

Supporting Information.

Non-rigid Diarylmethyl Analogs of Baloxavir as CAP-
Dependent Endonuclease Inhibitors of Influenza
Viruses

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Table S1. 5a and 5d protection of MDCK cells from death caused by influenza A and B virus ^a

Compound	EC ₅₀ ± SEM, nM ^b			
	A/Denmark/524/2009 (H1N1)pdm09	A/Fukui/20/2004 (H3N2)	B/Brisbane/60/2008 (Victoria Lineage)	B/Florida/4/2006 (Yamagata lineage)
5a	5.1 ± 3.9	3.6 ± 1.7	9.6 ± 1.0	5.1 ± 3.9
5d	12.5 ± 4.9	10.0 ± 2.8	10.5 ± 1.3	28.3 ± 6.7
3	1.1 ± 0.5	0.4 ± 0.2	5.0 ± 0.6	1.2 ± 0.5

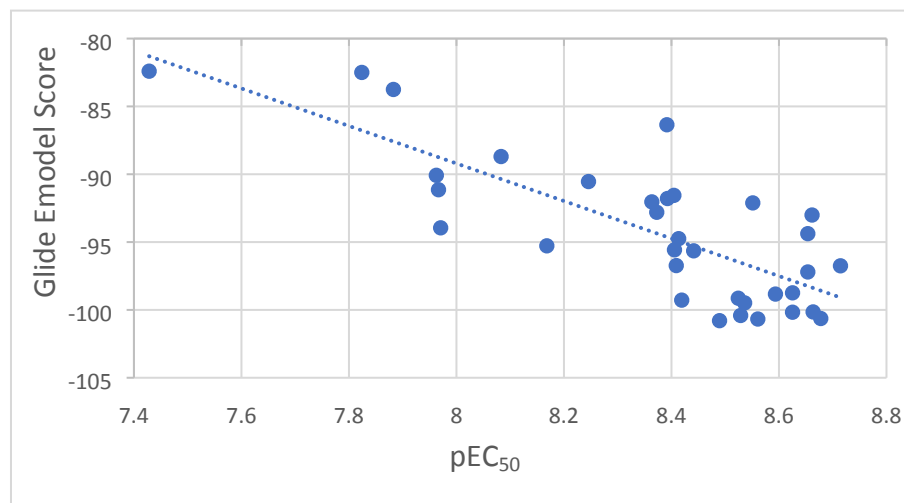
^a The cells were infected with the corresponding virus at a MOI = 0.001

^b The EC₅₀, 50% effective concentration, was assessed 72 or 96 hours post infection. 3 or 4 independent dose-response curves were averaged and mean ± SEM values presented.

Table S2. PK parameters of 3, 5a, 5b, 5d, and 5e in CD-1 female mice upon IV administration.

PK in mice, IV (2 mg/kg)						
		Compound				
Parameter	Units	5a	5b	5d	5e	3
kel	1/h	0.62	0.57	0.50	0.5	0.24
T1/2	h	1.11	1.21	1.39	1.3	2.83
Tmax	h	0.083	0.083	0.083	0.1	0.25
Cmax	ng/ml	654	511	600	977.7	198
C0	ng/ml	815	522	642	1073.8	156
AUClast	h*ng/ml	844	1073	927	2213.9	354
AUCinf	h*ng/ml	931	1085	937	2241.0	412
Vz	ml/kg	3446	3231	4279	1655.0	16747
Cl	ml/h/kg	2147	1844	2134	892.4	4101
MRTlast	h	2.02	1.24	1.59	1.9	2.12

Validation of Glide Emodel vs pEC₅₀ for Known Influenza Virus CEN inhibitors.



A virtual library containing BXA (**3**) and its potent structural analogues was used to validate the docking protocol. 2D structures of these compounds and their CEN inhibitory activity (EC₅₀) were manually mined from the patent application [1]. Collected structures were docked into the model of IFV cap-dependent endonuclease and were ranked by Glide Emodel score (Figure).

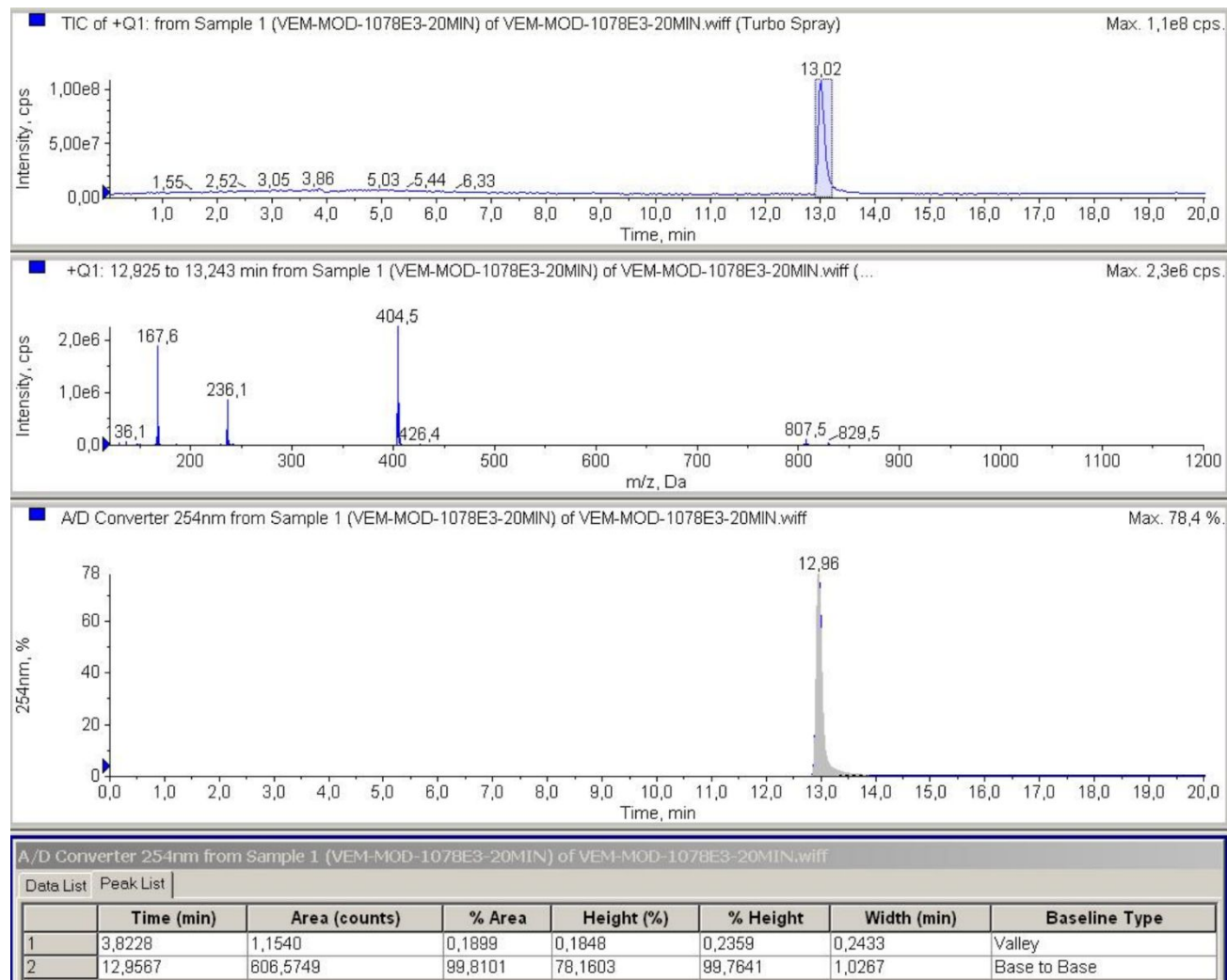
Maestro, release 2015-2, was used for the molecular modelling. The X-ray structure of CEN and BXA complex was downloaded from the Protein Data Bank (PDB code: 6FS6). The target structure was pre-processed using Protein Preparation Wizard tool. Pre-processing included addition of missing hydrogens, bonds assignment, protonation of BXA and generation of charge states for the cofactors (Epik, at pH of 7 ± 2), removal of water molecules, which form less than three hydrogen bonds, and H-bonds optimization (PROPKA, at pH 7). Next, a grid with BXA structure at the centre, was generated using Receptor Grid Generation and was applied for further docking simulations. 2D structures of the ligands were preliminary pre-processed with LigPrep tool. The stereo configurations were manually inspected, and the required isomers were selected. Docking simulations were performed exploiting Glide SP with the post-docking minimization. Compounds were ranked by the values of Glide Emodel scoring function and manually inspected.

Reference:

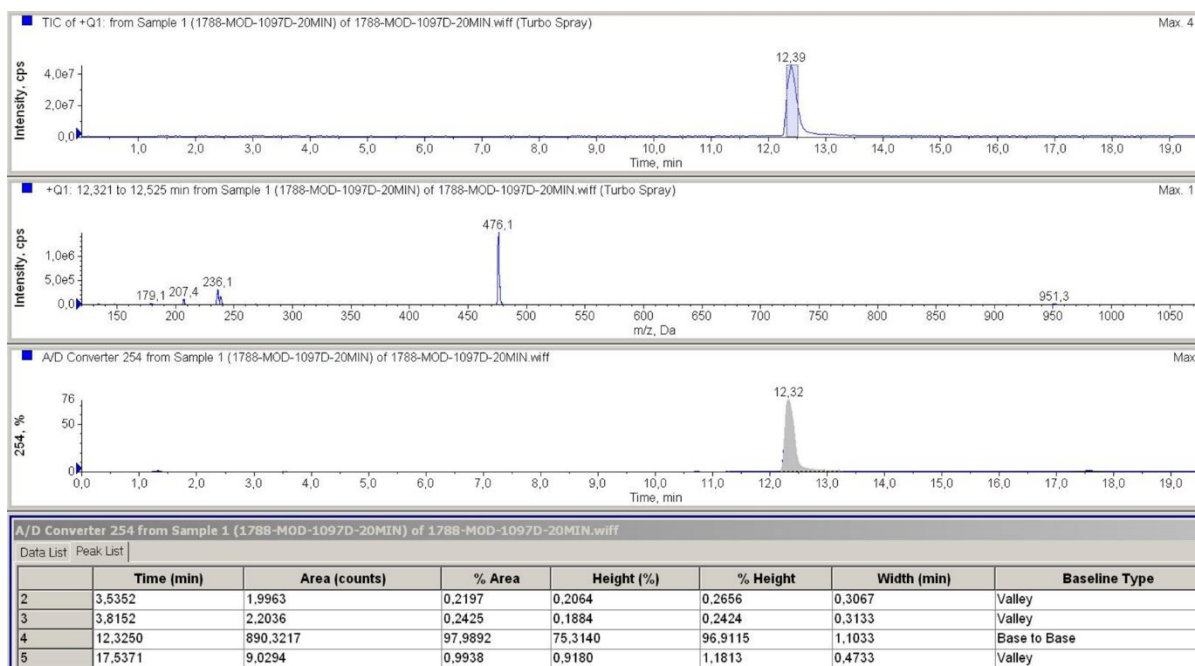
1. Makoto, K.; Tomita, K.; Akiyama, T.; Okano, A.; Miyagawa, M. Substituted polycyclic pyridone derivative and prodrug thereof. U.S. Patent Appl. US 2018/0118760, May 3, 2018.

HPLC-MS traces

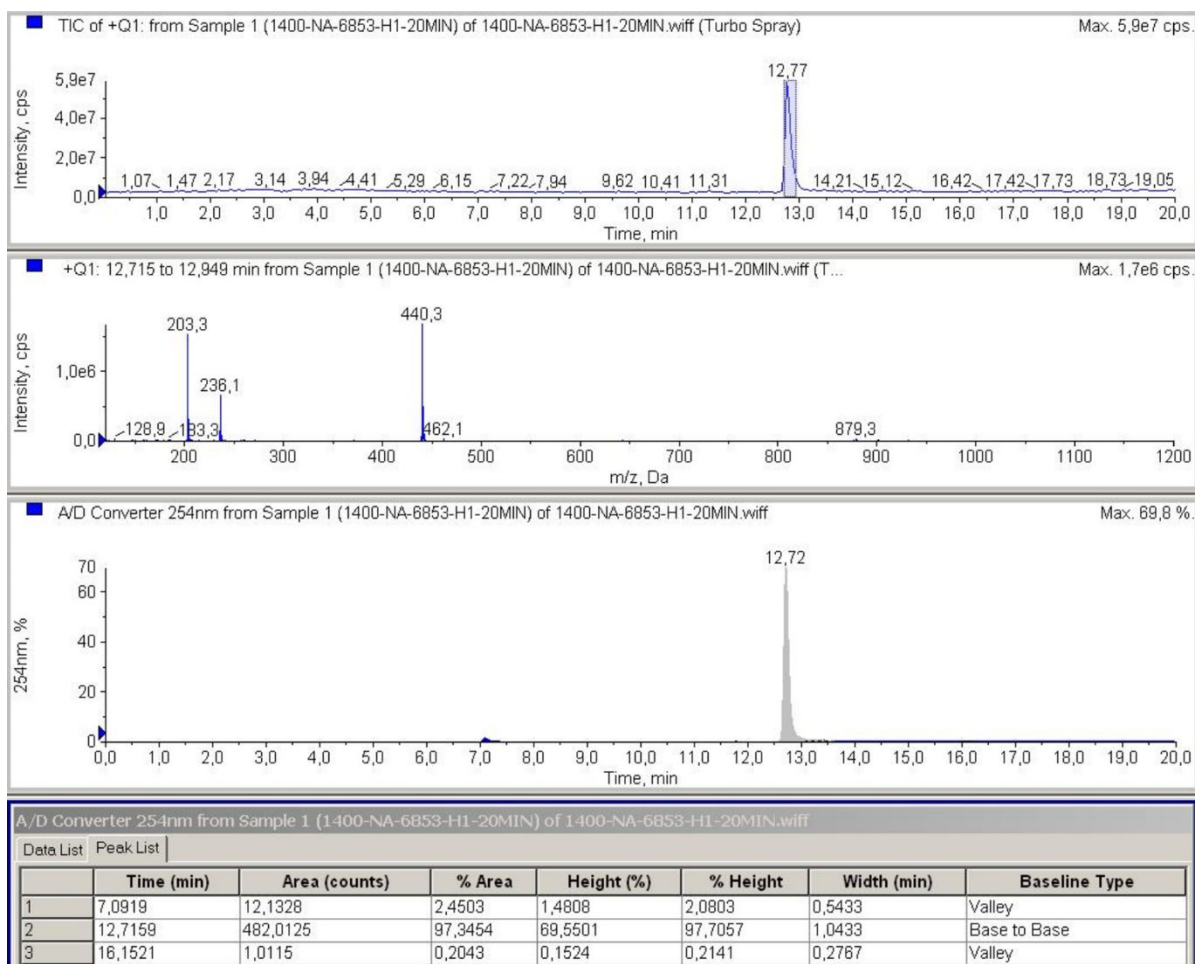
Compound 5a



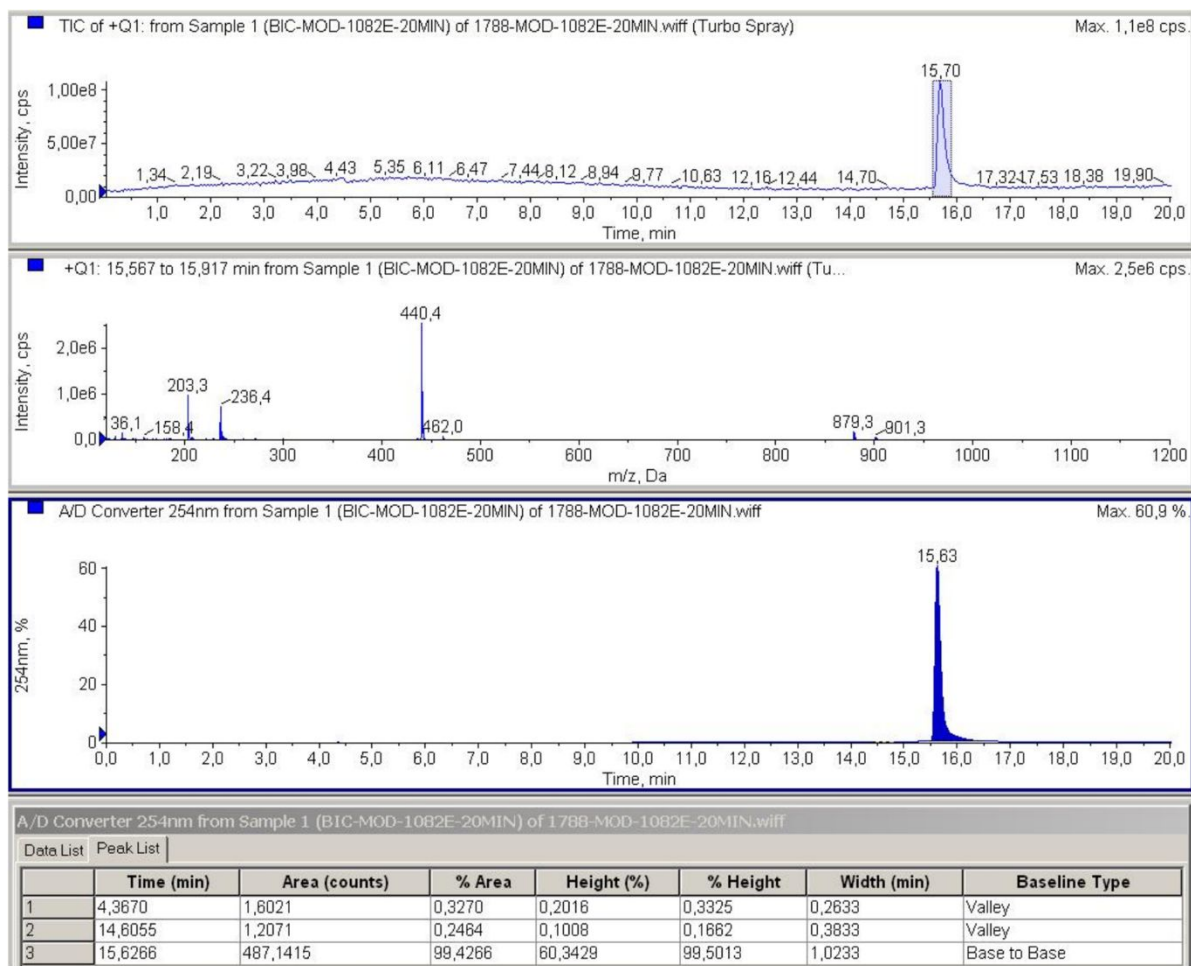
Compound 5b



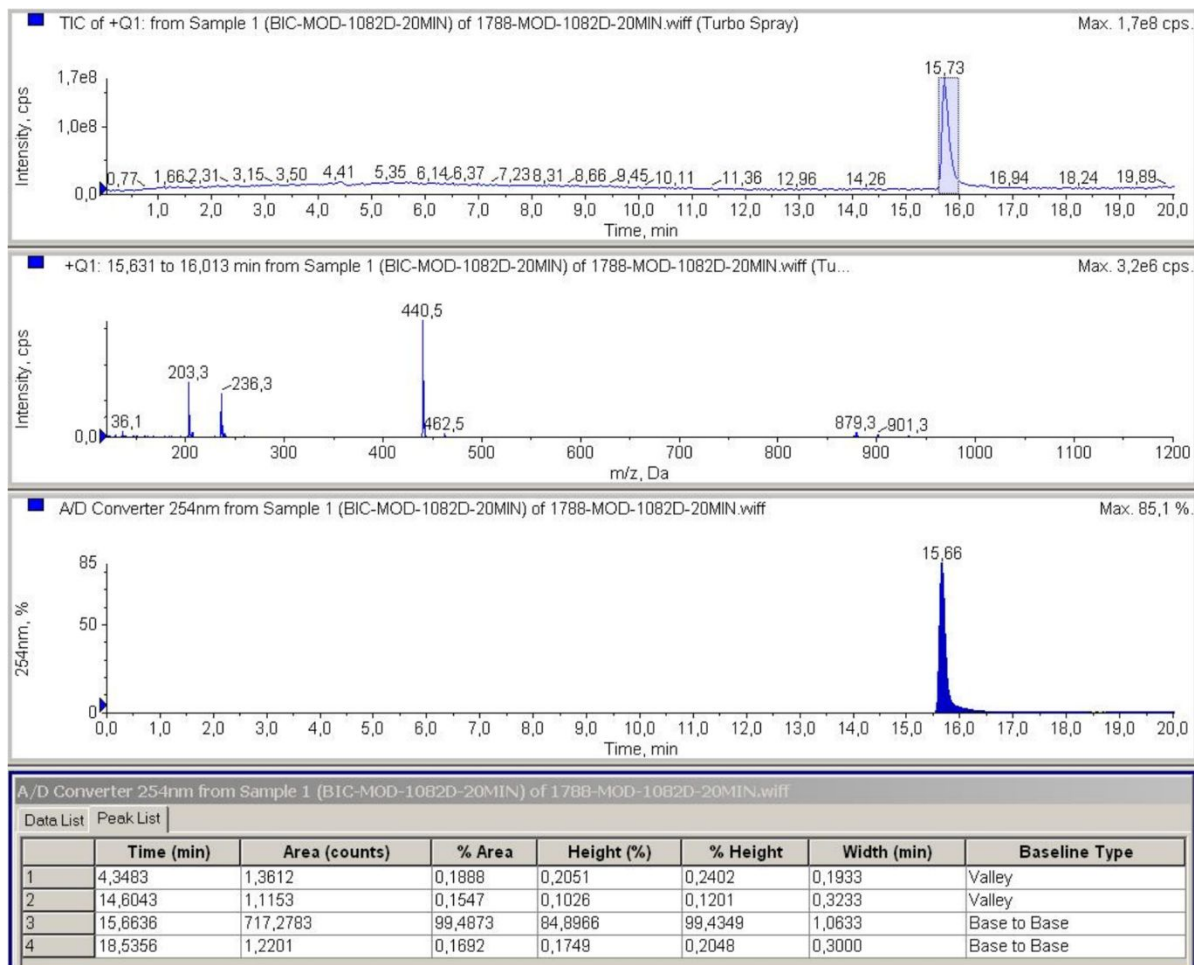
Compound 5c



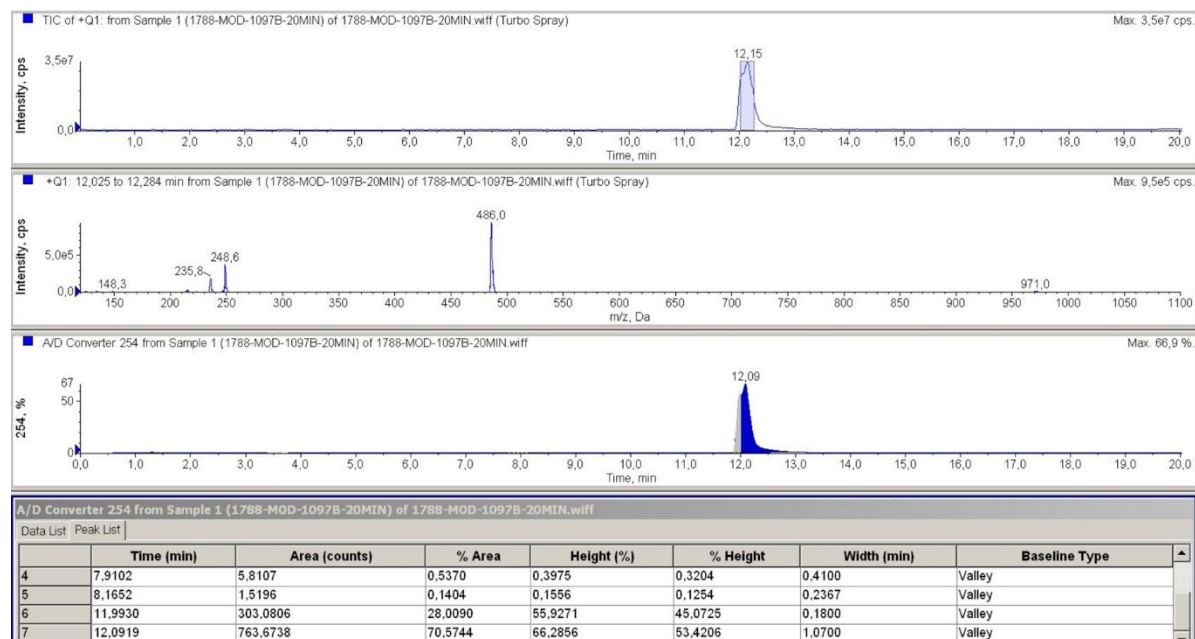
Compound 5d



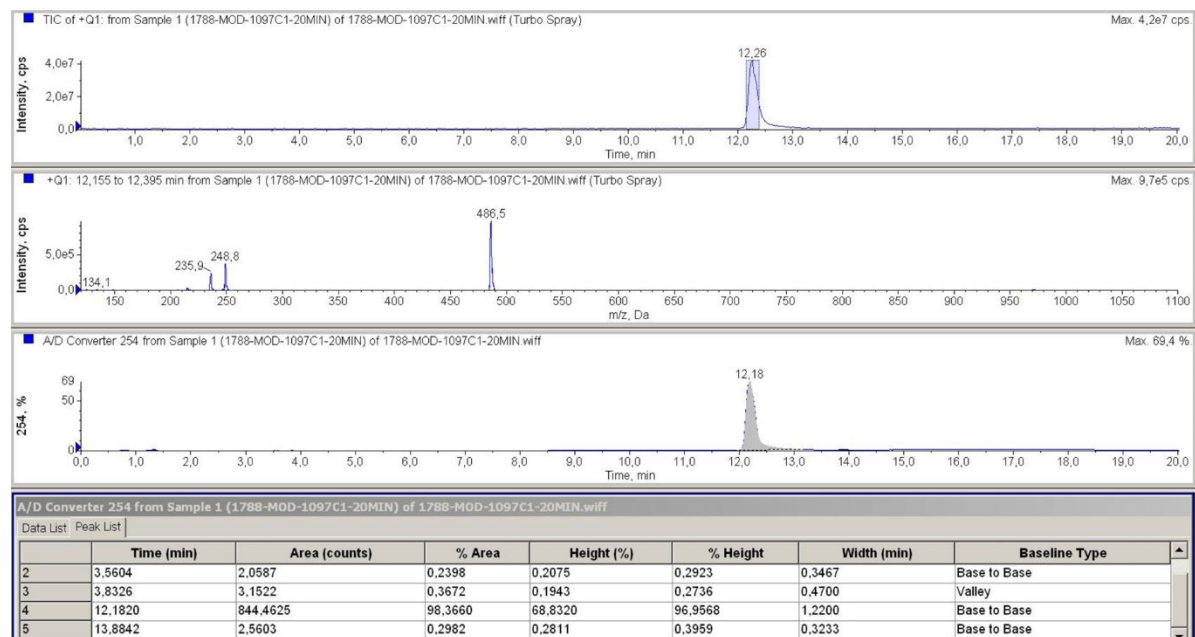
Compound 5e



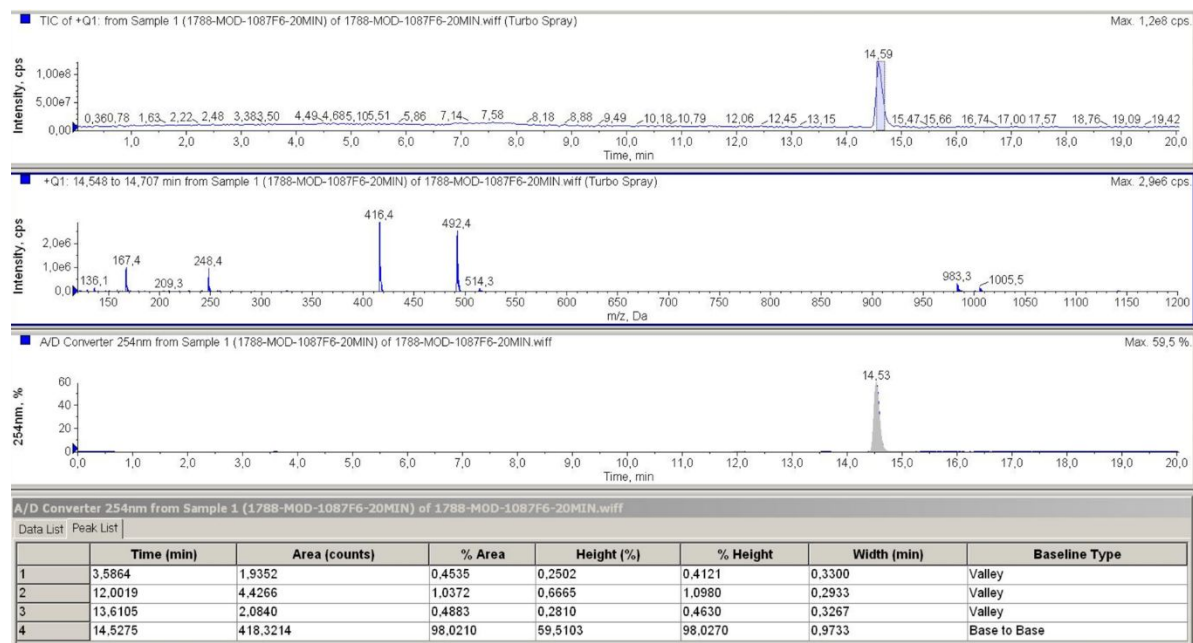
Compound 5f



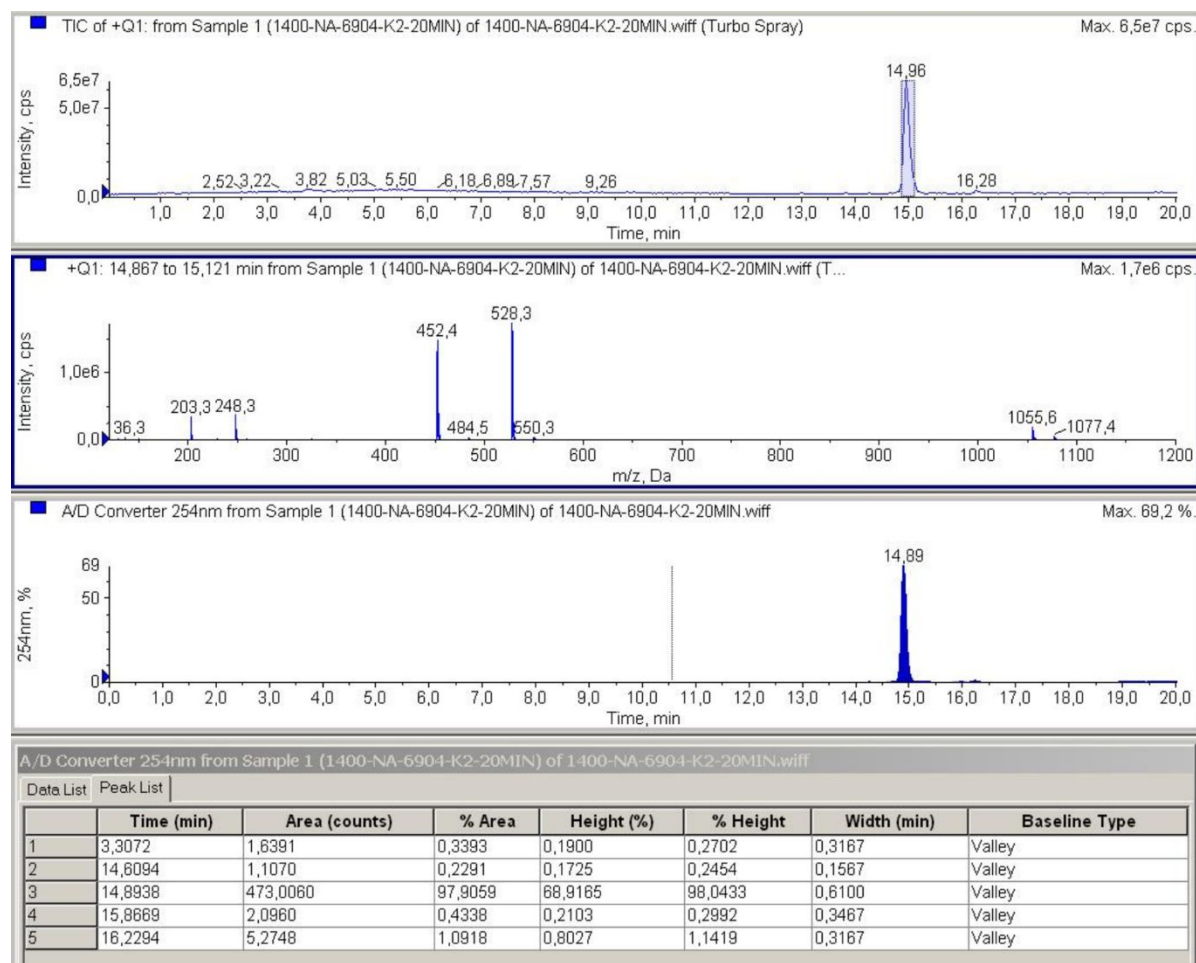
Compound 5g



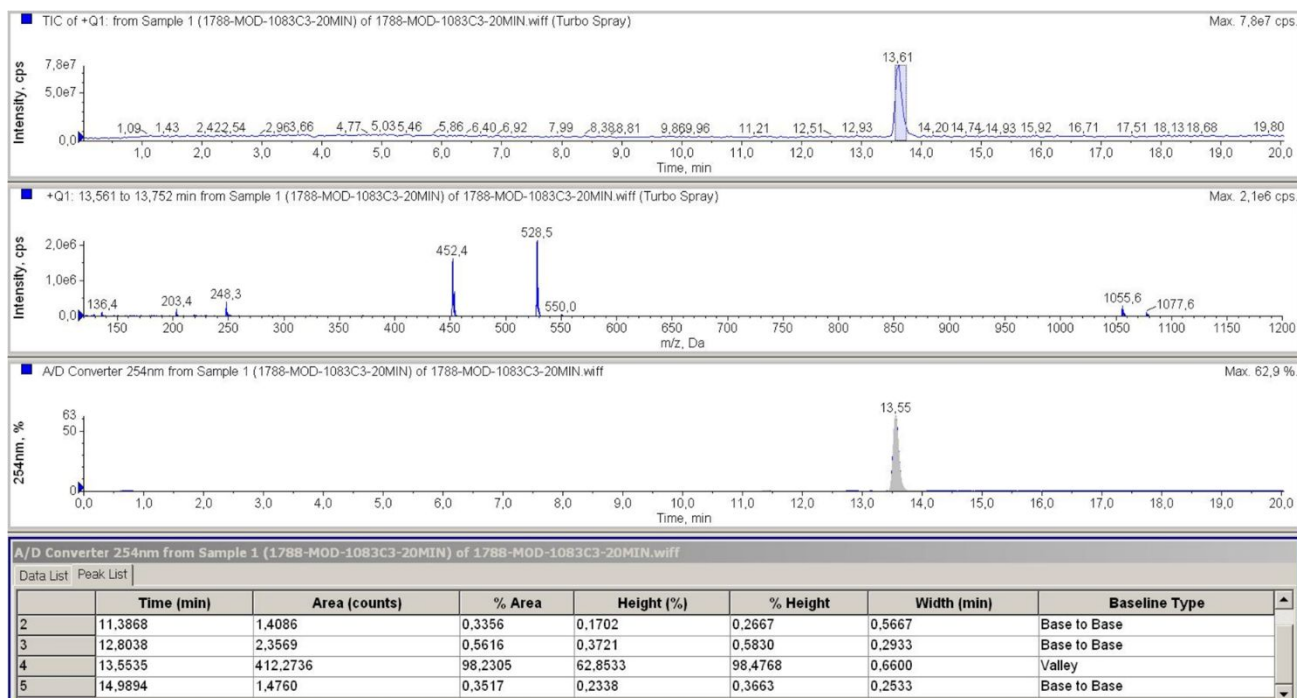
Compound 6a



Compound 6b



Compound 6d



Compound 6

