Space group	P3 ₂ 21	P3 ₂ 21	P3 ₂ 21
Cell dimension a, b, c (Å)	63.89, 63.89, 225.77	63.8, 63.81, 225.99	63.89, 63.89, 225.7
Cell dimension α , β , γ (°)	90, 90, 120	90, 90, 120	90, 90, 120
Resolution (Å)	44.58 (1.85)	49.64 (2)	45.2 (1.8)
Unique reflections*	46100 (7322)	31729 (5871)	50869 (8076)
Completeness*	98.2 (98.9)	100 (99.8)	99.9 (99.7)
Redundancy*	6.14 (5.26)	13.06 (13.65)	9.77 (9.53)
R _{merge} *	8.3 (141.4)	12.6 (128.6)	8.4 (158.3)
CC (1/2)	99.9 (45.8)	99.9 (70.5)	100 (55.1)
I/ σ I	15.17 (1.11)	17.69 (2.1)	19.93 (1.43)
Refinement			
R _{work} /R _{free}	19.81/22.18	18.9/22.6	19.28/22.51
RMSD bond (Å)	0.008	0.008	0.008
RMSD angle (°)	0.989	0.898	1.027
B-factor (Å ²)**	34.92/42.86/41.82	34.67/41.14/41.35	33.66/42.2/41.79
Ramachandran Favored	97.64	97.23	97.16
Ramachandran allowed	2.12	2.08	2.6
Ramachandran Disallowed	0.24	0.69	0.24
PDB ID:	7O0L	7O29	7O2E
Compound	8	20	21
Data Collection			
Space group	P3 ₂ 21	P3 ₂ 21	P3 ₂ 21
Cell dimension a, b, c (Å)	64.13, 64.13, 225.85	64.15, 64.15, 225.65	63.8, 63.8, 224.91
Cell dimension α , β , γ (°)	90, 90, 120	90, 90, 120	90, 90, 120
Resolution (Å)	45.18 (1.9)	45.13 (2.75)	44.92 (2.5)
Unique reflections*	43655 (6908)	14906 (2374)	19442 (3082)
Completeness*	99.7 (99.2)	99.9 (100)	99.9 (99.8)
Redundancy*	9.84 (10.04)	9.53 (9.28)	8.14 (8.55)
R _{merge} *	9.7 (195.1)	11.4 (107.5)	10.7 (160.8)
CC (1/2)	100 (18.4)	99.9 (71.4)	99.9 (49.6)
I/ σ I	19.28 (1.29)	19.12 (2.12)	17.13 (1.41)
Refinement			
R _{work} /R _{free}	19.6/22.63	20.23/25.54	20.57/27.3
RMSD bond (Å)	0.009	0.009	0.009
RMSD angle (°)	1.012	1.073	1.067
B-factor (Å ²)**	38.22/44.34/42.67	56.99/59.35/49.38	62.3/63.56/57.07
Ramachandran Favored	96.52	93.78	95.31
Ramachandran allowed	3.02	5.3	4.46
Ramachandran Disallowed	0.46	0.92	0.23

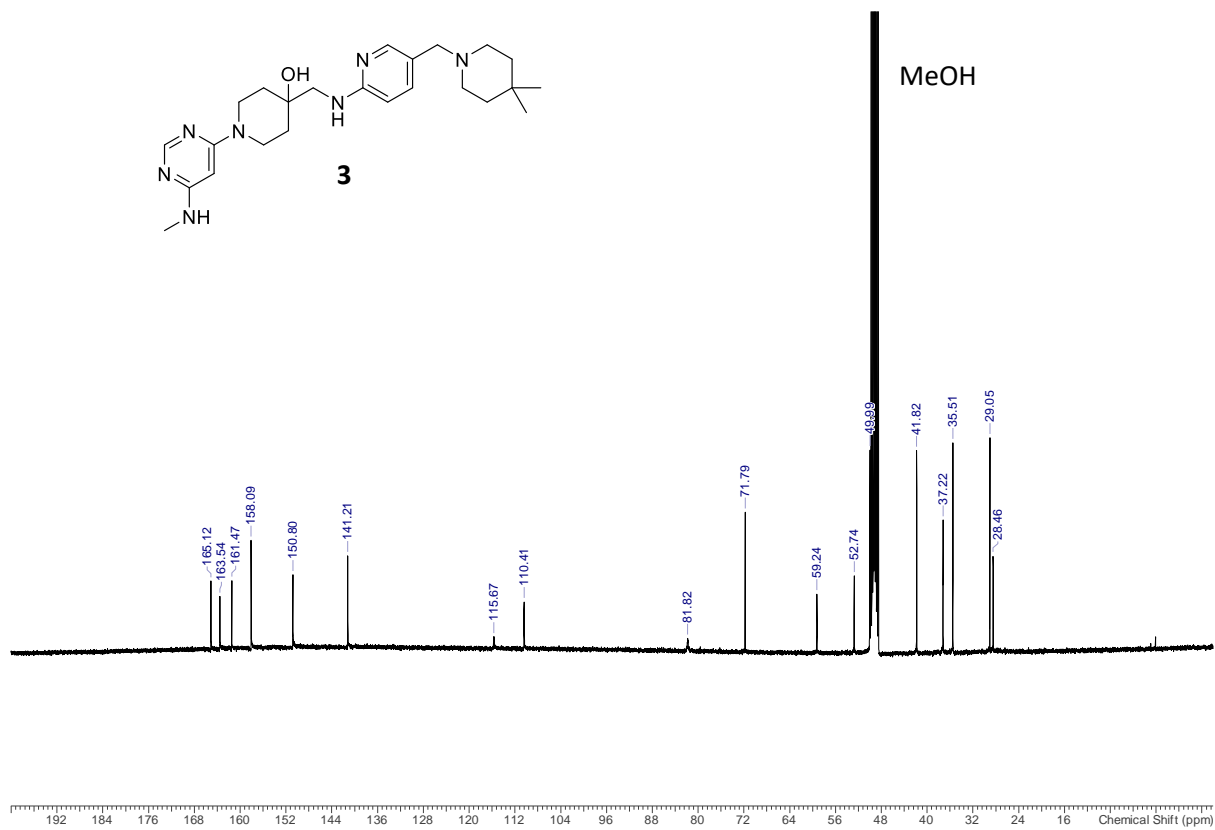
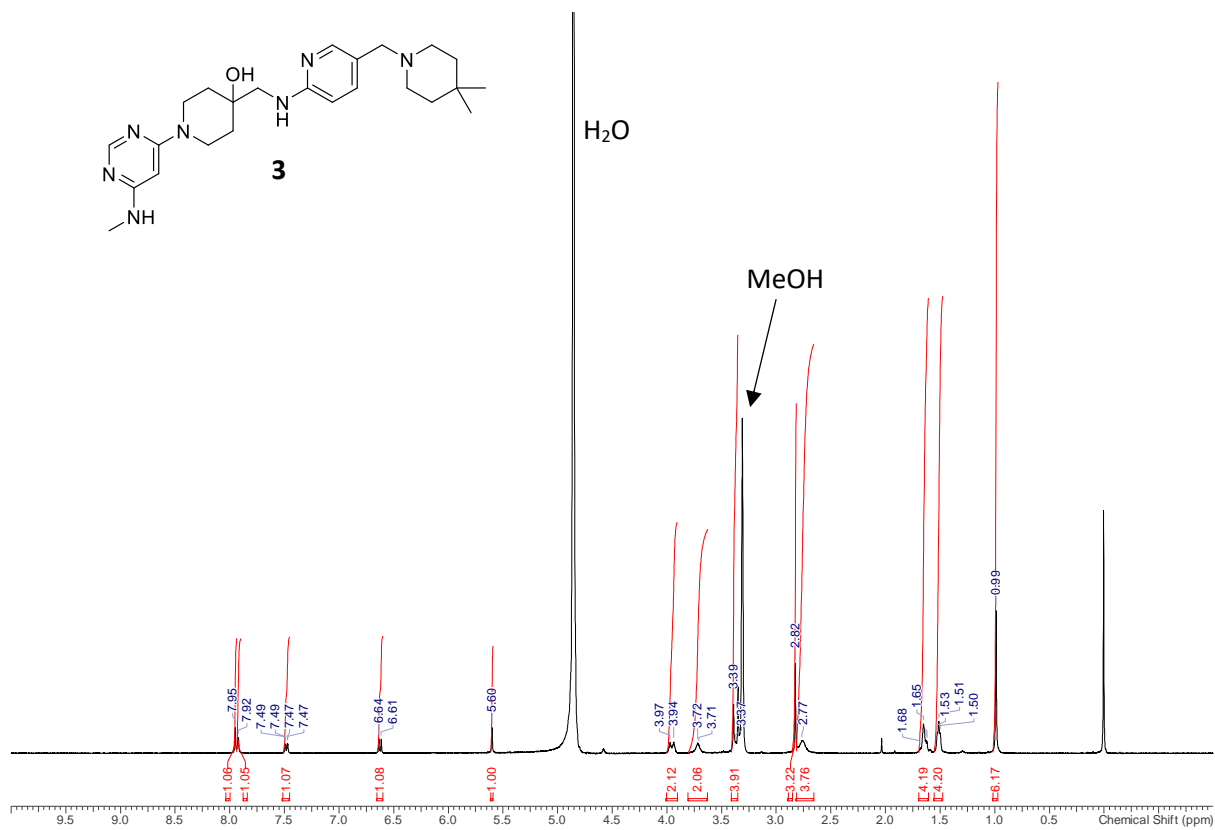
*Statistics for the highest resolution shell shown in parentheses. ** P/L/W indicate protein, ligand/ion and water molecules, respectively.

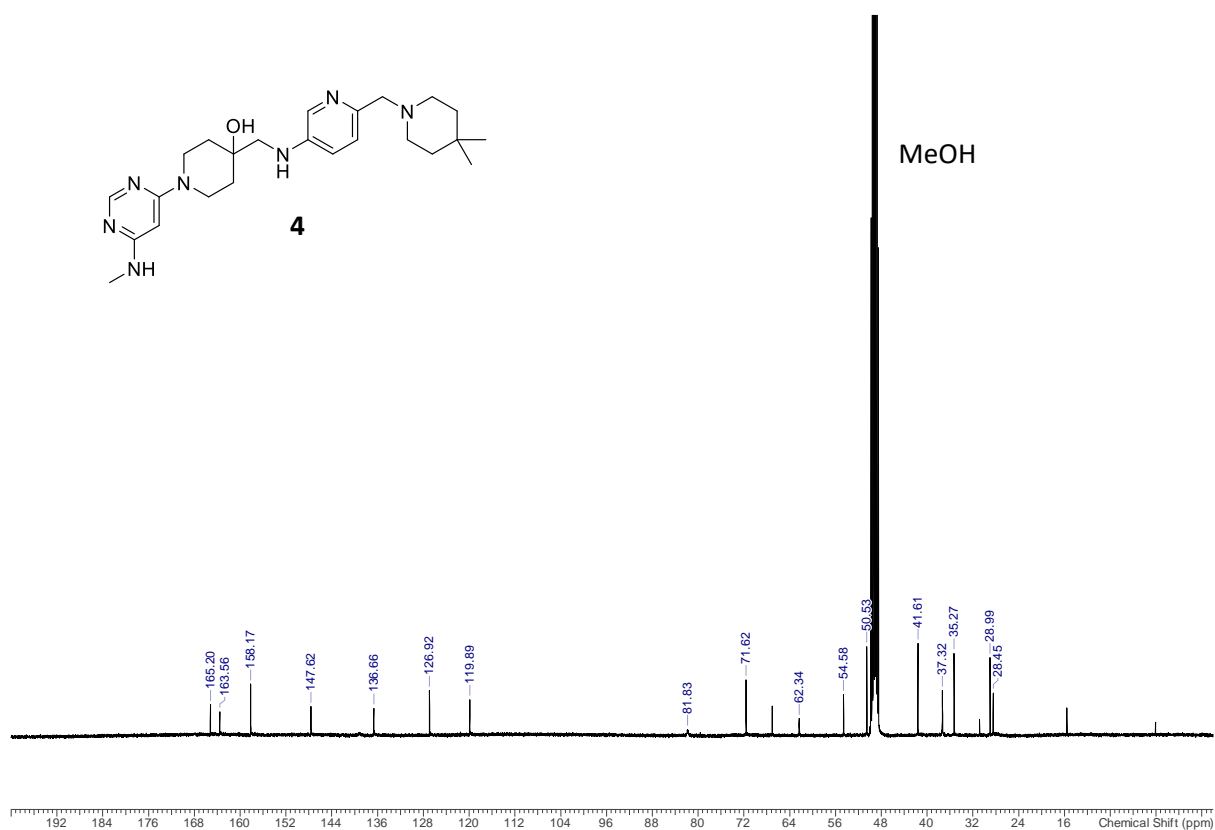
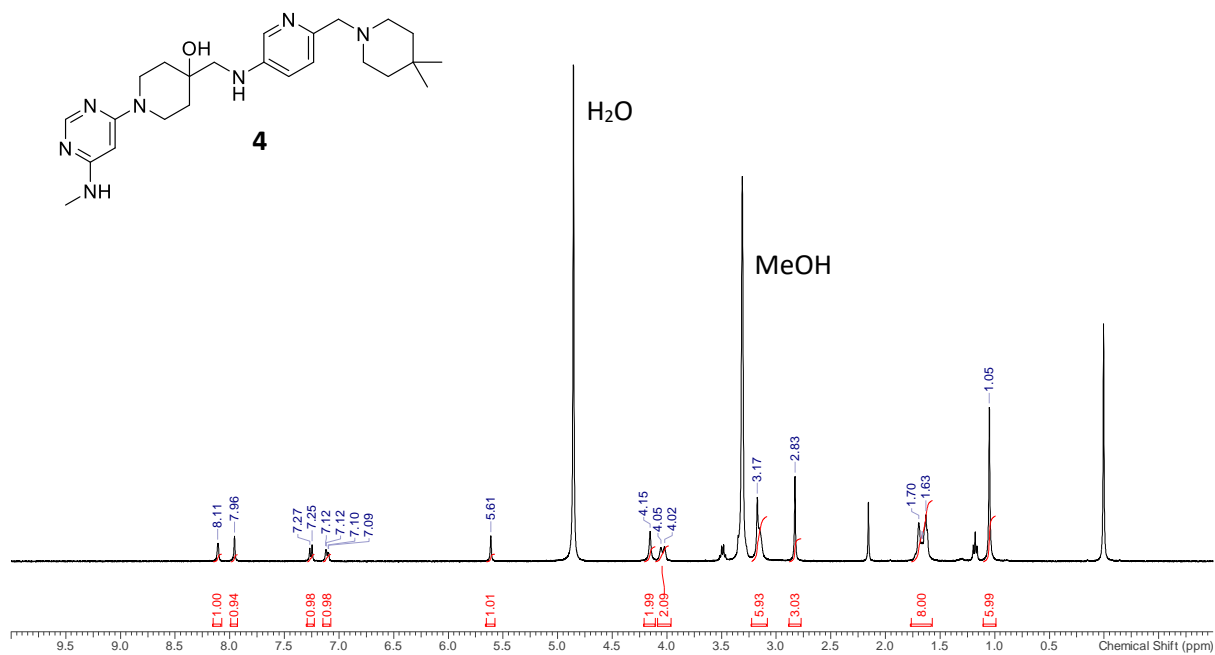
PDB ID:	7O2F
Compound	22 (UZH2)
Data Collection	
Space group	P3 ₂ 21
Cell dimension a, b, c (Å)	63.87, 63.87, 224.51
Cell dimension α , β , γ (°)	90, 90, 120
Resolution (Å)	44.74 (2.1)
Unique reflections*	32606 (5099)
Completeness*	99.3 (98.1)
Redundancy*	6.56 (4.96)
R _{merge} *	9.5 (87.8)
CC (1/2)	99.8 (61.4)
I/ σ I	12.77 (1.48)
Refinement	
R _{work} /R _{free}	19.71/24.21
RMSD bond (Å)	0.008
RMSD angle (°)	0.963
B-factor (Å ²)**	40.17/41.12/42.7
Ramachandran Favored	96.32
Ramachandran allowed	3.22
Ramachandran Disallowed	0.46

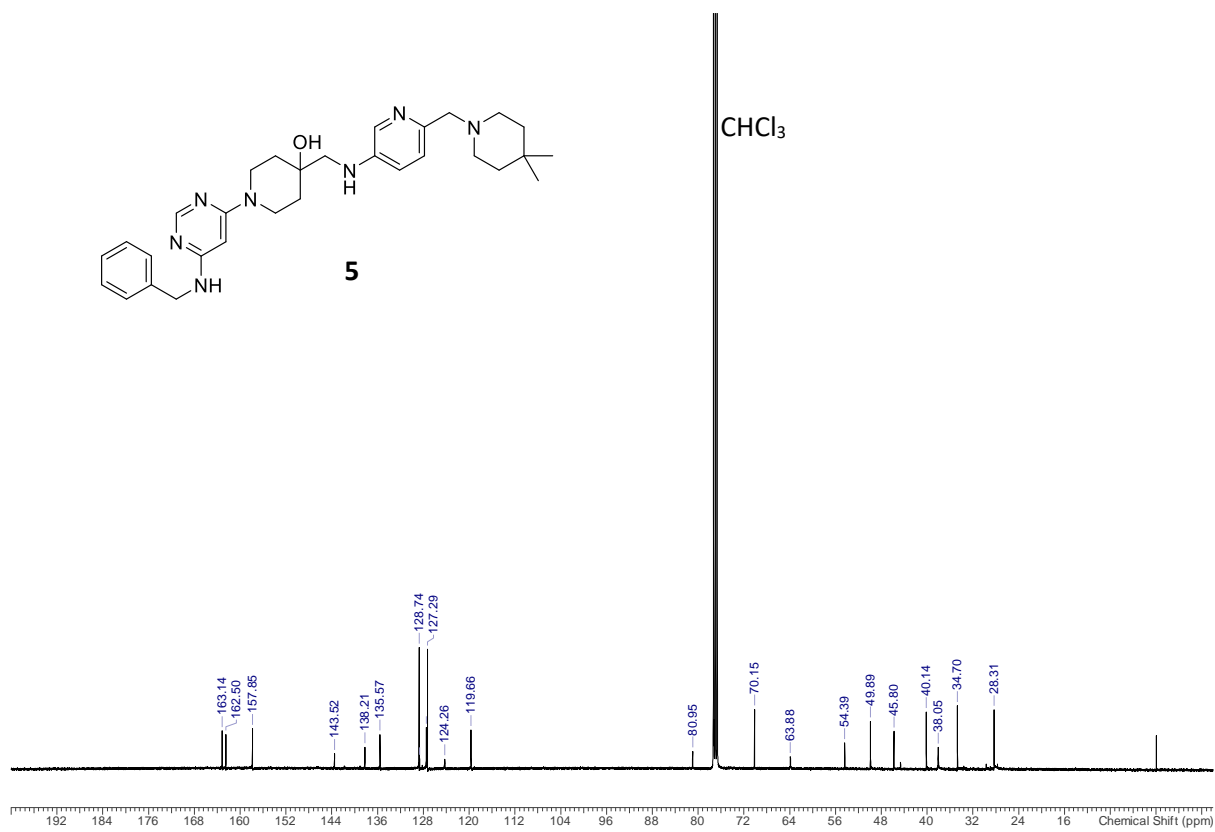
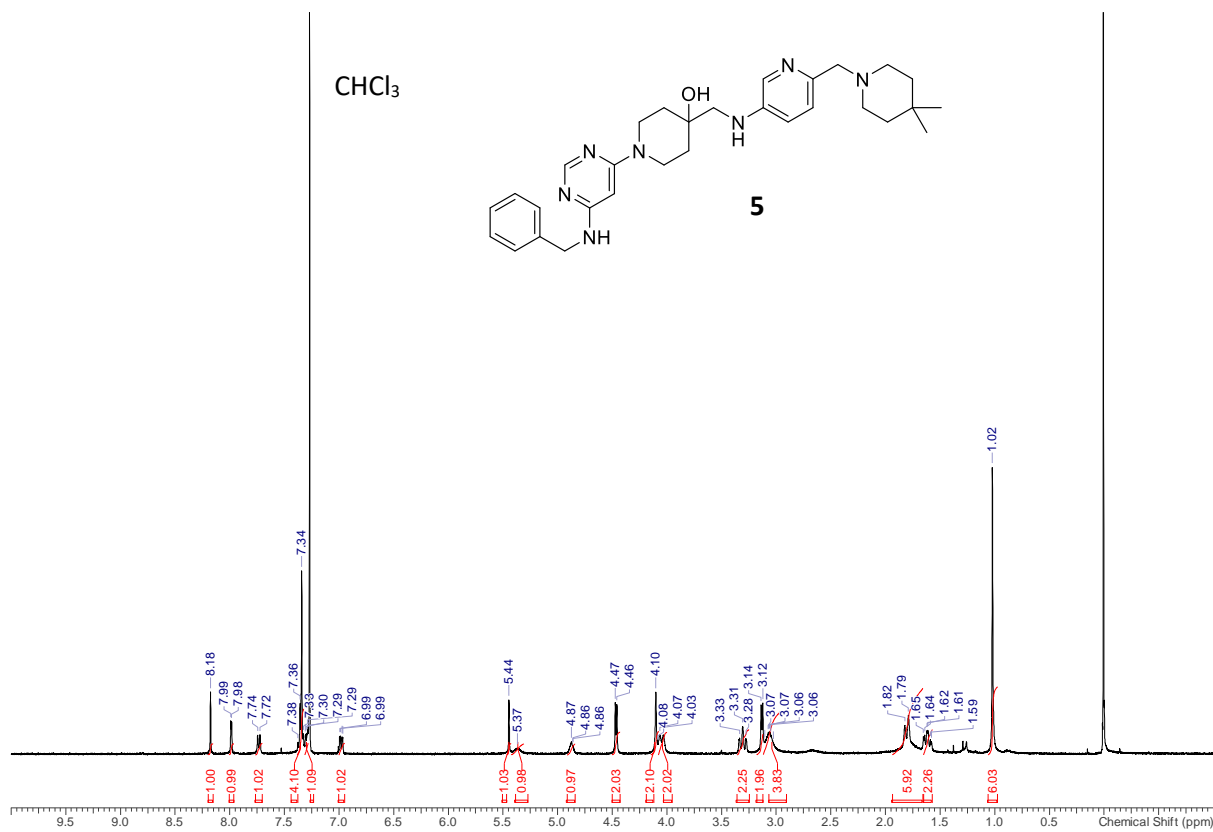
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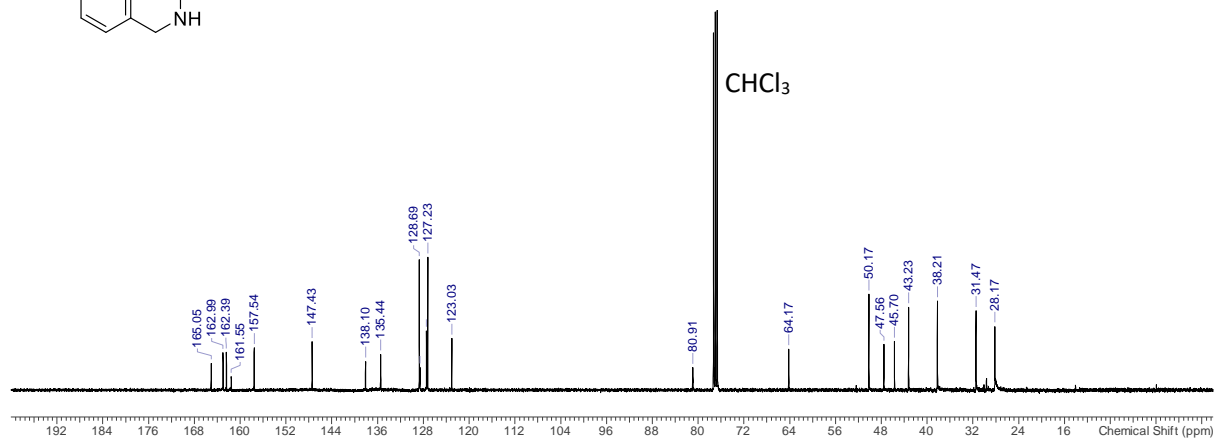
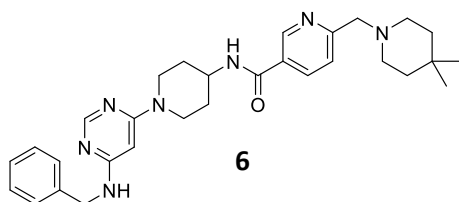
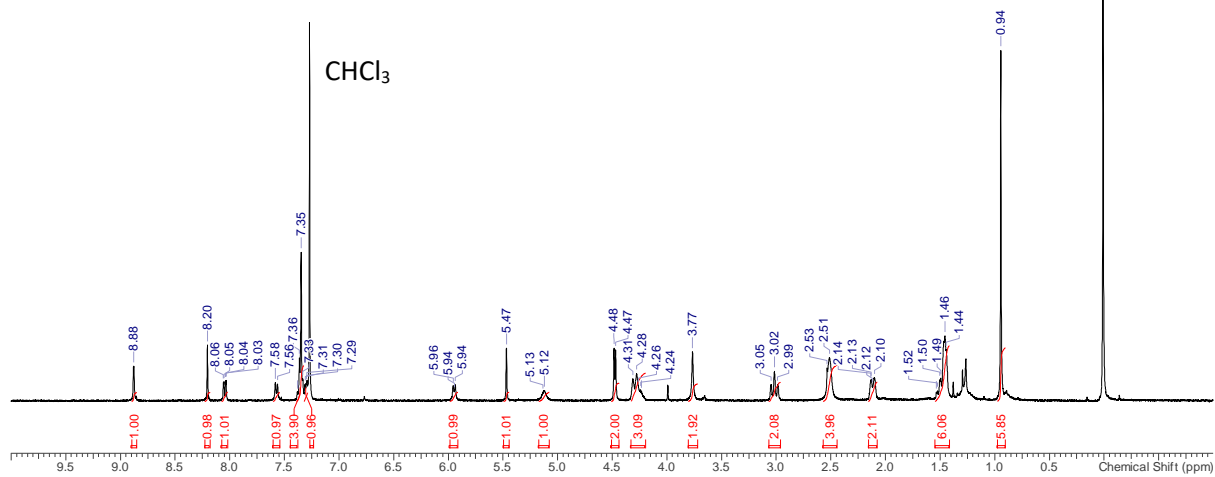
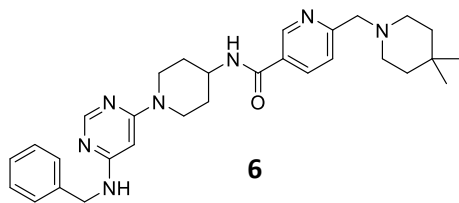
NMR traces of final compounds

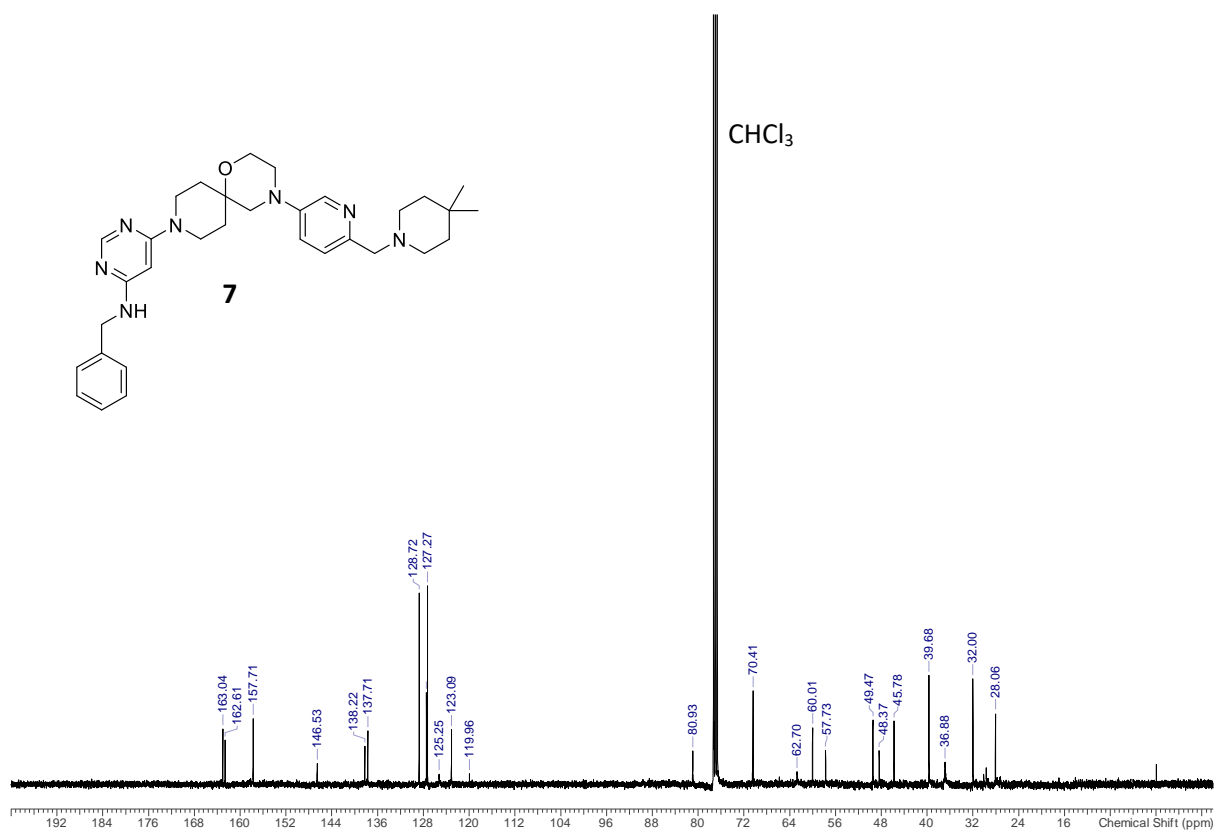
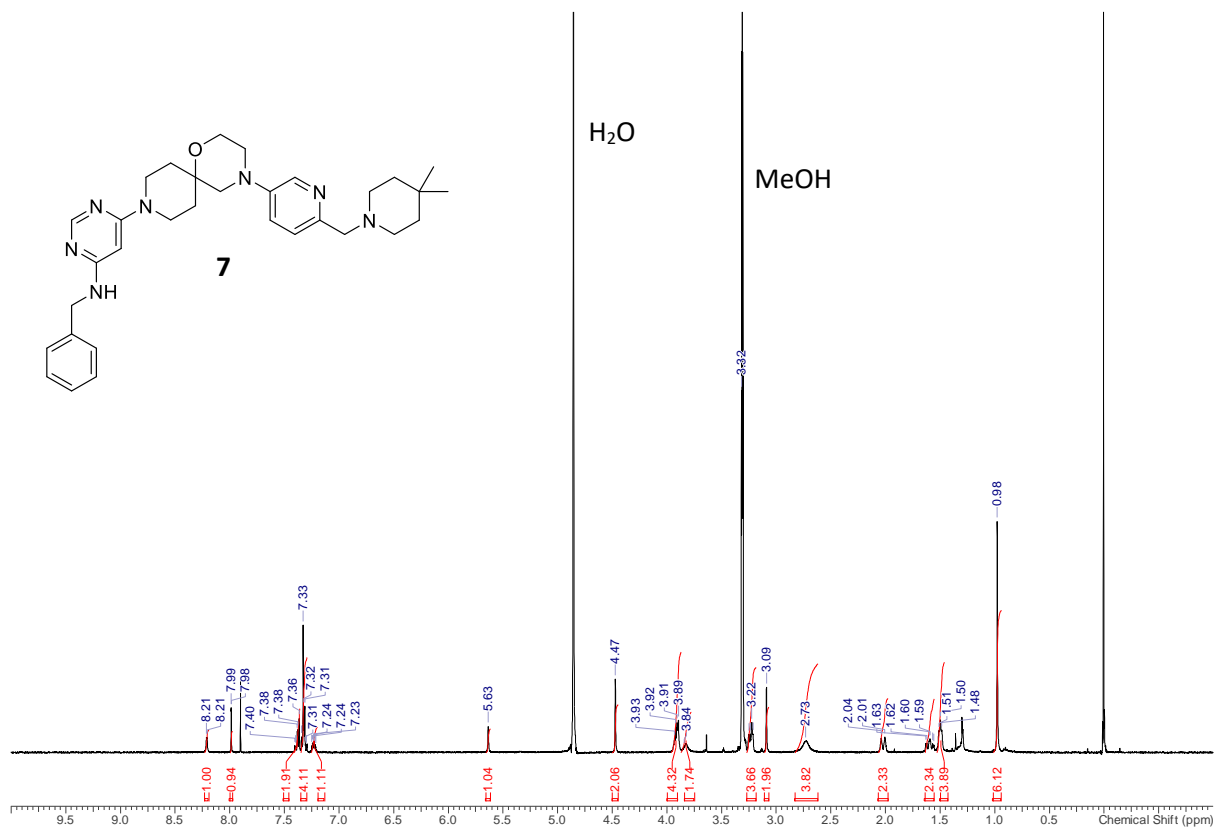


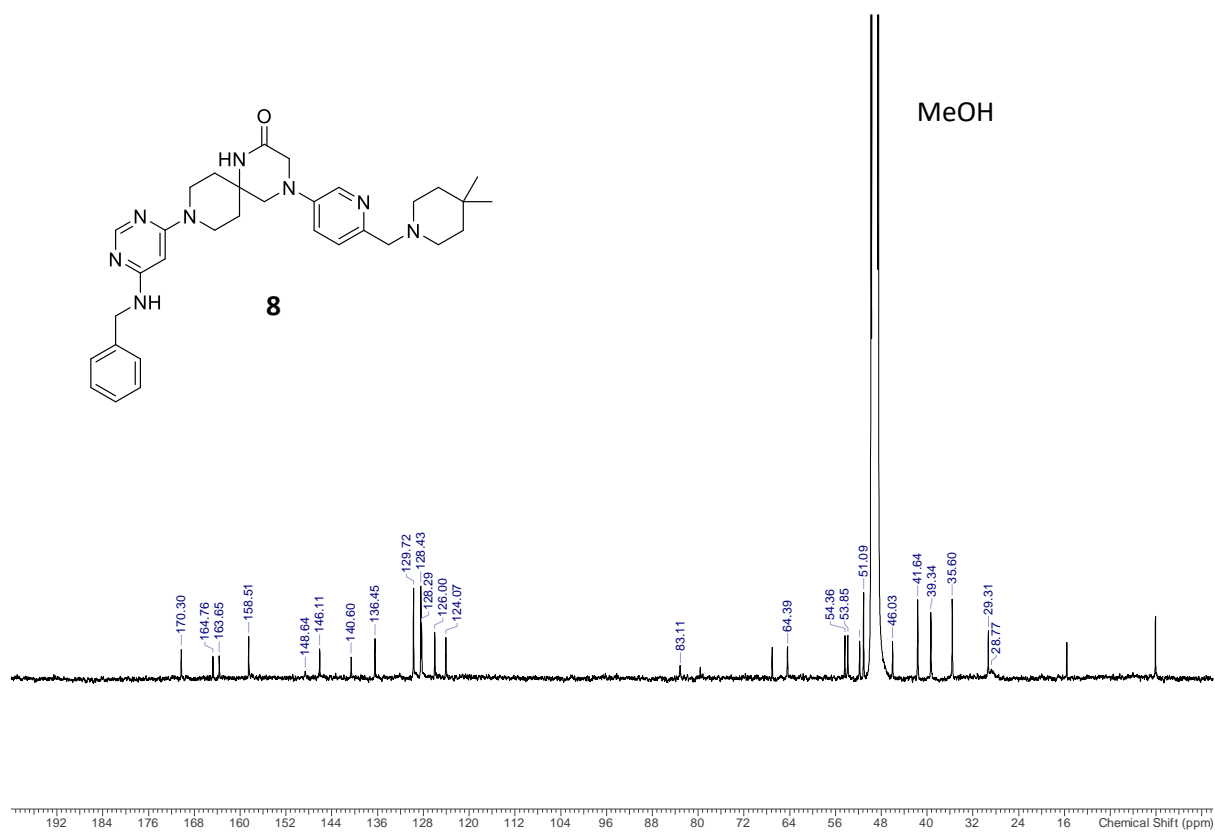
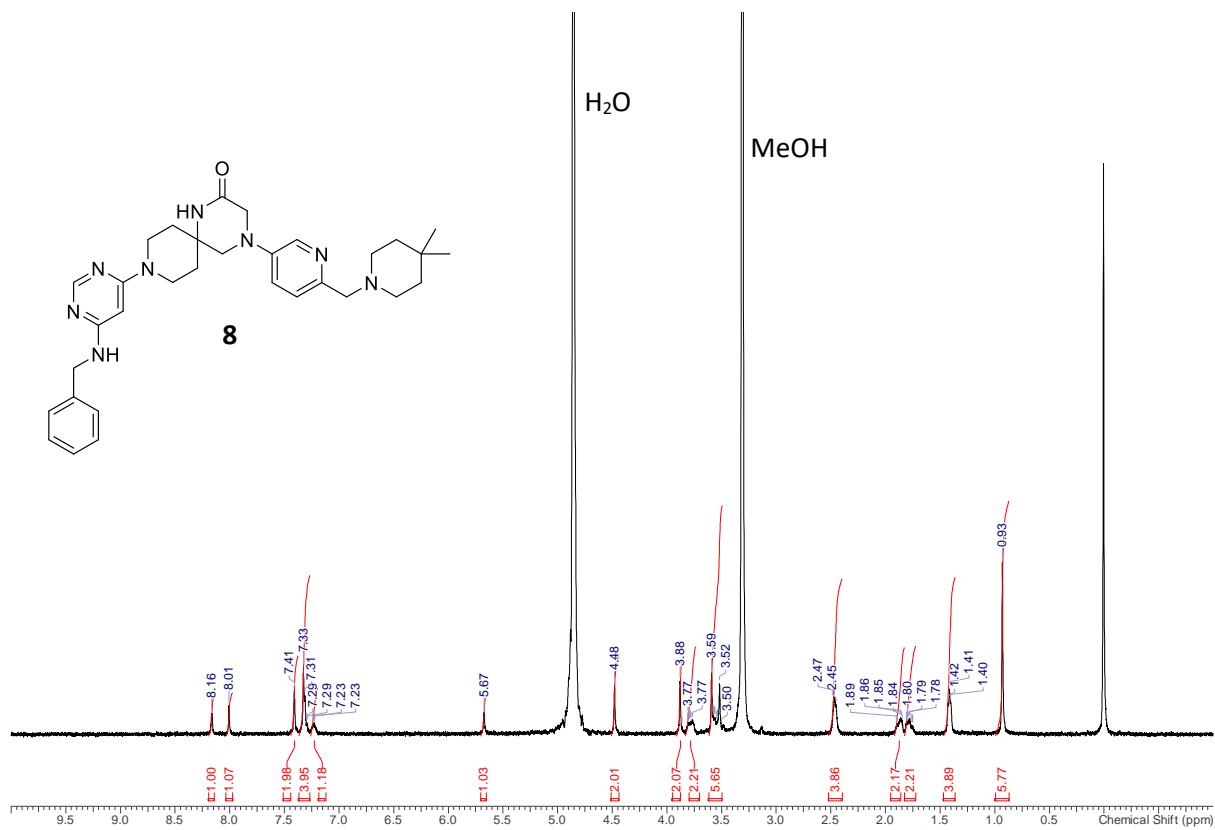


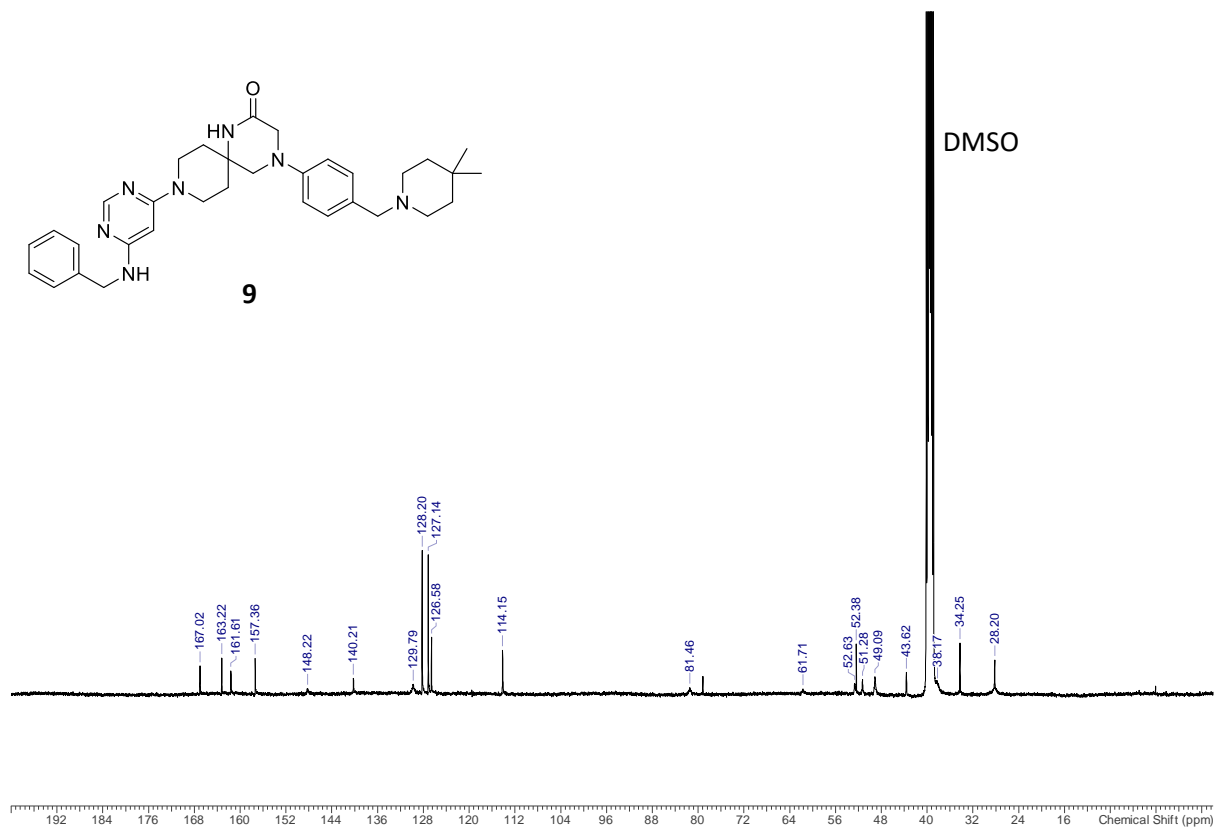
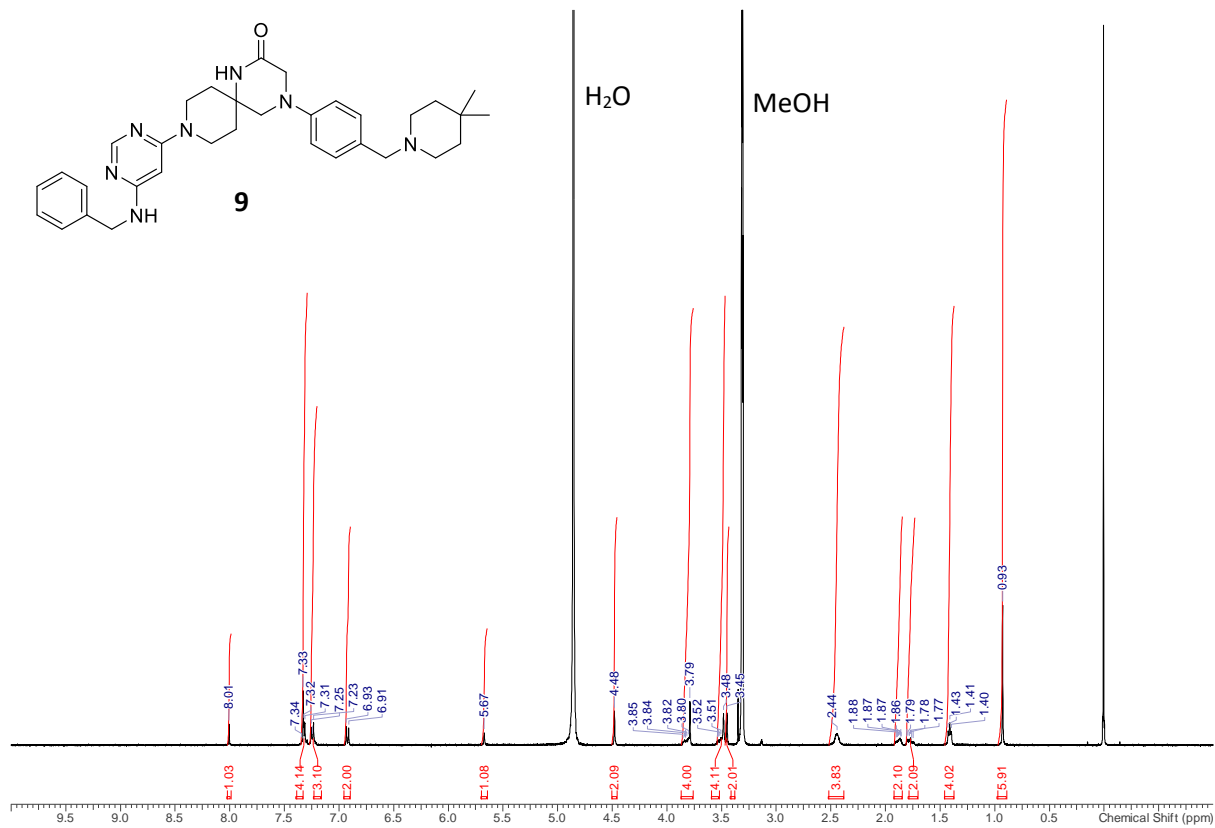


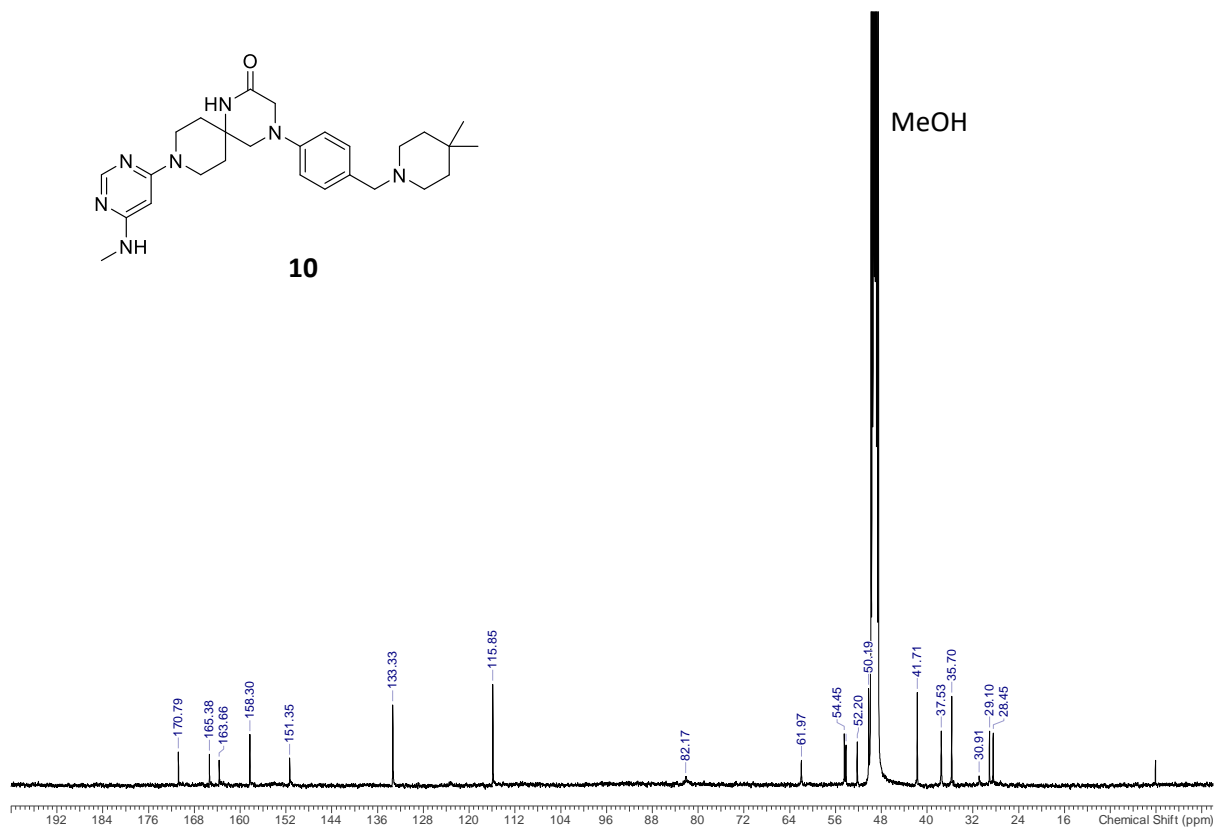
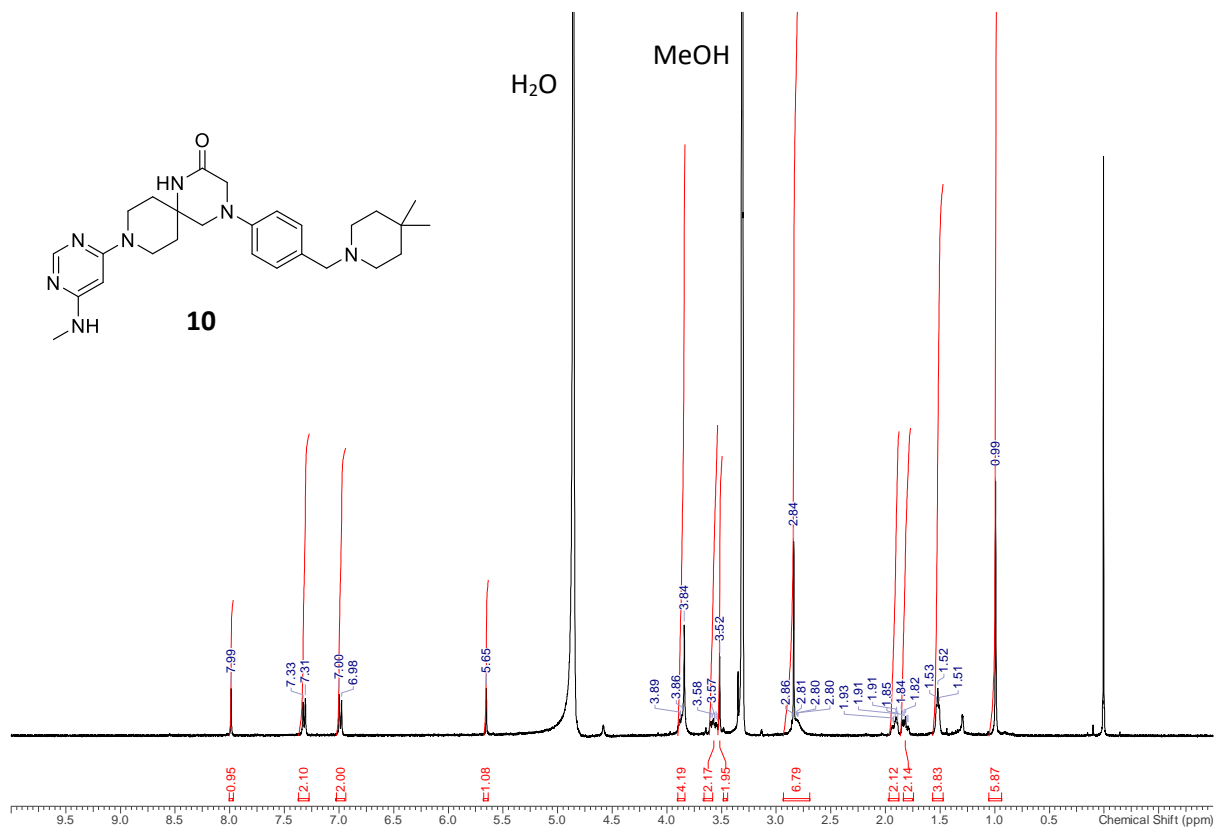


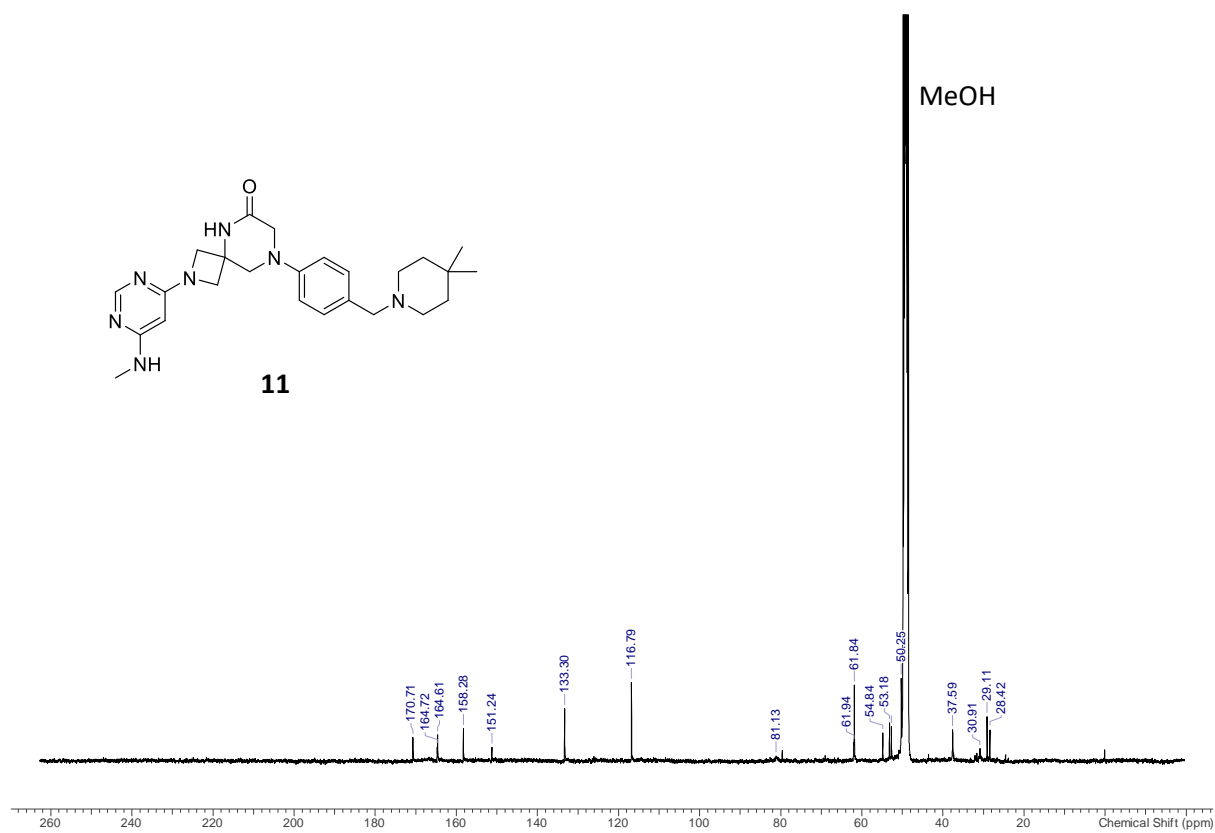
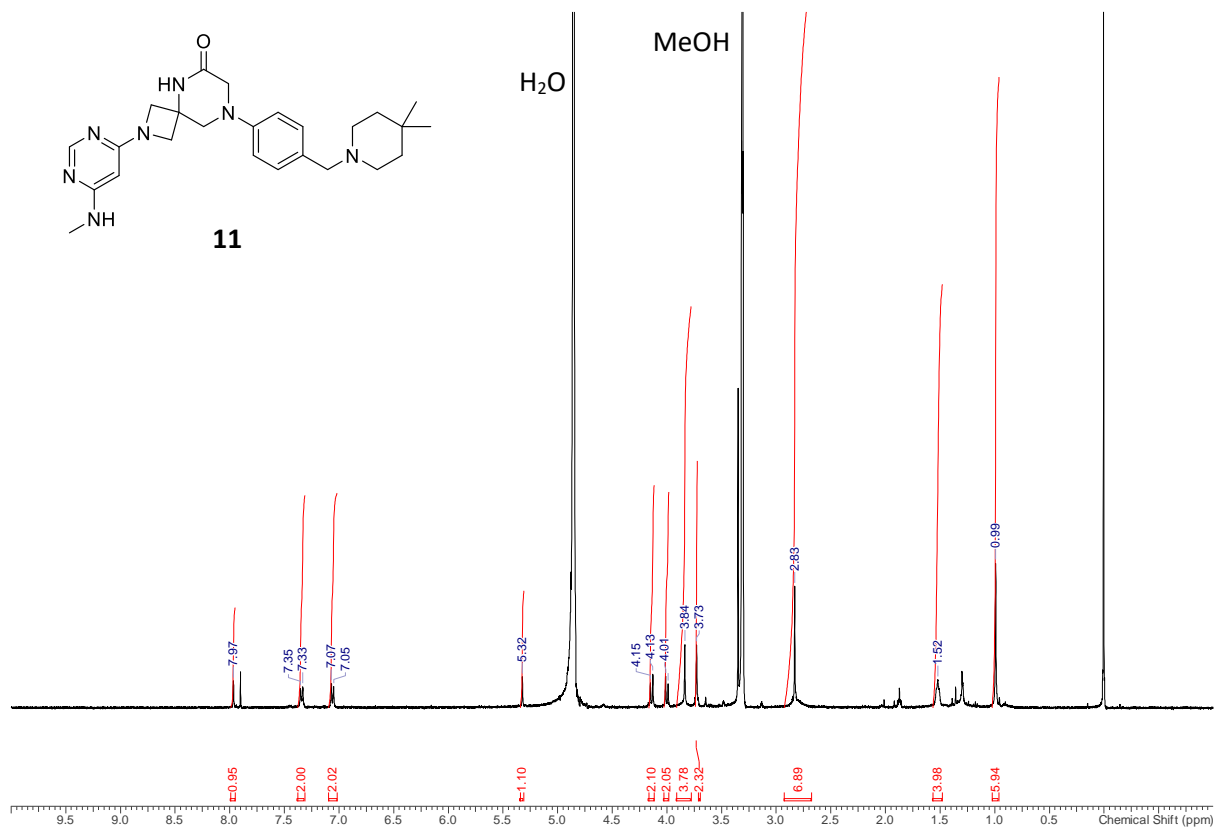


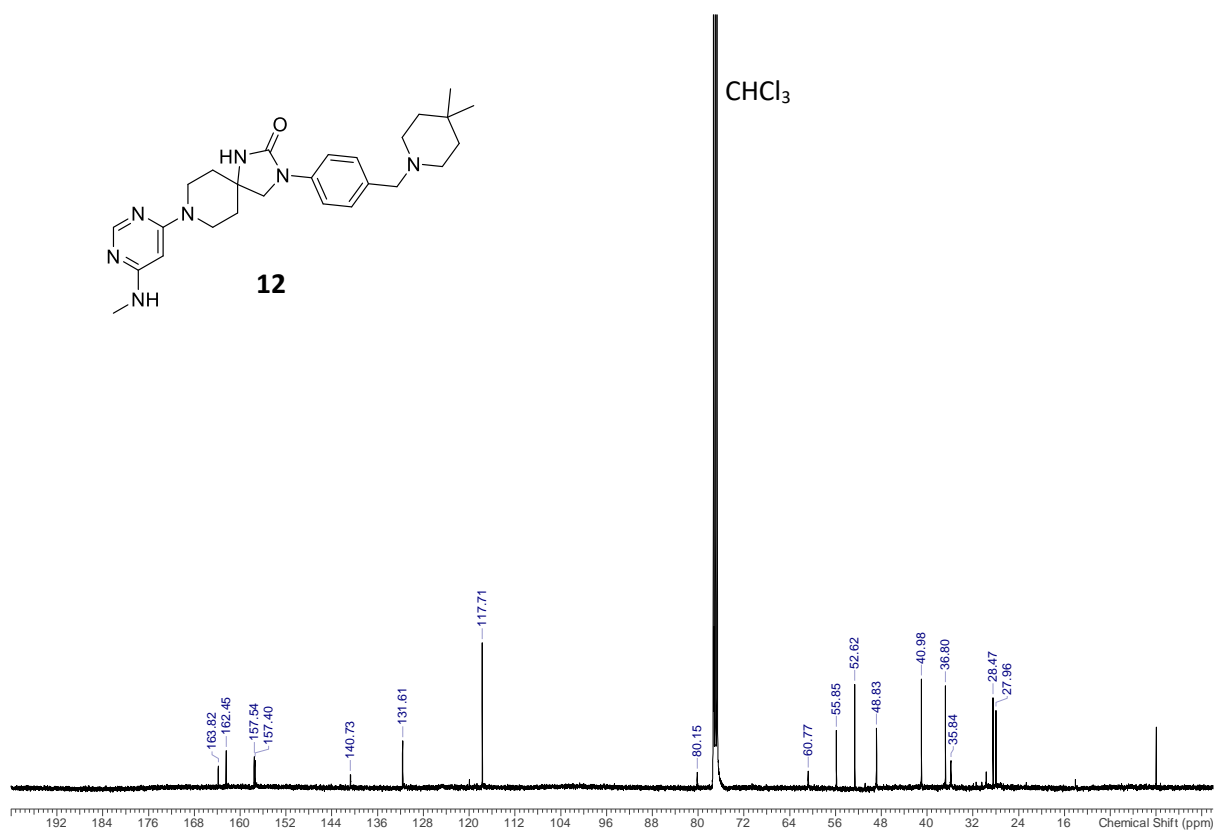
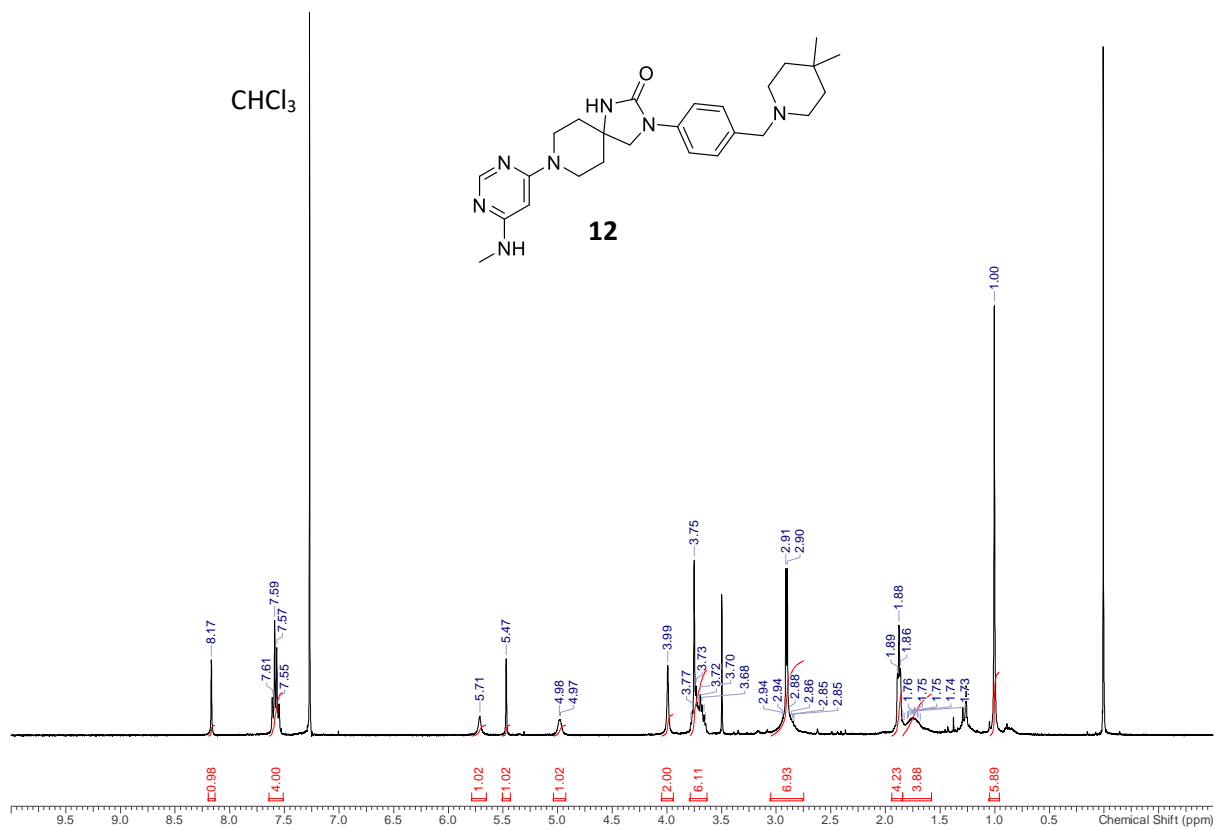


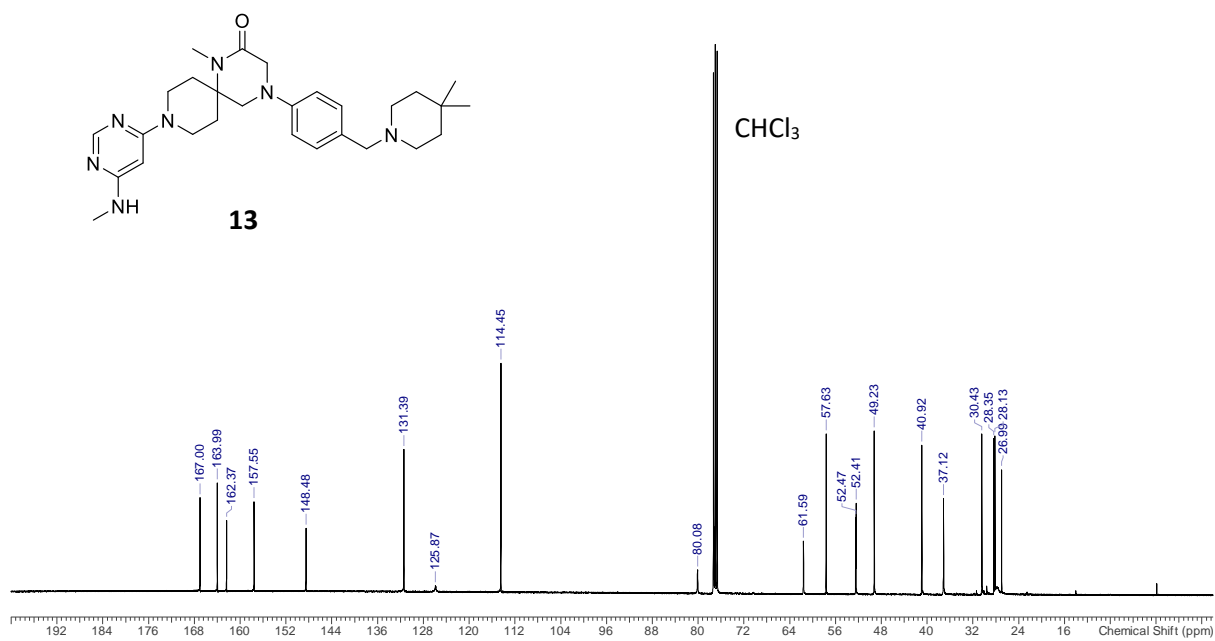
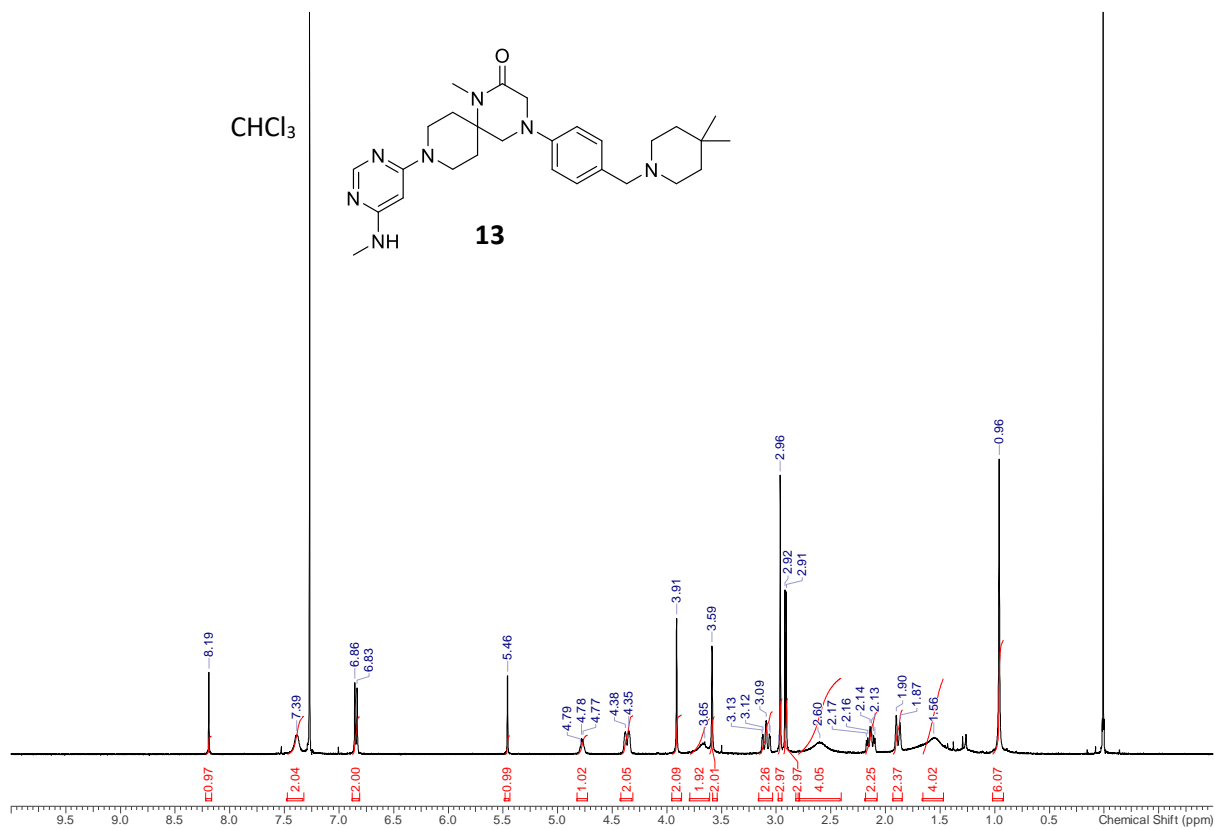


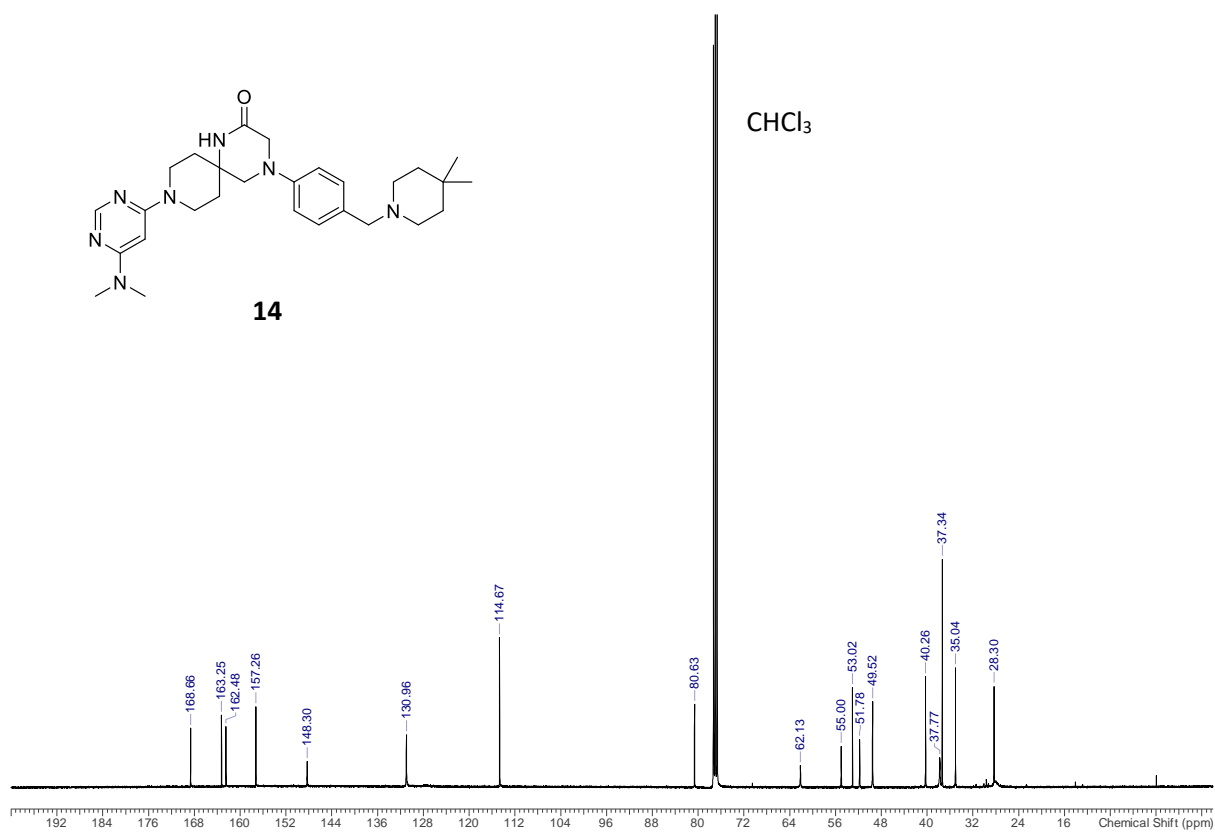
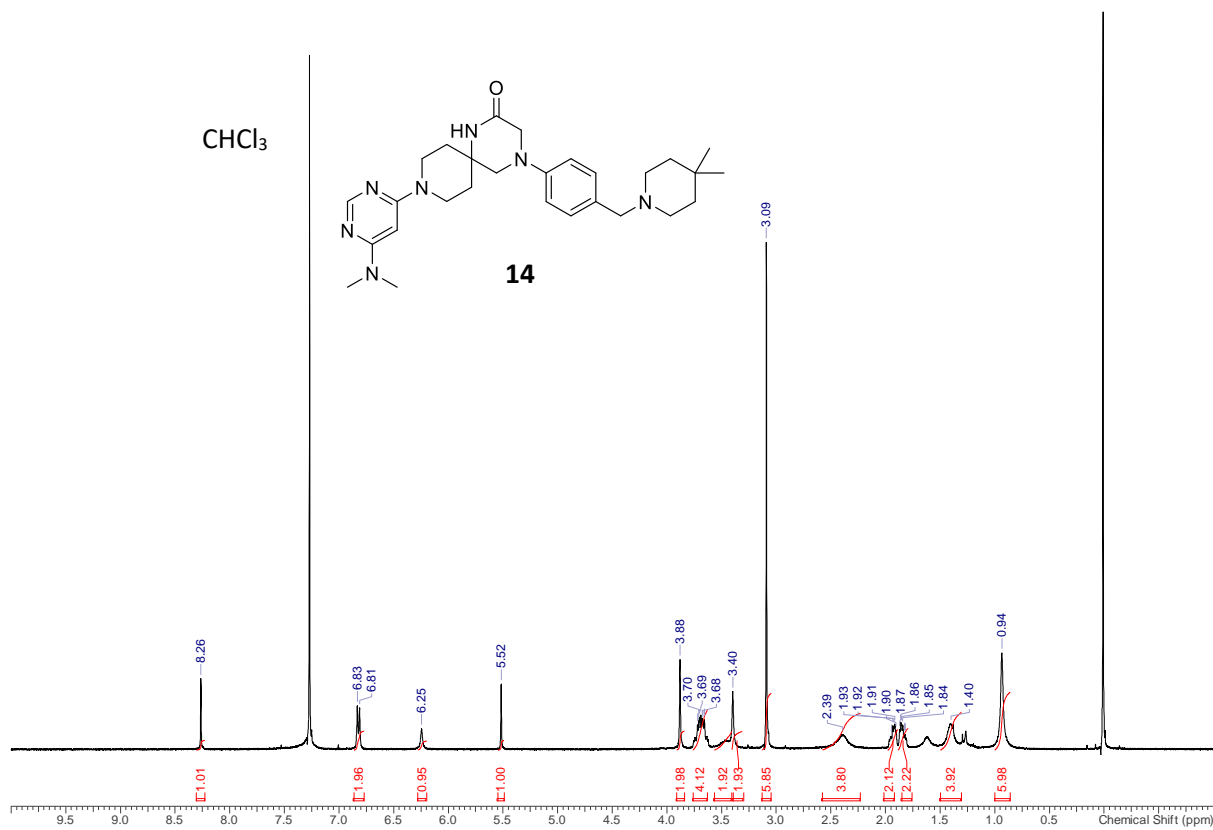


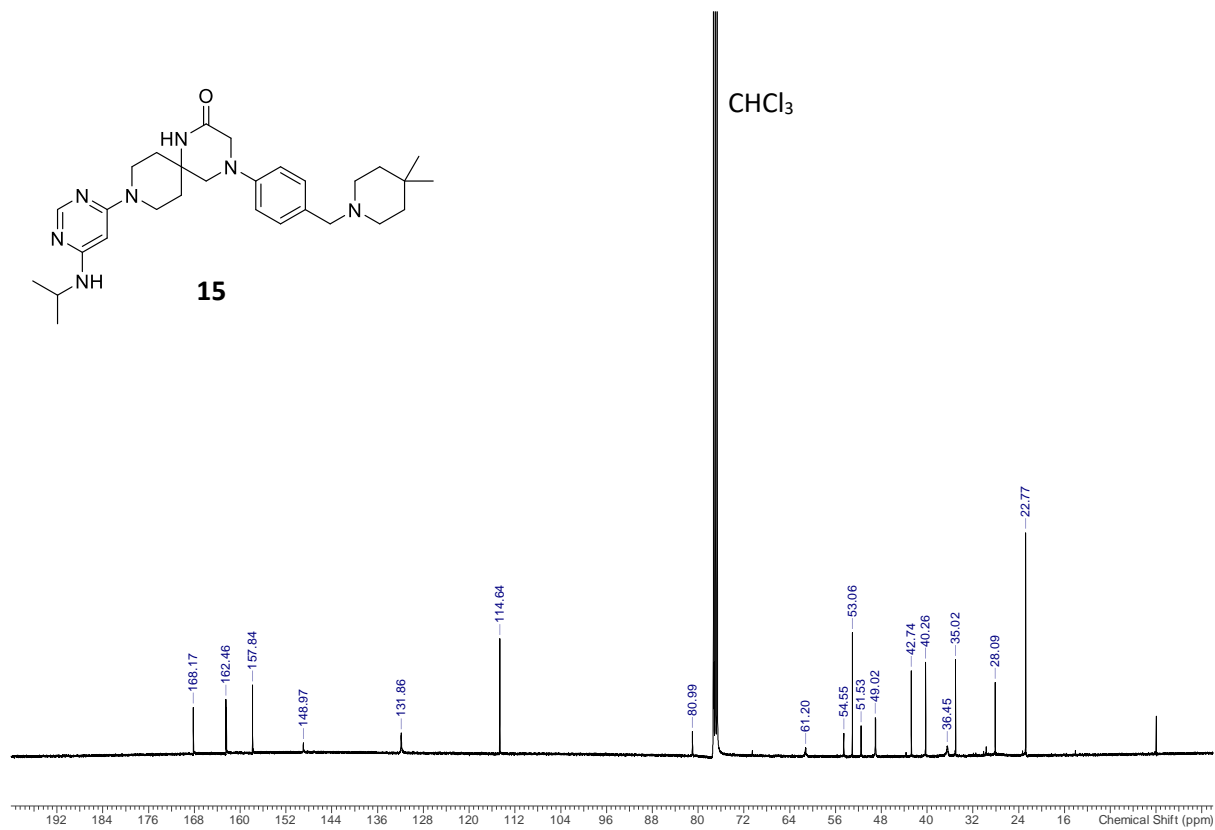
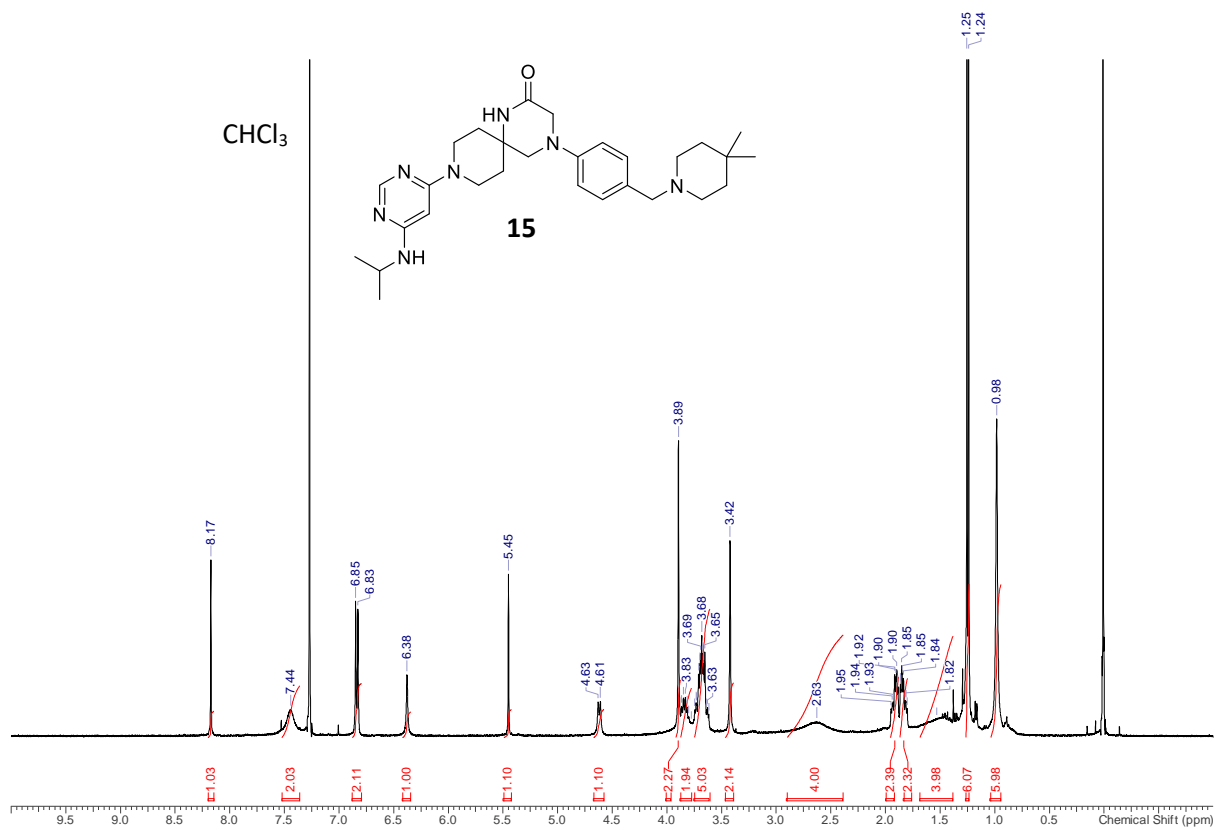


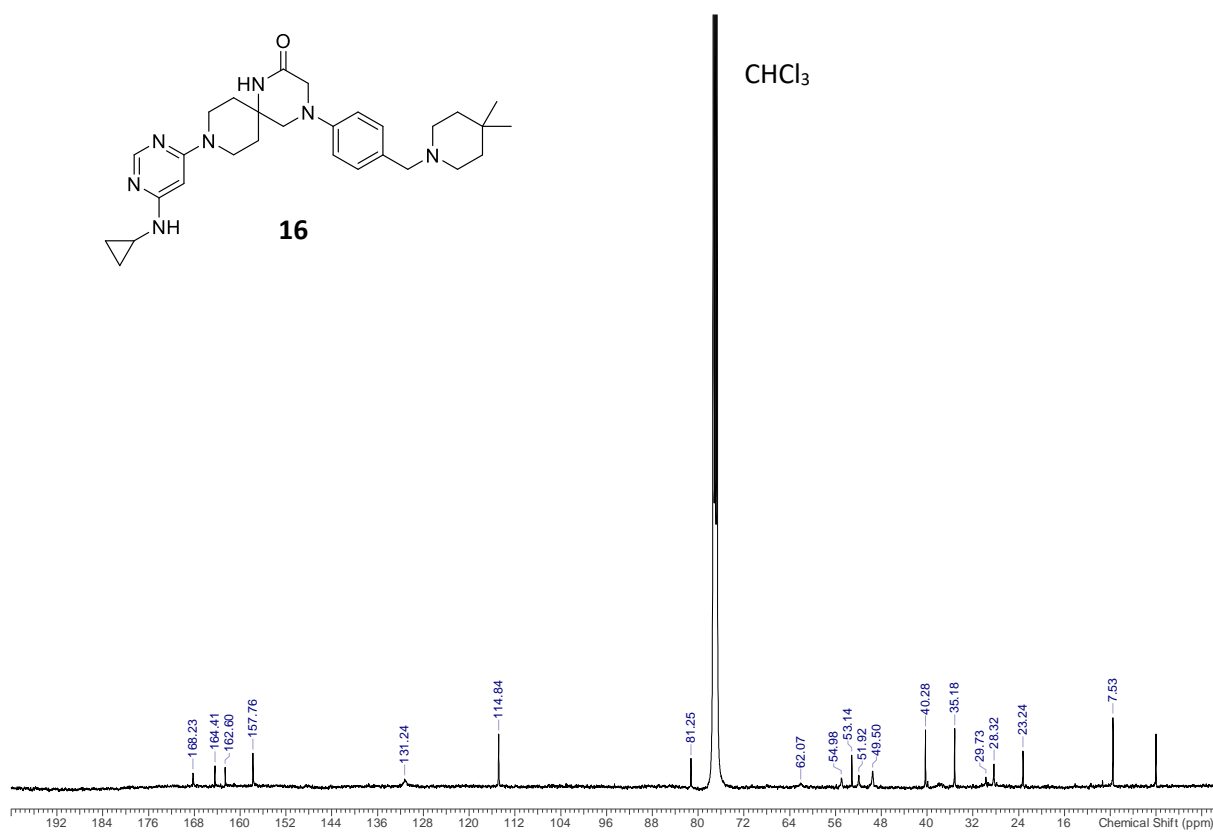
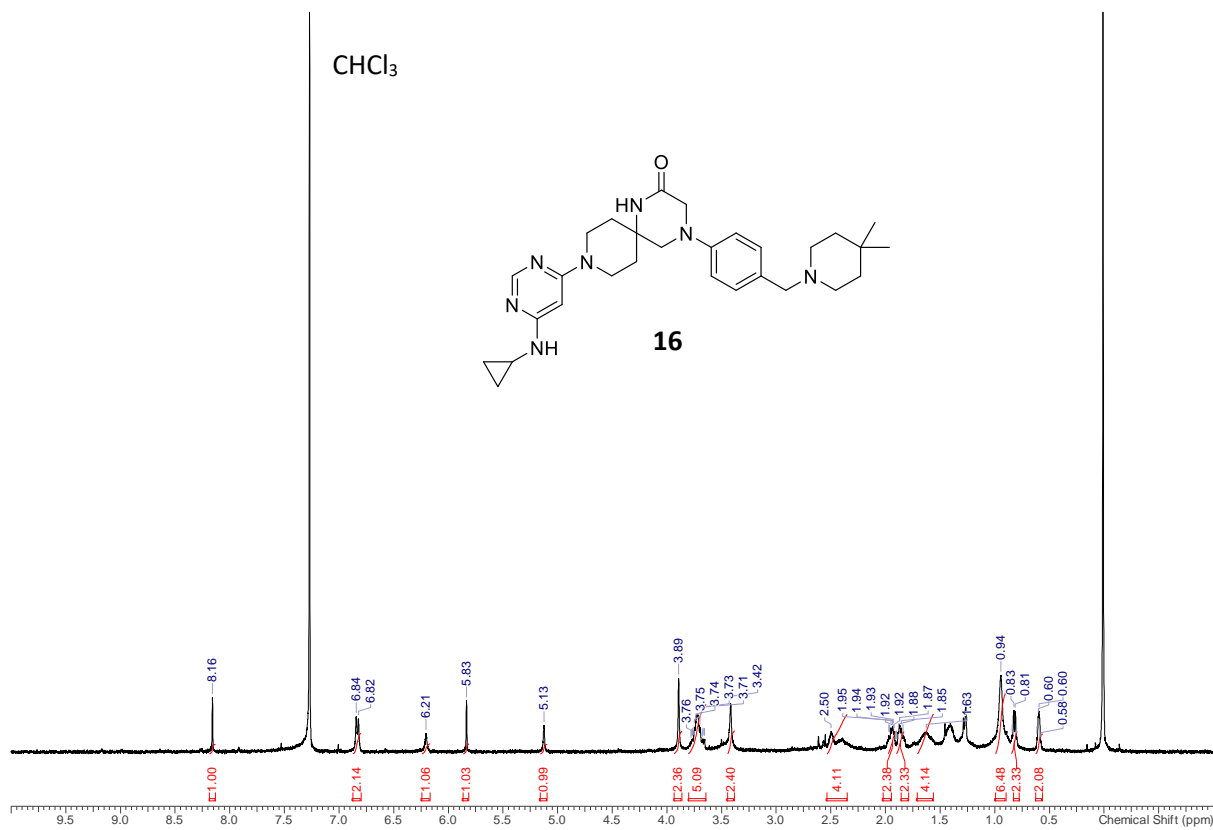


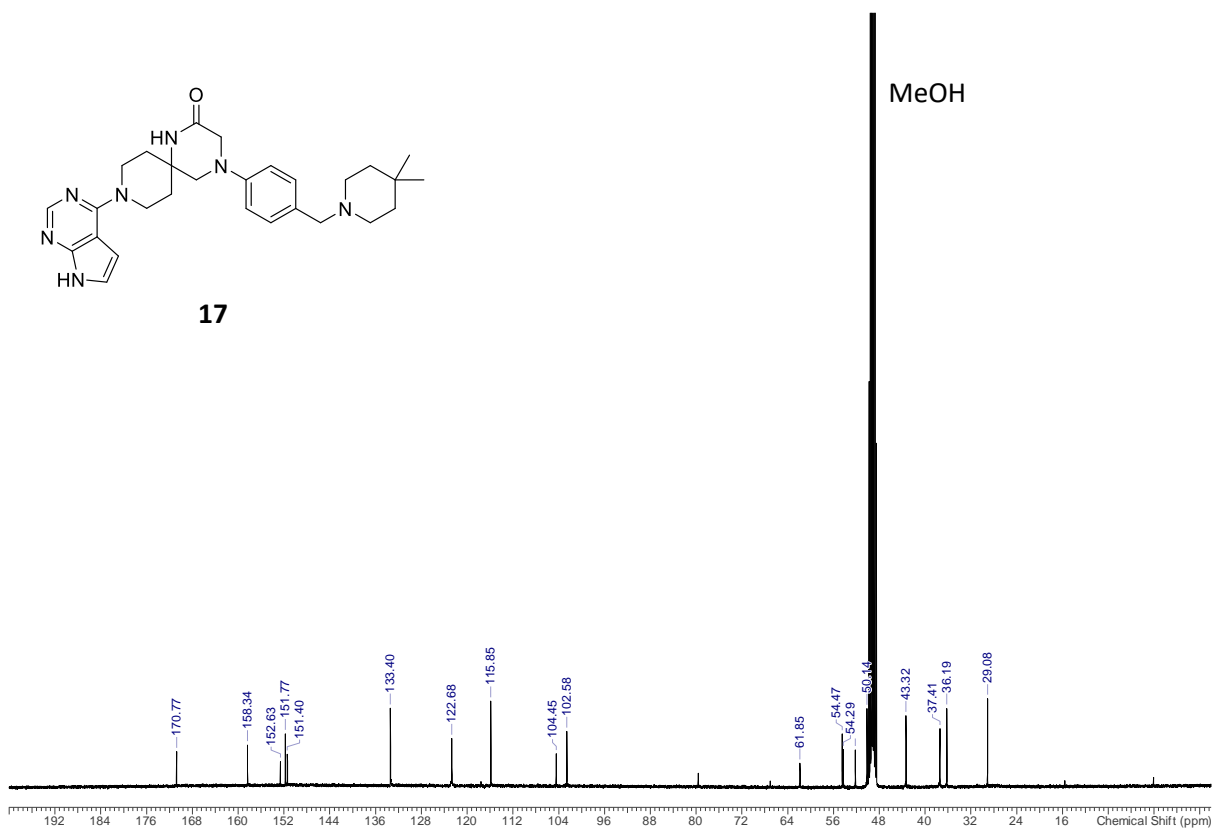
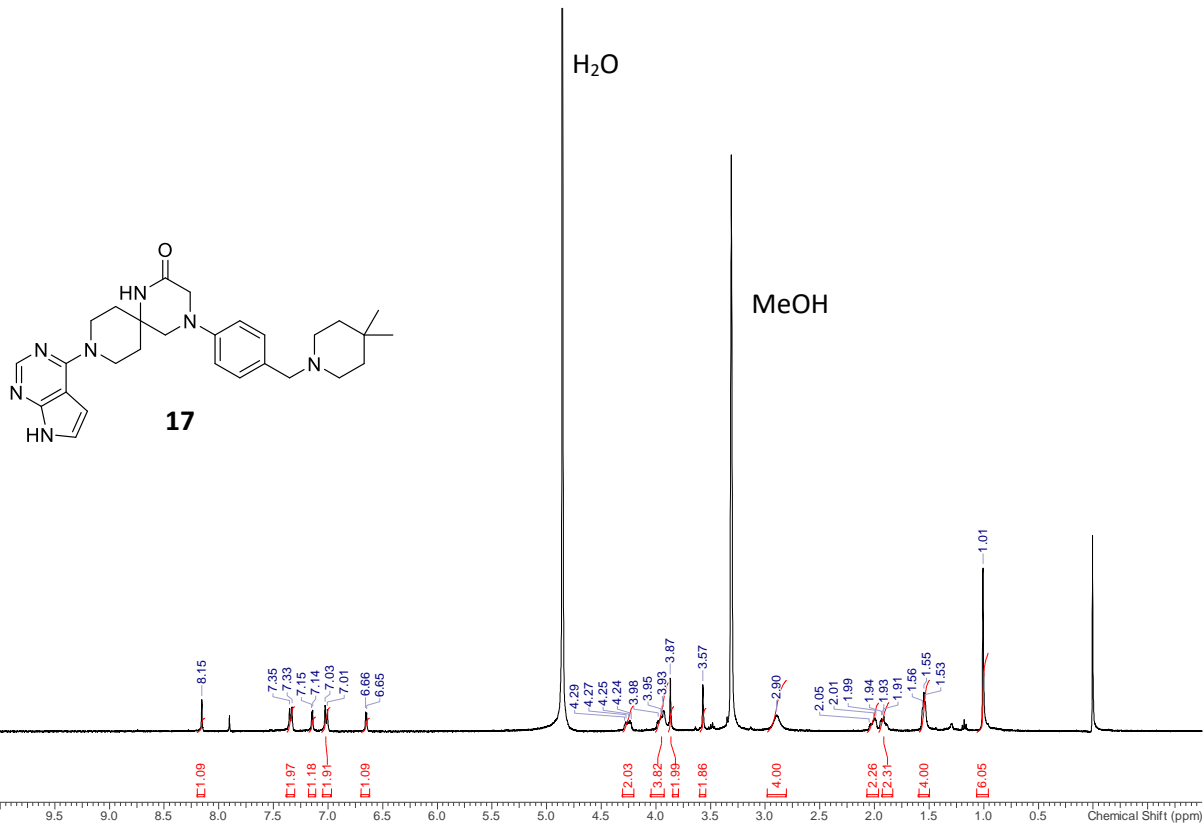


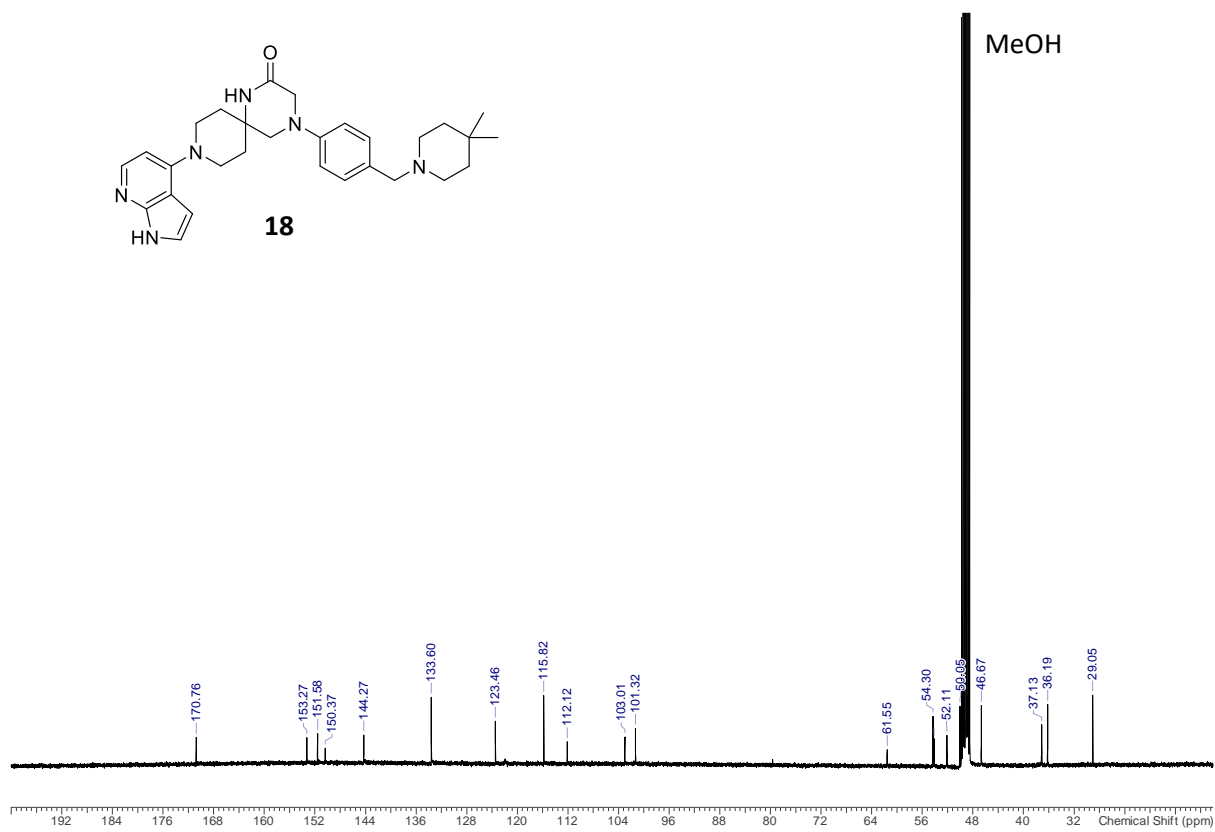
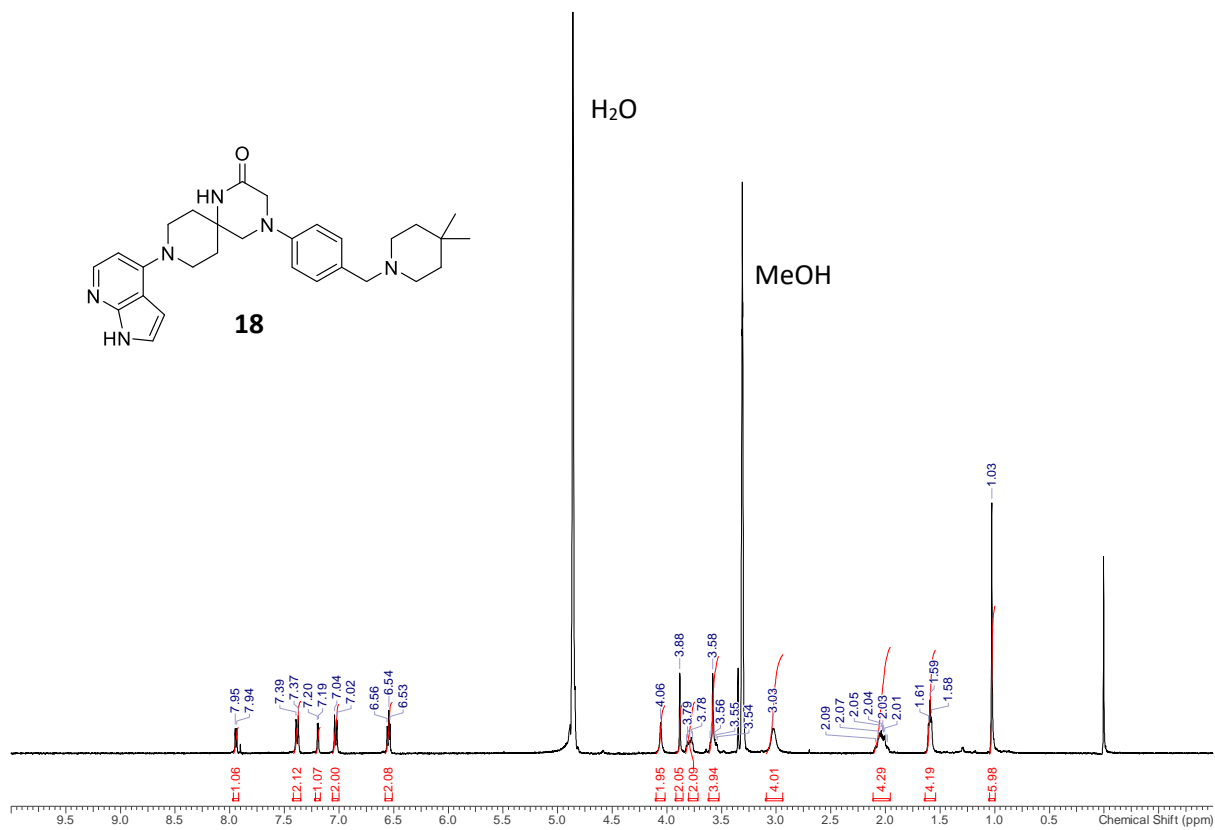


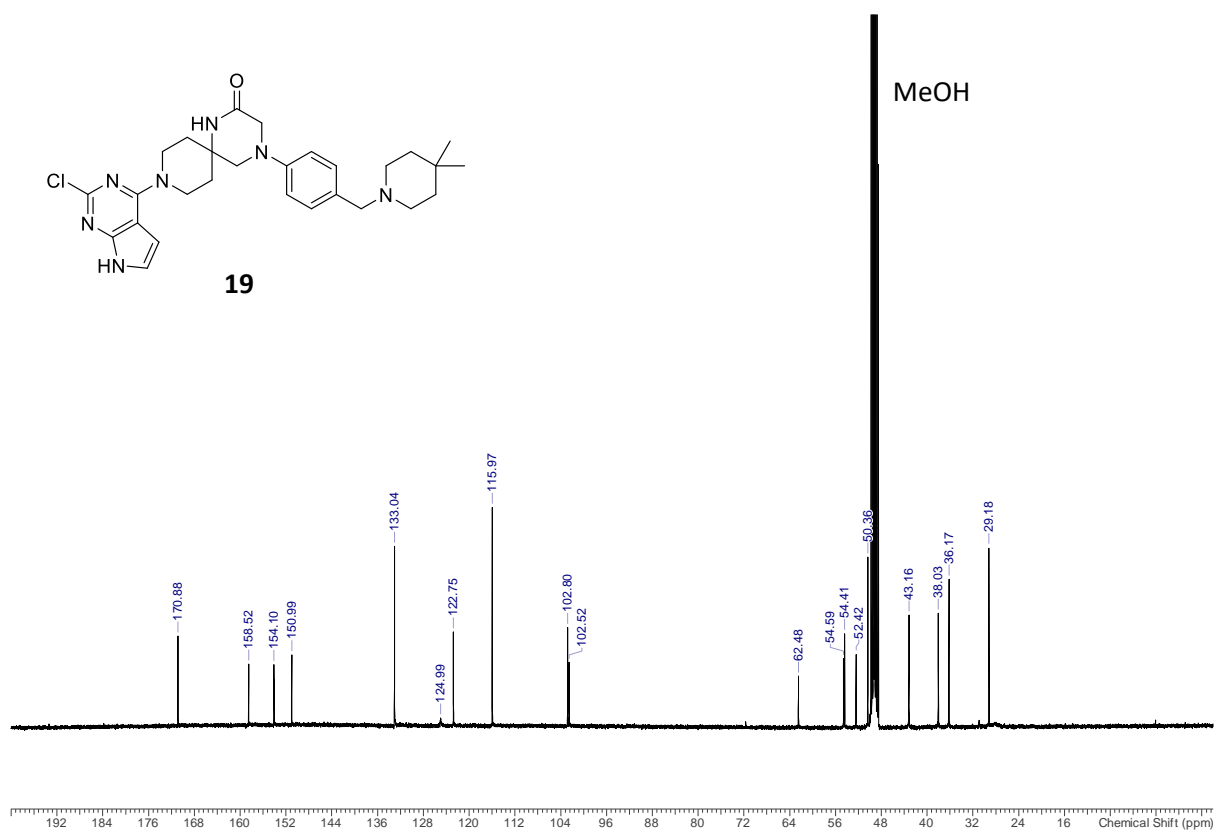
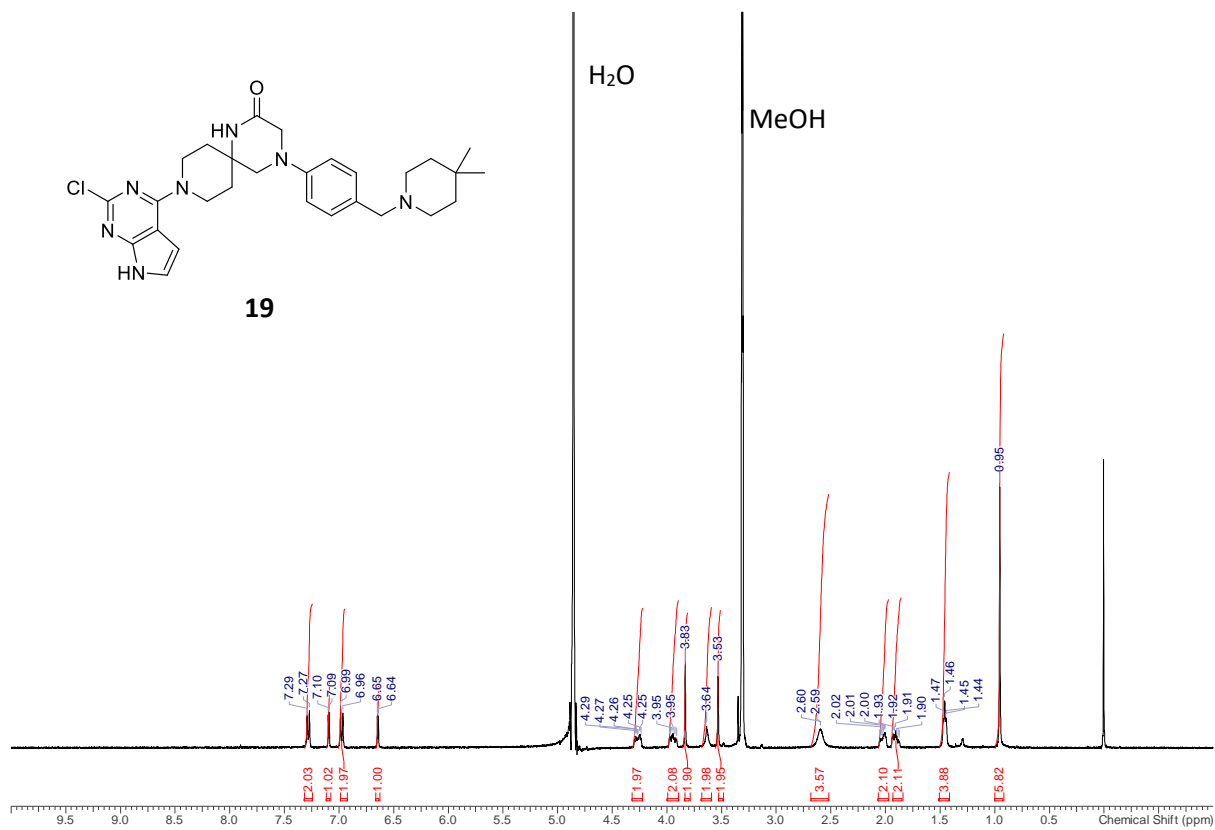


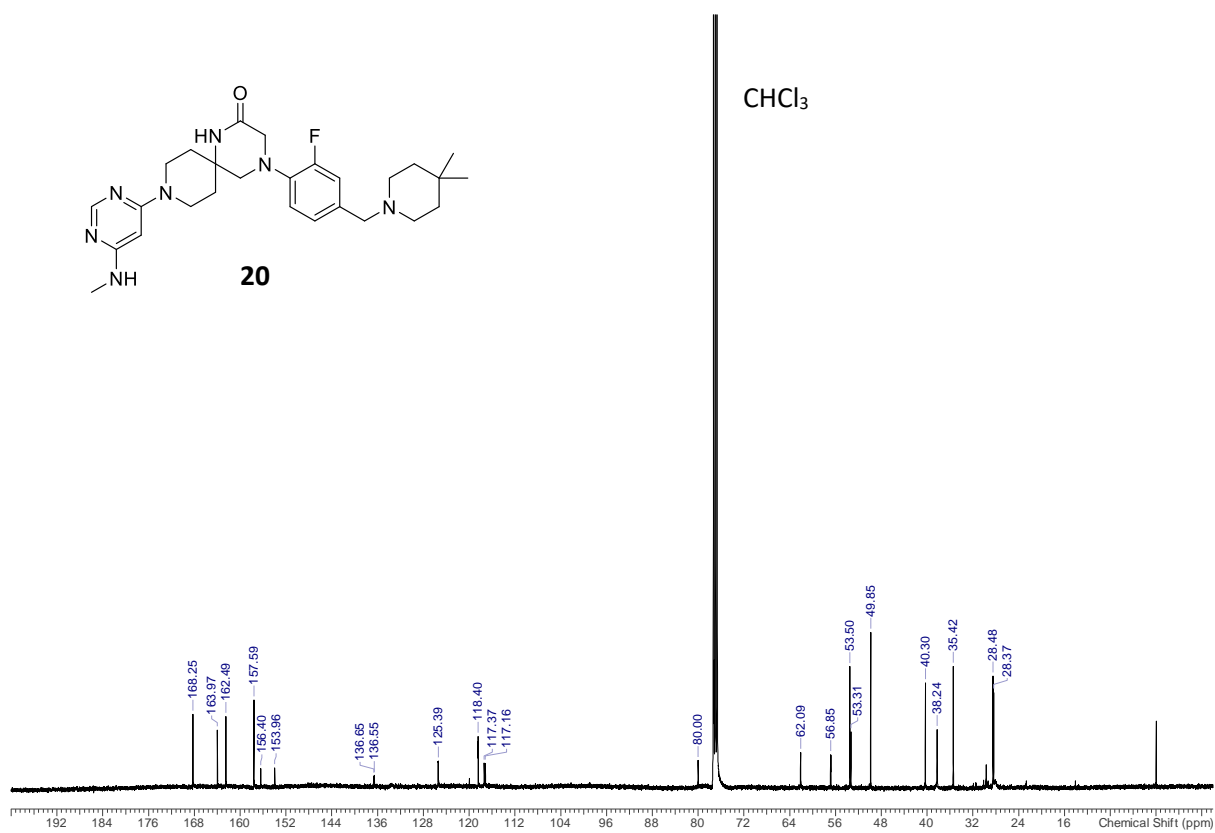
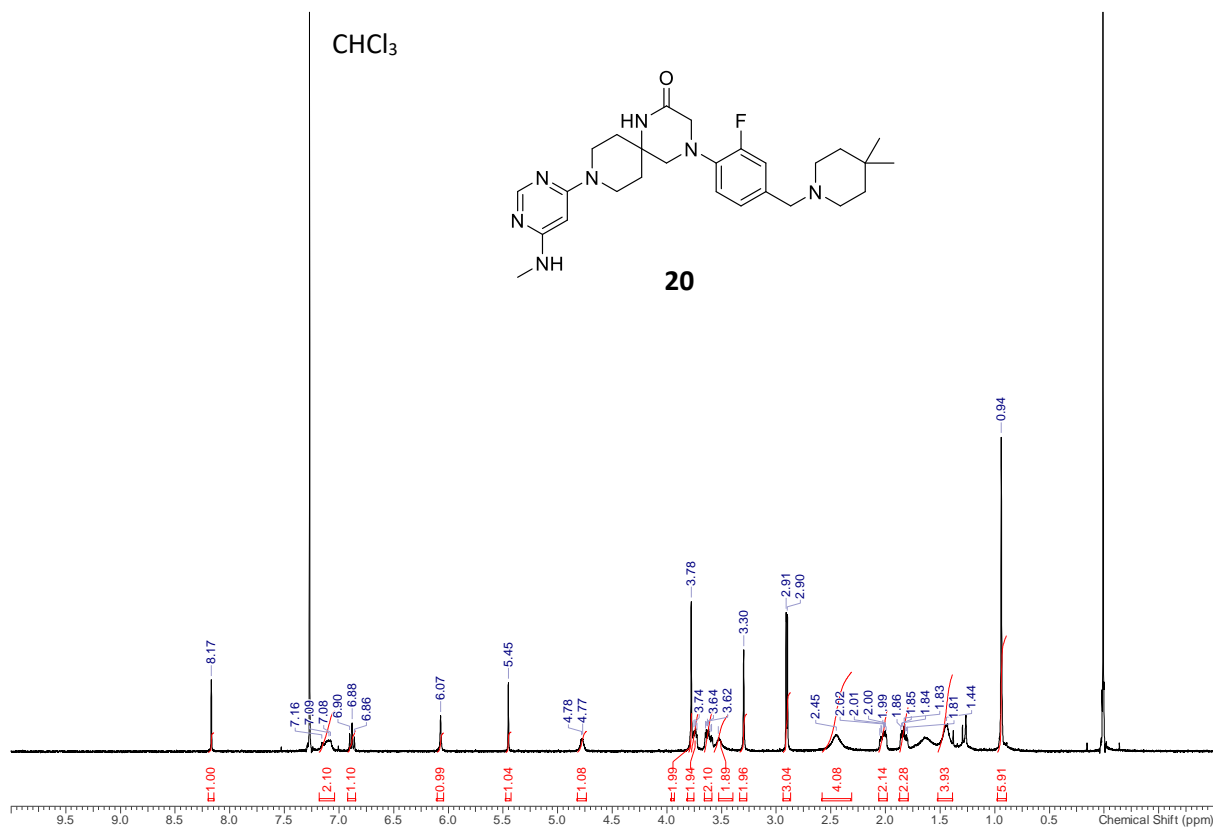


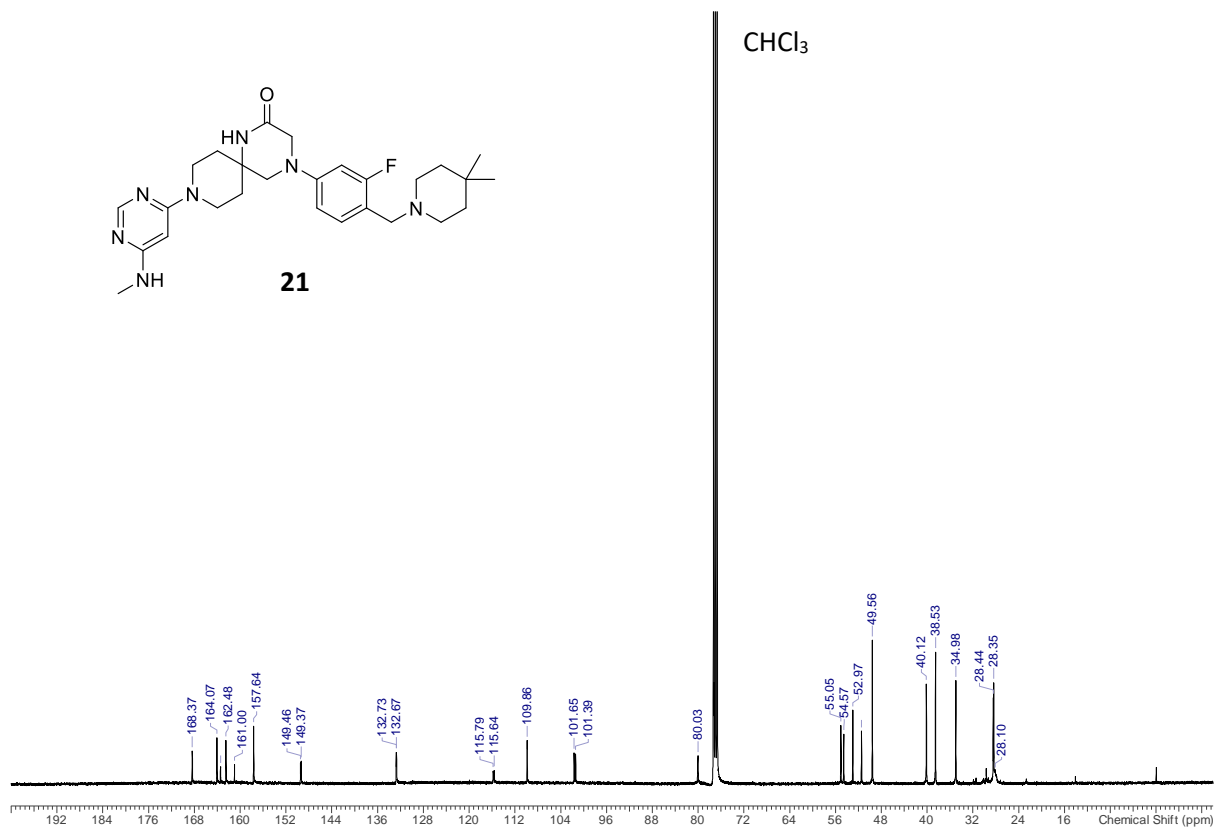
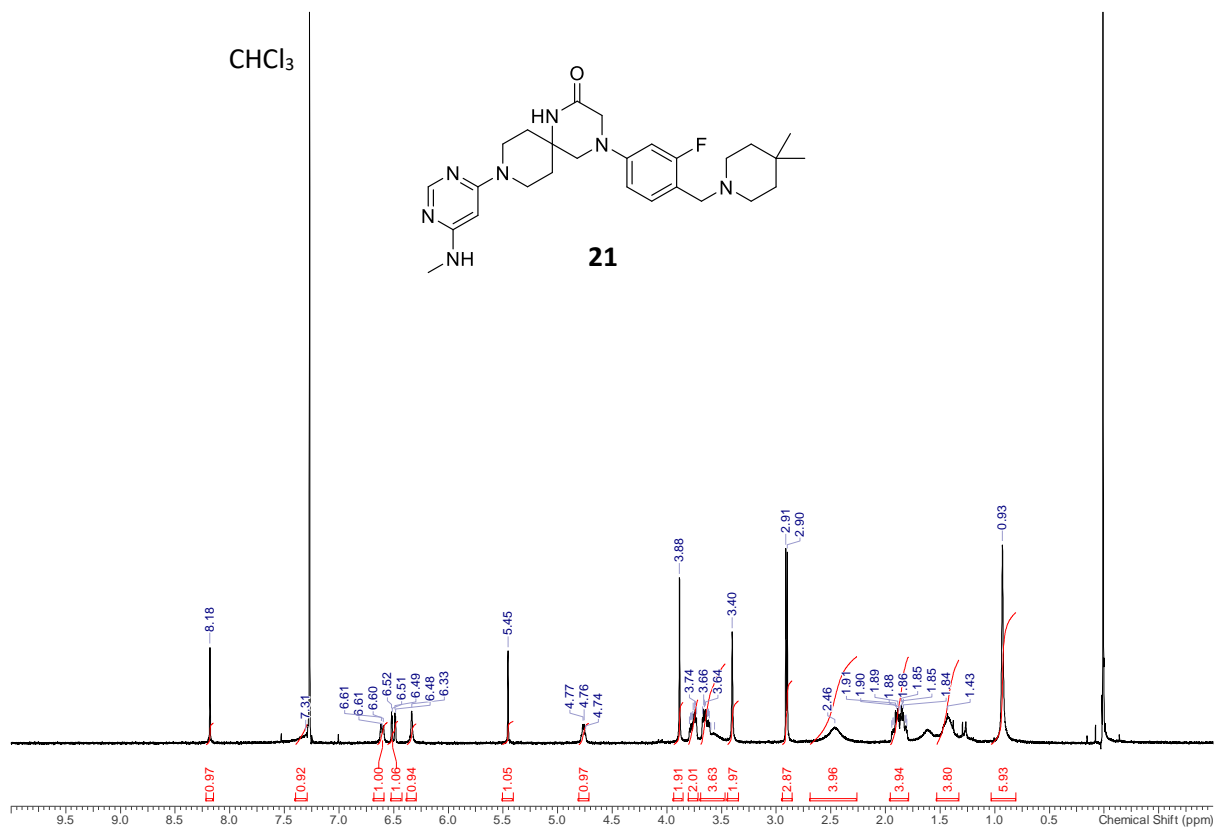


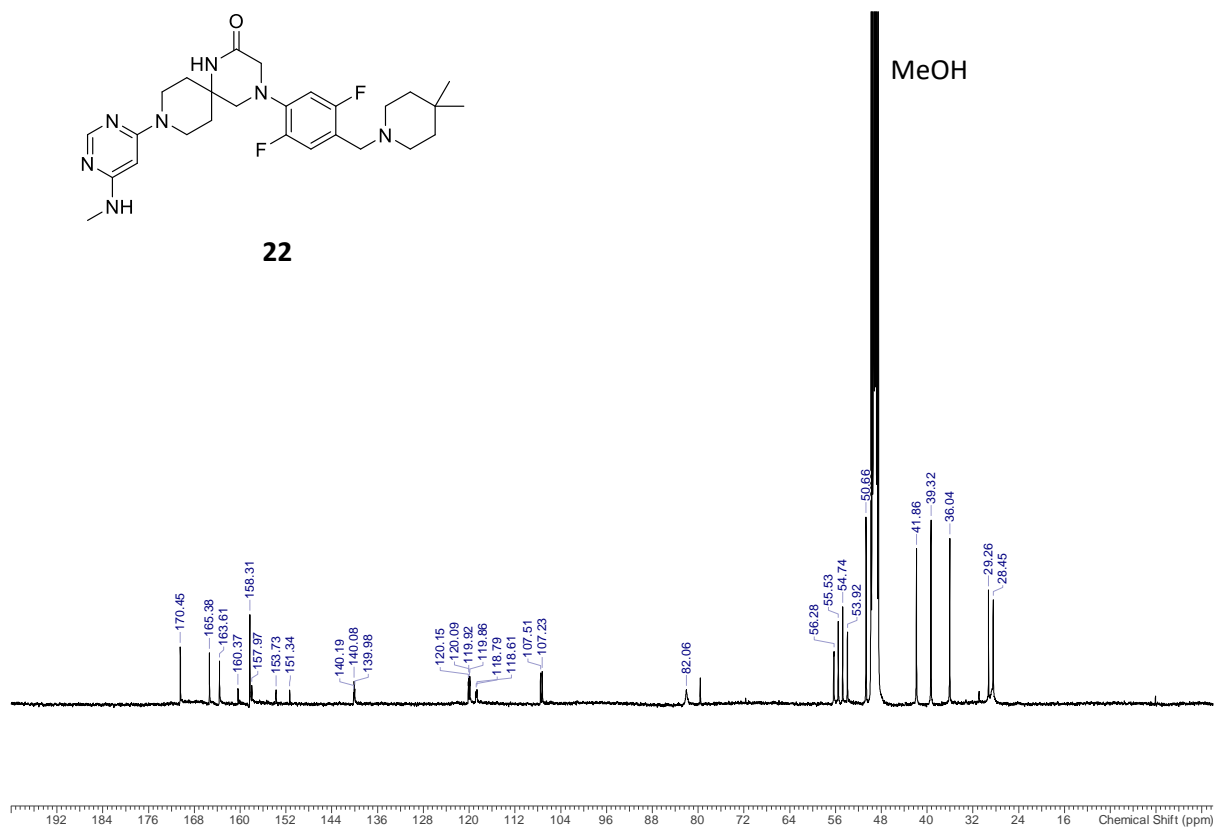
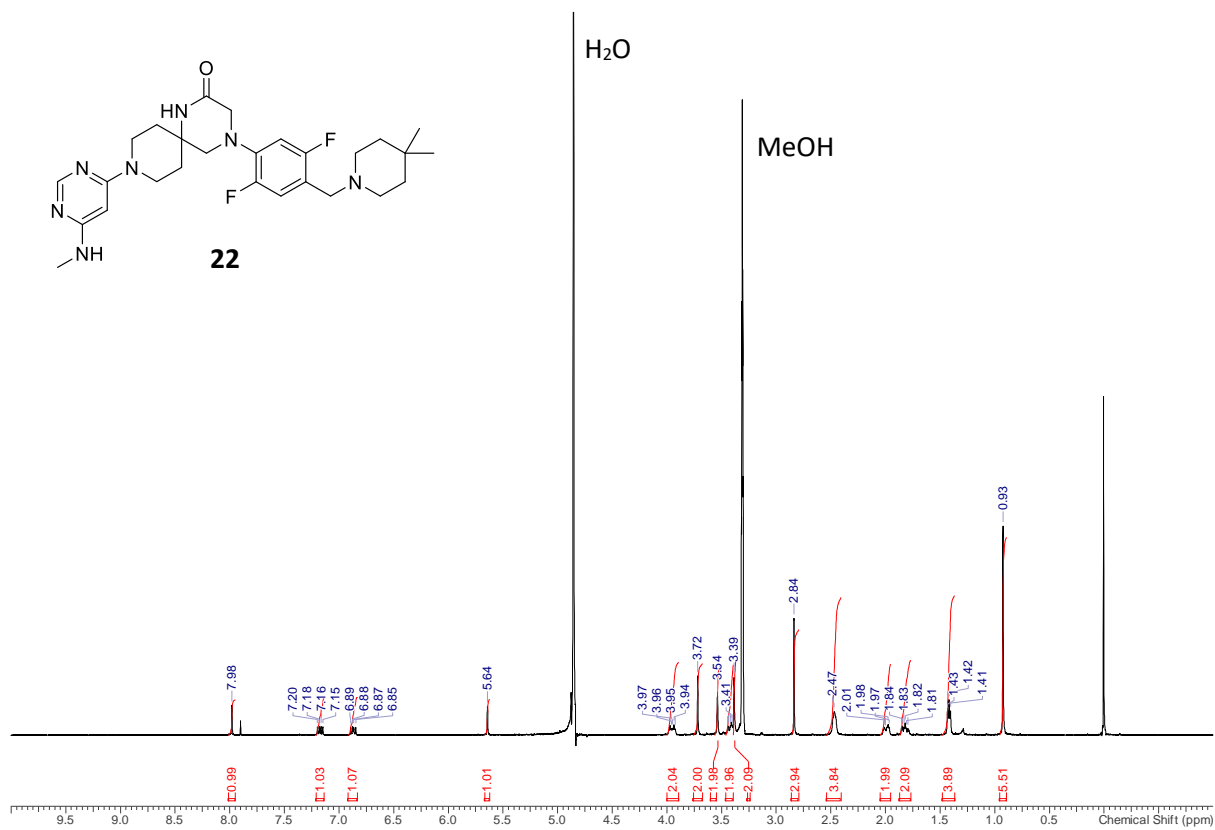












HPLC traces of final compounds

