ACS Medicinal Chemistry Letters

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Correction

Correction to "Sweet and Blind Spots in E3 Ligase Ligand Space Revealed by a Thermophoresis-Based Assay"

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ACS Med. Chem. Lett. **2021**, *12*, 1, 74−81. DOI: 10.1021/acsmedchemlett.0c00440

Cite This: *ACS Med. Chem. Lett.* 2022, 13, 148−149

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Regrettably, we noticed a mistake in the calculation of the IC_{50} (and hence the K_i) values for avadomide, iberdomide, lenalidomide, and pomalidomide. These were indicated in Figure 5, which also had the chemical structures of lenalidomide and pomalidomide reversed. In the main text, it should read that iberdomide has the highest affinity, pomalidomide the second highest affinity, and dasabuvir the third highest affinity of the hTBD binders tested in this study. Apart from this change in the ranking, the conclusions of the study remain valid. A corrected version of Figure 5 is provided below; the correct values are as follows: avadomide: $IC_{50} = 19.4 \pm 1.8\ \mu M$, $K_i = 6.66 \pm 0.94\ \mu M$; iberdomide: $IC_{50} = 8.02 \pm 0.60\ \mu M$, $K_i = 0.765 \pm 0.31\ \mu M$; lenalidomide: $IC_{50} = 18.9 \pm 1.5\ \mu M$, $K_i = 6.40 \pm 0.8\ \mu M$; pomalidomide: $IC_{50} = 12.9 \pm 2.7\ \mu M$, $K_i = 3.28 \pm 1.4\ \mu M$. In addition, Figure S1 and Figure S3 are interchanged in the Supporting Information: Figure S1 shows "Influence of initial fluorescence on MST behavior", while Figure S3 shows "FRET assay data for avadomide, nitrofurantoin and UMP".

Published: December 28, 2021

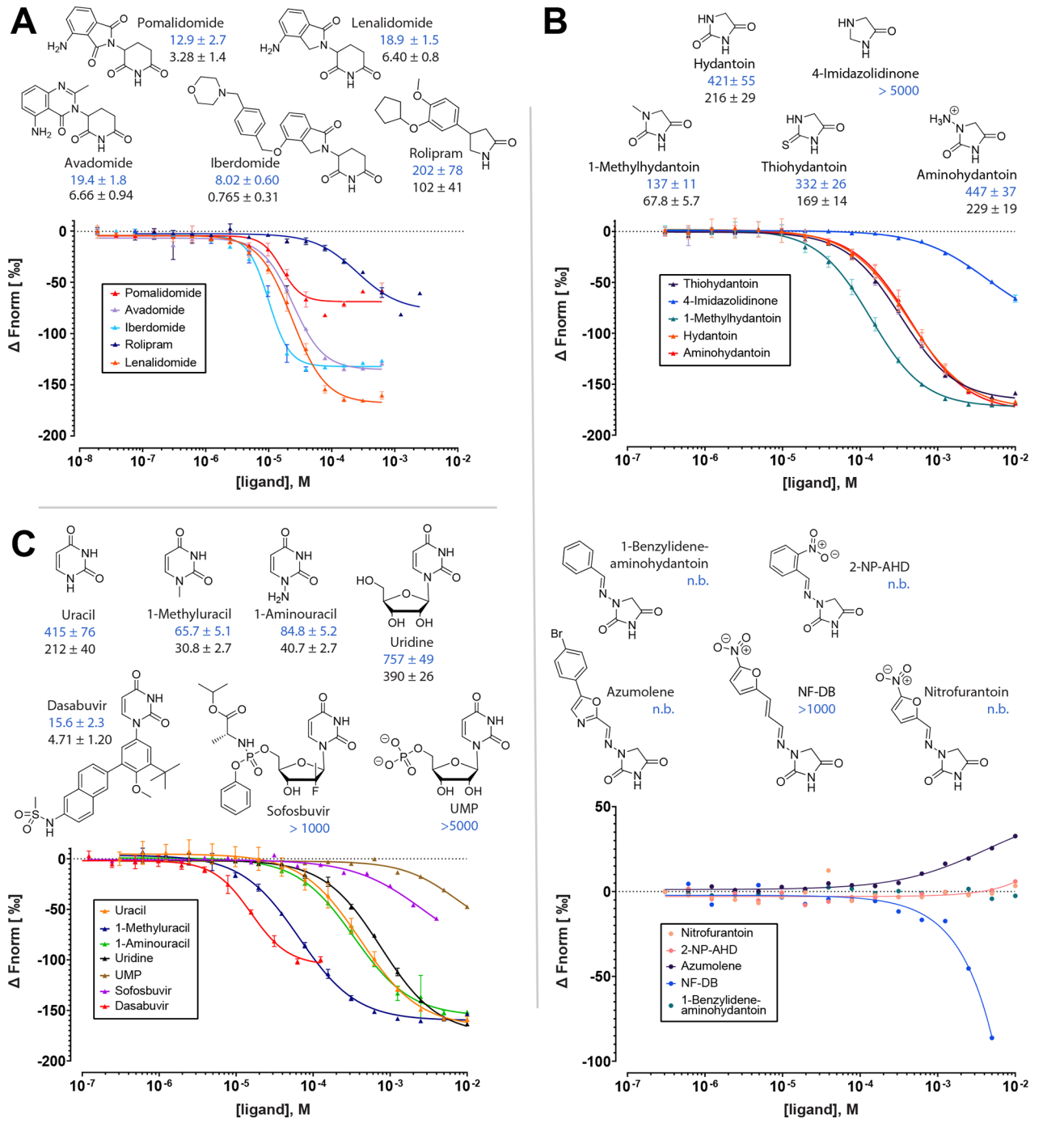

Figure 5. Chemical structures, dose−response curves and affinity values for (A) IMiDs and rolipram, (B) small hydantoins and hydantoins branched via hydrazo groups, and (C) uracils to hTBD. IC_{50} and derived K_i values are shown in blue and black, respectively, together with their standard deviations. All values are in μM. n.b., no binding. 2-NP-AHD, 1-(2-nitrobenzylideneamino)hydantoin; NF-DB, 1-(3-(5-nitrofuran-2-yl)allylidene)amino)hydantoin.

https://doi.org/10.1021/acsmedchemlett.1c00693
ACS Med. Chem. Lett. 2022, 13, 148−149