Electronic Supplementary Material (ESI) for Analyst.

Supplemental Data

Identification of a p53-based portable degron based on the MDM2-p53 binding region

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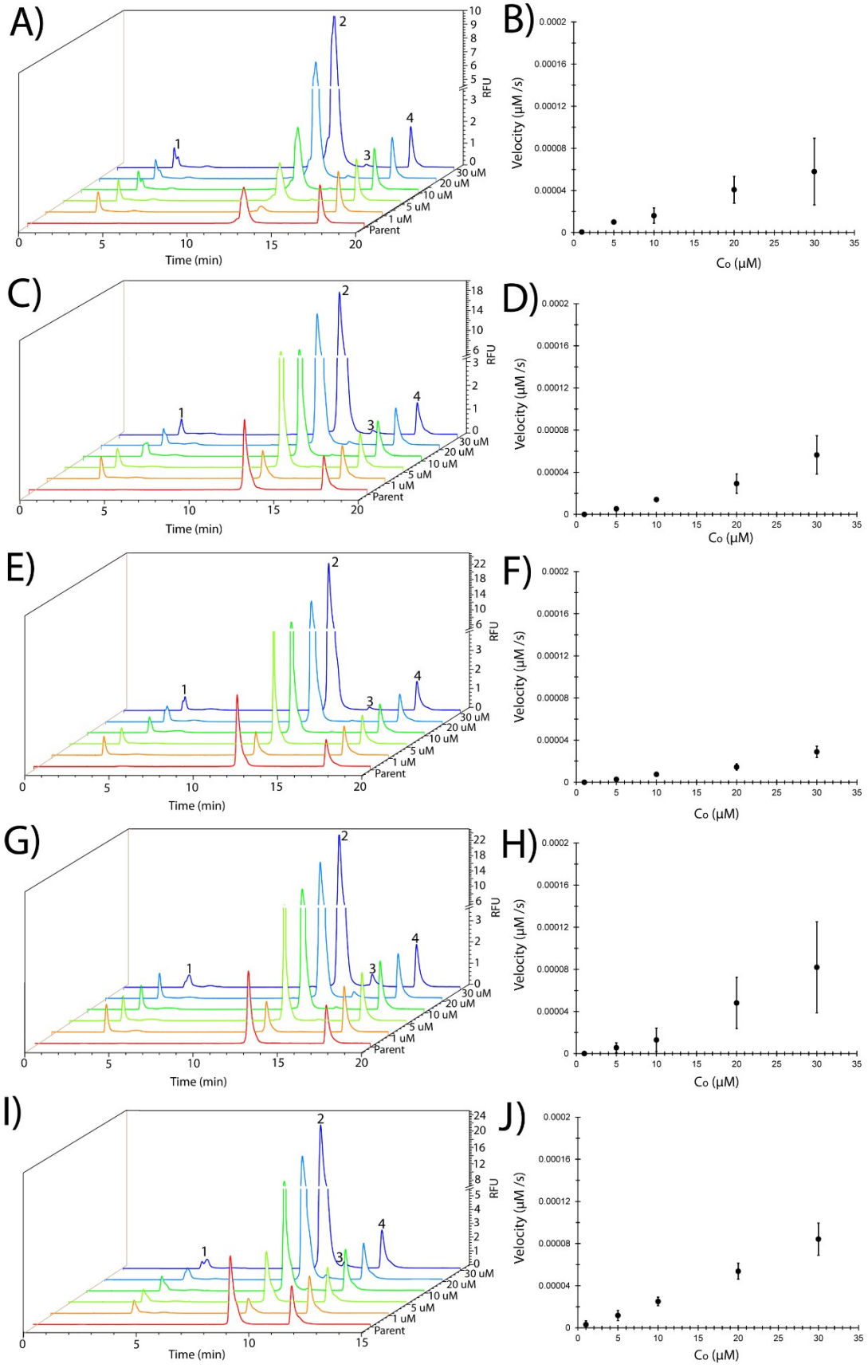
A)
B)
C)
D)
E)
F)
G)
H)
I)
J)
Time (min)
RFU
Velocity (µM /s)
Co (µM)
Parent
1 uM
5 uM
10 uM
20 uM
30 uM

Figure S1. Quantification of ubiquitination of the remaining members of the p53-based substrate library. Chromatograms depicting the separation of parent peptide from Ub~peptide for peptides **3** (A), **4** (C), **5** (E), **6** (G), **8** (I) using initial peptide concentrations of 1 μM (orange), 5 μM (yellow), 10 μM (green), 20 μM (blue), and 30 μM (indigo) as marked on the right side of each trace. Separation of parent peptide from the internal standard (FAM, carboxyfluorescein) was also performed (red) and is labeled "Parent". Peaks are labeled as parent peptide (peak 2), Ub~peptide (peak 3), internal standard (FAM, peak 4), and the unidentified, non-reactive contaminant (peak 1). The initial concentration of peptides **3** (B), **4** (D), **5** (F), **6** (H), and **8** (J) against the velocity of peptide ubiquitination (μM/s). The data presented here is the average of three independent experiments with the standard deviation of the data points depicted by the error bars.